Antibodies against medically relevant arthropod-borne viruses in the ubiquitous African rodent *Mastomys natalensis*

Short title: Antibodies against arboviruses in *Mastomys natalensis* from Tanzania

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Abstract

Over the past decades, the number of arthropod-borne virus (arbovirus) outbreaks has increased worldwide. Knowledge regarding the sylvatic cycle (i.e., non-human hosts/environment) of arboviruses is limited, particularly in Africa, and the main hosts for virus maintenance are unknown. Previous studies have shown the presence of antibodies against certain arboviruses (i.e., chikungunya-, dengue- and zika virus) in African non-human primates and bats. We hypothesize that small mammals, specifically rodents, may function as amplifying hosts in anthropogenic environments. The detection of RNA of most arboviruses is complicated by the virus's short viremic period within their hosts. An alternative to determine arbovirus hosts is by detecting antibodies, which can persist several months. We developed a high-throughput multiplex immunoassay to detect antibodies against 15 medically relevant arboviruses. We used this assay to assess almost 1,300 blood samples of the multimammate mouse, *Mastomys natalensis* from Tanzania. In 24% of the samples, we detected antibodies against at least one of the tested arboviruses, with high seroprevalences of antibodies reacting against dengue virus serotype one (7.6%) and two (8.4%) and chikungunya virus (6%). Seroprevalence was higher in females and increased with age, which could be explained by inherent immunity and behavioral differences between sexes and the increased chance of exposure to an arbovirus with age. We evaluated whether antibodies against multiple arboviruses co-occur more often than randomly and found that this may be true for some members of the *Flaviviridae* and *Togaviridae*. In conclusion, the development of an assay against a wide diversity of medically relevant arboviruses enabled the analysis of a large sample collection of one of the most abundant African small mammals. Our findings suggest a role in the transmission of multiple arboviruses by this ubiquitous rodent and

provide a solid foundation for future molecular screening to elucidate the role in the arbovirus transmission cycle.

Author summary

One of the main causes of zoonotic related human morbidity and mortality is the transmission of arthropod-borne viruses such as dengue virus, Yellow Fever virus, and chikungunya virus. These viruses cannot only infect humans but also livestock, pets, and wildlife, though our understanding of their non-human hosts remains limited. Rodents are thought to be an interesting host for these viruses because they can be abundant, often live near humans and some are already known to be viral hosts. However, research has focused on non-human primates, neglecting other potential hosts. To address this gap, we have developed a high-throughput antibody test to screen rodent blood against 15 different arboviruses. Our findings reveal that a proportion of *Mastomys natalensis*, a common African rodent species, carry antibodies that (cross-)react against these viruses. We hypothesize that immunologically naïve juveniles may drive transmission, particularly during population outbreaks. These outbreaks coincide with environmental conditions that are favorable for mosquitoes, the vectors of these viruses. Thus, increasing the risk of spillover to humans, livestock, and wildlife. Understanding the role of rodents in arbovirus transmission dynamics is crucial for mitigating zoonotic disease risks.

67 # Introduction

68 The African continent harbors a diverse array of infectious diseases with profound
69 impacts on public health, economic development, and general well-being [1,2]. Diseases
70 caused by arthropod-borne viruses, collectively known as arboviruses, are a growing threat
71 for Africa and the rest of the world especially in relation to climate and environmental
72 changes [3,4]. Arboviruses are a polyphyletic clade that includes several viral families, of
73 which the most important are *Flaviviridae, Togaviridae, Bunyaviridae,* and *Reoviridae* [5].
74 Some well-known arboviruses, notorious for their devastating effects on human health, are
75 dengue virus, Yellow Fever virus, Zika virus, and chikungunya virus. Mosquitoes, ticks,
76 sandflies, and midges are the primary vectors responsible for arbovirus transmission as they
77 engage in hematophagy. These vectors do not only affect humans and livestock, but also a
78 wide range of wildlife hosts [6–8]. Indeed, while for some arboviruses morbidity and mortality
79 can be high in humans, similar impacts have been detected in other animals by arboviruses
80 such as Rift Valley Fever virus in goats and sheep, West Nile virus in birds and horses and
81 Japanese Encephalitis virus in birds and pigs [4,5,9–11]. The (re-)emergence of arboviruses
82 appears, at least partially, to be caused by the increased urbanization and global connectivity,
83 natural genetic evolution of viruses, and adaptations of the vectors to changing climate and
84 environments [11,12]. Emerging arboviruses pose a threat for humans, livestock, as well as
85 wildlife, therefore it needs to be approached from a One health perspective (i.e., including
86 human, animal, and environment health) [13,14]. Nevertheless, our knowledge about the
87 extent to which wild animals can serve as sylvatic hosts for human-infecting arboviruses and
88 the natural diversity of arboviruses remains insufficient. This significantly limits our

89 understanding of arbovirus transmission dynamics, which is required to develop effective
90 control measurements.

91 For decades, efforts have been made to identify natural reservoirs of arboviruses to
92 monitor, prevent, and control sources of infection that pose a threat to human health [15–
93 17]. Several studies have proposed non-human primates as significant potential reservoirs for
94 arboviruses, as they have found arbovirus antibodies and viral RNA in this animal group [18–
95 20]. However, other animal groups such as small mammals have often been neglected as
96 arbovirus hosts [21]. Sporadic reports of arboviruses in small mammal species suggest that a
97 more comprehensive investigation of their potential role as a host is needed [22–24].

98 Rodents have a number of characteristics that could make them potentially important
99 hosts for several pathogens, including arboviruses [23]. Particularly the high species diversity,
100 the fact that many species can reach high population abundances and turnover rates. The risk
101 of pathogen spillover to humans increases with the role of some rodents as a pest species,
102 due to their proximity to humans [25,26]. A notable example of such a pest species is the
103 ubiquitous rodent *Mastomys natalensis*, commonly known as the multimammate mouse. This
104 species inhabits many regions of sub-Saharan Africa, with a preference for crop fields, fallow
105 land, and typically occurring within or at the fringes of urban settlements [27,28]. In east
106 Africa, and especially in Tanzania, the reproductive cycle of *M. natalensis* is strongly
107 correlated with seasonal rainfall which leads to strong seasonal fluctuations in density (20 -
108 500 individuals/hectare), and occasionally even severe population outbreaks (>1000
109 individuals/hectare) [29–32]. This has large ecological and societal impacts due to crop
110 damage and influences seasonal transmission dynamics of different pathogens [33–35]. The
111 multimammate mouse is a known host for several zoonotic pathogens such as *Lassa*
112 *mammarenavirus*, *Yersinia pestis*, *Leptospira interrogans*, *Leishmania major* as well as

113 different ecto- and endoparasites [31,36–52]. No studies have investigated or reported on
114 arboviruses in *M. natalensis*, except Diagne et al. (2019) who have detected Usutu virus RNA
115 in *M. natalensis*. However, other studies have reported on sporadic arbovirus detections in
116 other rodent species in sub-Saharan Africa [22,24,53,54]. These findings, along with the
117 ecology of *M. natalensis* (i.e., high abundance during population outbreaks, proximity to
118 humans, and its status as a proven pathogen host) may suggest that this species plays a role
119 in the natural transmission cycle of arboviruses. Consequently, *M. natalensis* could thus pose
120 a risk to humans in east Africa, particularly in Tanzania as an amplifying host.

121 The human population in Tanzania has experienced several outbreaks of chikungunya
122 virus, Rift Valley fever virus, West Nile virus, and dengue virus in the past decades [55–59].
123 Due to the symptomatic similarities between arbovirus and malaria infections, which has a
124 prevalence of around 20% in Tanzania, it is probable that arbovirus cases are underreported
125 [60,61]. While these studies confirm that the local human population is indeed exposed to
126 arboviruses, the specific dynamics of arbovirus transmission in this region remains unclear.

127 The goal of this study was to investigate the potential of wild *M. natalensis* to serve as
128 a host for arboviruses in their natural environment. To achieve this, we first developed a
129 multiplex immune assay to detect immunoglobulin G (IgG) antibodies against 15 different
130 arboviruses causing disease in humans and subsequently conducted a comprehensive
131 screening of almost 1,300 blood samples obtained from *M. natalensis* from Morogoro,
132 Tanzania.

Materials and Methods

Sample origin

The samples used in this study were collected during previous published and unpublished studies conducted by the University of Antwerp (UAntwerp) and Pest Management Center of the Sokoine University of Agriculture on *M. natalensis* in Morogoro, Tanzania, between 2010 and 2019 [31,62,63] (Fig 1). In this study, the samples were divided in two screening sessions. The first session consisted of approximately 500 dried blood spot (DBS) samples, from wild captured mice that were used in infection and behavioral experiments in six different years (i.e., 2010, 2011, 2015, 2017, 2018, and 2019) with an average of 80 samples per year. The second session consisted of 800 DBS samples from mice involved in capture mark recapture experiments in 2017 and 2019. All samples were randomly selected from the studies regardless of individual characteristics or trapping period.

During these studies, *M. natalensis* were live caught using Sherman traps (H.B. Sherman Traps, Tallahassee, USA) in a heterogeneous landscape (e.g., woodlands, maize fields, and fallow land) on the premises of the Sokoine University of Agriculture in Morogoro, Tanzania. Blood was collected from the retro-orbital plexus using a 50µL hematocrit capillary tube and preserved on filter paper (Serobuvard; LDA 22; Zoopole, France). The filter paper was dried for 12 hours at room temperature and archived at -20°C in envelopes with desiccant. Additional data related to characteristics such as sex, reproductive status, weight, and body measurements were recorded. More detailed Information pertaining to the trapping procedures and sampling methodology can be found in the primary research documents associated with these studies [31,62–64].

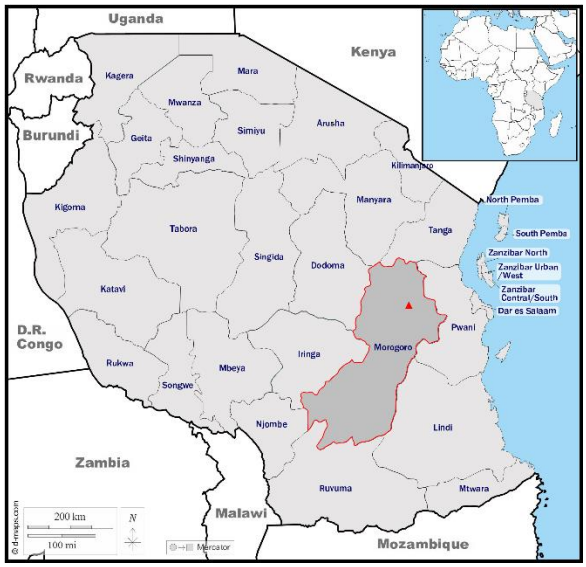

Fig 1. African continent with a focus on Tanzania. Samples were collected in the city of Morogoro (red triangle) which is located in the Morogoro region.

Analysis set up and protocol.

To assess the presence of arbovirus antibodies in DBS against a panel of arboviruses, we first developed a multiplex immune assay using Luminex technology [18,65]. Recombinant virus-derived proteins (Table 1) were covalently coupled to carboxyl-functionalized fluorescent magnetic beads (1-3µg/1.25*10^6 beads) (Luminex Corp. MagPlex® Microspheres; Bio-Rad; Temse, Belgium) employing the BioPlex amine coupling kit (Ref.: 171406001; Bio-Rad; Temse, Belgium) following the manufacturer's instructions.

To obtain positive control samples we inoculated captive *M. natalensis* individuals (age: 5-12 months) from our breeding colony at UAntwerp with recombinant virus-derived proteins (Table 1) [66–68]. We subcutaneously injected 4µg of the respective virus protein and 1µL of vaccine adjuvant (Quil-A® adjuvant; InvivoGen; Toulouse, France), dissolved in autoclaved phosphate buffered saline (PBS) to achieve a final volume of 1mL. This inoculum was evenly divided, with 0.5mL administered into the scruff and 0.5mL into the hindlimb of the animal, using a 25-gauge, 12.5mm needle and a 0.5mL syringe. This inoculation was duplicated for each viral protein (i.e., performed in two mice) and repeated twice for each

174 mouse (i.e., inoculation on day 0 and day 20). We collected blood, according to the same
175 method as in the previous studies, every 10 days from day zero until day 30, at day 30 we also
176 collected whole blood from which serum was extracted. Serum from day 30 from individuals
177 were the antibody response increased over time were considered as positive samples. Day 30
178 had the highest antibody titer in our tests and is also a time point at which IgG antibody
179 development is anticipated to have reached a peak [69,70].

180 **Table 1. Recombinant arbovirus proteins for the inoculation of captive *Mastomys natalensis*.**

Viral family	Virus	Protein (reference)	Supplier
Bunyaviridae	Rift Valley Fever virus (RVFV)	Nucleoprotein (REC31640)	The native antigen company (Kidlington, United Kingdom)
Flaviviridae	Yellow Fever virus (YFV)	Nonstructural protein 1 (YFV-NS1)	The native antigen company (Kidlington, United Kingdom)
Flaviviridae	Zika virus (ZIKV)	Nonstructural protein 1 (40544-V07H)	Interchim (Montluçon Cedex, France)
Flaviviridae	Dengue virus serotype 1 (DENV1)	Nonstructural protein 1 (DEN-004)	Prospecbio (Rehovot, Israel)
Flaviviridae	Dengue virus serotype 2 (DENV2)	Nonstructural protein 1 (PIP048A)	BioRad (Temse, Belgium)
Flaviviridae	Dengue virus serotype 3 (DENV3)	Nonstructural protein 1 (DENV3-NS1)	The native antigen company (Kidlington, United Kingdom)
Flaviviridae	Dengue virus serotype 4 (DENV4)	Nonstructural protein 1 (DENV4-NS1)	The native antigen company (Kidlington, United Kingdom)
Flaviviridae	Usutu virus (USUV)	Nonstructural protein 1 (Ab218552)	The native antigen company (Kidlington, United Kingdom)
Flaviviridae	West Nile virus (WNV)	Nonstructural protein 1 (40346-V07H)	Sinobiological (Eschborn, Germany)
Flaviviridae	Tick-borne Encephalitis virus (TBEV)	Nonstructural protein 1 (TBEV-NS1)	The native antigen company (Kidlington, United Kingdom)
Flaviviridae	Wesselsbron virus (WSLV)	Nonstructural protein 1 (REC31698)	The native antigen company (Kidlington, United Kingdom)
Nairoviridae	Crimean Congo Hemorrhagic Fever virus (CCHFV)	Nucleoprotein (REC31639)	The native antigen company (Kidlington, United Kingdom)
Togaviridae	Chikungunya virus (CHIKV)	Envelope protein 2 (CHI-003)	Prospecbio (Rehovot, Israel)
Togaviridae	Mayaro virus (MAYV)	Envelope protein 2 (REC31644)	The native antigen company (Kidlington, United Kingdom)
Togaviridae	O'nyong nyong virus (ONNV)	Envelope protein 2 (B4TG40)	Interchim (Montluçon Cedex, France)

181

182 Screening was done in 96 flat-bottom well plates, each plate contained DBS samples
183 of 80 wild *M. natalensis*, two background controls, eight negative controls and a six step
184 dilution series (1:200 – 1:625,000) of a positive pool sample. Each well in the plate contained
185 50µL of the corresponding sample type. The samples of the wild *M. natalensis* were acquired
186 by placing a punched-out DBS (round, 0.5 cm diameter) in 200 µL of dilution buffer (1% bovine
187 serum albumin, 0.2% Tween-20, 5% fetal calf serum, 45% distilled water, 50% Hypertonic PBS
188 {0.08% NaH_2PO_4, 0.25% Na2HPO_4, 8.8% NaCl}). One single DBS punch corresponds to
189 approximately 10µL of blood [71]. The punched DBS were left to elute overnight, in a 1.5mL
190 Eppendorf tube, maintained at a temperature of 4°C on a plate shaker. This elution was
191 considered a 1:100 dilution and was diluted, with dilution buffer, to 1:200 prior to loading in
192 the 96 well plate. This dilution gave the best signal to noise ratio in our preliminary tests and
193 are in line with previous studies [18,72]. The background control was reading buffer (1%
194 bovine serum albumin, 0.05% NaN_3, 100% phosphate buffered saline). The eight negative
195 controls were four DBS, treated the same as the wild *M. natalensis* DBS, and four serum
196 samples in a 1:200 dilution. All negative controls originated from the breeding colony at
197 UAntwerp. The positive pool sample was compiled from serum from the positive individuals
198 acquired through the arbovirus protein inoculation experiment. Serum from 15 positive
199 individuals (i.e., one for each arbovirus antigen) was pooled to create the positive pool
200 sample, each individual serum had a final dilution in the pool of 1:200.

201 In each well of the 96 well plate, 25µL of bead mixture was added. The bead mixture
202 consisted out of ~1000 protein-coated beads per arbovirus antigen suspended in reading
203 buffer. The bead mixture of the first screening session did not contain ONNV beads.

204 Plates, containing 50µL of sample and 25µL of bead mixture per well, were incubated
205 for one hour at room temperature, in the dark and on a plate shaker (Heidolph Titrimax 100;

206 VWR; Leuven, Belgium) at 400rpm/min. After incubation, plates underwent washing with
207 dilution buffer using an automated plate washer (Tecan Hydroflex plate washer; Tecan
208 Benelux; Mechelen, Belgium). Subsequently, we added 50µL Biotin anti-mouse IgG (4µg/mL)
209 (Sigma-Aldrich B7022; Merck Life Science; Hoeilaart, Belgium) to each well and incubated for
210 40 minutes. After another round of washing, we added 50µL of Streptavidin-R-phycoerythrin
211 (1µg/mL) (10655783; Fisher Scientific; Brussel, Belgium) to each well, followed by a 10-minute
212 incubation. The last wash step used reading buffer, and the final bead pellet was resuspended
213 in 150µL of reading buffer. Beads were read on a Bio-Plex 200 System (Bio-Rad; Temse,
214 Belgium). Results were quantified as the median fluorescent intensity (MFI) based on a
215 minimum of 100 beads per antigen.

216 Data analysis and statistics

217 All data preparation, analysis and statistical procedures were conducted using R
218 Statistical Software (R version 4.3.3) [73]. We used the body weight of the wild-caught *M.*
219 *natalensis* individuals at the time of sample collection as a rough proxy for age, which we
220 subdivided into three categories based on the 1/3 quantiles of weight; juvenile (5 - 26.7g),
221 subadult (>26.7 - 42g) and adult (>42 - 91g). These weight classes coincide to the expected
222 sexual maturity, with sexual maturity estimated to occur between 30 - 40g [29,32].

223 To control for variation between different assay plates and testing days, the MFI
224 results were transformed to relative antibody units using the positive dilution series as a
225 standard curve. The MFI result of the positive control starting dilution (i.e., 1:200) was
226 equalized to 3,125 units and each following dilution step was adjusted proportionally (i.e., the
227 final dilution step 1:625,000 corresponded to 1 unit). The results of the two sessions were
228 combined by linear alignment adjustment. This alignment was based on 86 duplicate samples

229 encompassing the measurable range, allowing the adjustment of the results from the first
230 session.

231 Finally, each sample was categorized as a binary value (i.e., 1= positive, 0= negative)
232 for each of the tested arboviruses. This was done based on whether the unit value exceeded
233 the mean cutoff value for that specific arbovirus antigen. Five cutoff values were determined
234 for each arbovirus antigen: I) the mean plus three times the standard deviation of the negative
235 controls (i.e. *'NegCtrl'*) [18,65]; the change-point analysis, using R package *'changepoint'*
236 (version: 2.2.4), calculated at most one changepoint based on the II) mean (i.e. *'CHP.m'*), III)
237 variance (i.e. *'CHP.v'*) and IV) a combination of mean and variance (i.e. *'CHP.mv'*) of wild-
238 caught samples [74,75] and V) the maximum value of an average antibody curve (i.e. *'Recap'*).
239 This curve was based on wild-caught individuals that were recaptured at least three times and
240 showed seroconversion. Seroconversion of an individual was considered when the
241 individual's maximum unit value was at least four-fold the minimum unit value. This four-fold
242 increase is a standard seroconversion confirmation measure in human antibody studies [76].
243 An average antibody curve, with days as the explanatory variable, was created for each
244 antigen by aligning the maximum unit value of each recaptured seroconverted individual to
245 the same day. The binary results were used to calculate the seroprevalence for each arbovirus
246 along with a 95% confidence interval (CI), using the *'binom.exact'* from the package *'binom'*
247 (version: 1.1.1.1) [77]. The seroprevalence according to the different cutoff methods was
248 compared to the seroprevalence of the antibody curve cutoff using the *'chisq.test'* from the
249 package *'stats'* (version 4.3.3) [73]

250 As an indication of cross-reactivity in antibody response between the tested
251 arboviruses, pair-wise Pearson correlations were calculated on the binary results, according
252 to the antibody curve cutoff, of all samples using the *'corr.test'* function of R package *'psych'*

253 (version: 2.4.1) [78]. The cross-reactivity in antibody response was visualized using the
254 *'heatmap.2'* function of the R package *'gplots'* (version: 3.1.3) [79].

255 A generalized linear model (logit link function and binomial error distribution) was
256 constructed with the package *'stat'* (version: 4.3.1), with the response variable being the
257 binary serostatus of each sample [73]. Age (juvenile, subadult and adult), sex and their
258 interaction were included as explanatory variables. The analysis of variance was performed
259 using a likelihood ratio test, with p-values calculated assuming a chi-squared distribution.
260 Pairwise comparison of the seroprevalence was performed between the six combinations of
261 the explanatory variables (two levels of sex and three levels of age), using the *'emmeans'*
262 package (version: 1.8.9) [80]. To prevent reporting statistical findings based on the reliance of
263 an arbitrary p-value of 0.05, we instead present significance in terms of levels of statistical
264 support based on p-values. P-values exceeding 0.1 are labeled as "no" support and values
265 around 0.05 (range 0.1 - ≥ 0.01, symbol: *) as "weak" support. "Moderate" support was
266 assigned to p-values clearly below 0.05 (range < 0.01 - ≥ 0.001, symbol: **), while "strong"
267 support is reserved for p-values lower than 0.05 (< 0.001, symbol: ***). This representation
268 in terms of statistical support is based on current statistical reporting practices [81].

269 Results

270 In total 1,280 DBS samples were tested of which 660 were female, consisting of 256
271 juveniles, 172 subadults and 232 adults, 620 samples were male with 199 juveniles, 313
272 subadults and 108 adults. Samples of recaptured individuals were considered as individual
273 samples for all analysis.

274 ## Seroprevalence

275 The seroprevalences according to the different cutoff methods showed at least a weak
276 statistical support for a different seroprevalence compared to the antibody curve
277 seroprevalence for almost all arboviruses. Histograms of the data and seroprevalence for each
278 tested arbovirus antigen according to the different cutoff methods is shown in S1 and S2 Figs.
279 The cutoff value according to the antibody curve based on the recaptured seroconverted
280 individuals was used as the main cutoff value for all further calculations.

281 The overall arbovirus seroprevalence, defined as at least positive for one of the tested
282 arboviruses, except ONNV, was almost 24% (95% CI: 21.89 – 26.66%; N= 1280). ONNV was
283 excluded since the samples of the first session were not screened for antibodies against the
284 ONNV antigen. The seroprevalence for *Flaviviridae* was 20% (95% CI: 17.99 – 22.46%; N=
285 1280) and for *Togaviridae*, excluding ONNV, almost 7% (95% CI: 5.48 – 8.32%; N= 1280).
286 Overall, seroprevalences ranged from 0.62% for DENV3 (95% CI: 0.27 – 1.23%; N= 1280) and
287 MAYV (95% CI: 0.27 – 1.23%; N= 1280) to 8.44% for DENV2 (95% CI: 6.97 – 10.10%; N= 1280),
288 see Table 2.

289 **Table 2. Total seroprevalence of each arbovirus and virus family in the wild-caught *M. natalensis* sample set.**

	Seroprevalence (%)	95% CI (%)	Nr. positive	Cutoff
Arbovirus[a]	24.22	21.89 – 26.66	310	
Bunyaviridae				
RVFV	2.58	1.78 – 3.60	66	37.94
Flaviviridae	20.16	17.99 – 22.46	258	
YFV	2.03	1.33 – 2.96	26	3.45
ZIKV	3.44	2.51 – 4.59	44	15.23
DENV1	7.58	6.19 – 9.17	97	42.11
DENV2	8.44	6.97 – 10.10	108	101.09
DENV3	0.62	0.27 – 1.23	8	32.27
DENV4	5.62	4.43 – 7.03	72	40.66
USUV	4.61	3.53 – 5.91	59	6.47
WNV	2.42	1.65 – 3.42	31	25.60
TBEV	1.64	1.02 – 2.50	21	50.85
WSLV	3.52	2.58 – 4.68	45	4.16

Nairoviridae				
CCHFV	2.81	1.98 – 3.87	36	5513.61
Togaviridae[a]	6.80	5.48 – 8.32	87	
CHIKV	6.17	4.92 – 7.63	79	43.95
MAYV	0.62	0.27 – 1.23	8	11.91
ONNV	2.18	1.30 – 3.42	18	77.10

A 95% confidence interval (CI) is provided and the calculated cutoff value is in units. Sample size was 1280 for each tested arbovirus except for ONNV which had 826 samples. [a] Indicates that ONNV was not included for that calculation.

Pairwise arbovirus serostatus correlation

The correlations in serostatus of samples between the tested arboviruses are visualized in Fig 2. Correlation between two arboviruses is depicted in color scale with the statistical symbol, lower triangle, and the number of positive samples in the upper triangle. The matrix is accompanied by a dendrogram based on the hierarchical clustering of the correlation coefficients. The branch lengths are a proxy for relative distance between arboviruses based on the serostatus response of the samples.

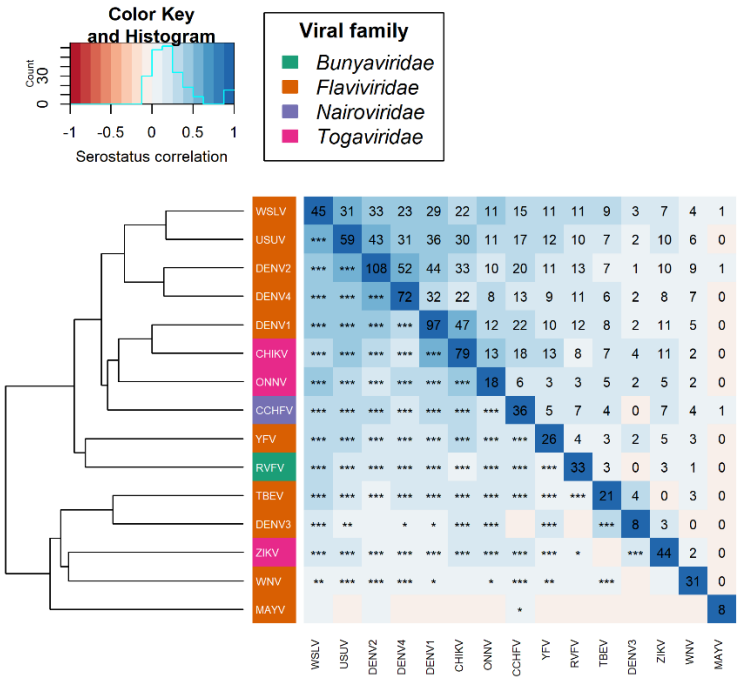

Fig 2. Correlation of the serostatus response between the tested arboviruses with a dendrogram of hierarchical clustering. Symbols in lower triangle represent significance of correlation, values in upper triangle, including diagonal line, represents the number of positive individuals for the corresponding arboviruses.

304 The correlation in sample response between the tested arboviruses ranged from -
305 2.44% for TBEV and ZIKV with no statistical support (p= 0.384) to almost 59% between WSLV
306 and USUV with a strong statistical support (p< 0.001). The dendrogram based on the
307 hierarchical clustering of the correlation showed that WSLV – USUV (correlation= 58.52%; p<
308 0.001), DENV2 – DENV4 (correlation= 56.03%; p< 0.001) and DENV1 – CHIKV (correlation=
309 50.31%; p< 0.001) are relatively closer to each other than to other tested arboviruses.

310 Model analysis of antibody response

311 Sex, age, and interaction effects on serostatus

312 The generalized linear model indicated that there was a weak statistical interaction
313 between the effects of sex and age on serostatus for DENV4 (Deviance [Df.= 2; Res.Df.= 1274]= 5.44;
314 p= 0.066) and USUV (Deviance [Df.= 2; Res.Df.= 1274]= 7.72; p= 0.021). For the other tested arboviruses,
315 no support for a statistical interaction was detected, the interaction was thus removed from
316 those models. In the case of RVFV, no statistical support was found for an effect of sex, age,
317 or the interaction on the serostatus. All results from generalized linear model's analysis of
318 variance are reported in S1 Table.

319 The analysis of the sex variable showed a moderate support for males having a lower
320 seroprevalence compared to females for DENV2 (Est. $_{males}$ ± SE= -0.665 ± 0.242; p= 0.006) and WSLV
321 (Est. $_{males}$ ± SE= -1.446 ± 0.483; p= 0.003). A weak statistical effect of a lower seroprevalence in males
322 compared to females was detected in ZIKV (Est. $_{males}$ ± SE= -0.643 ± 0.386; p= 0.096), TBEV (Est. $_{males}$ ±
323 SE= -1.103 ± 0.635; p= 0.083), CCHFV (Est. $_{males}$ ± SE= -0.821 ± 0.460; p= 0.074) and CHIKV (Est. $_{males}$ ± SE= -
324 0.633 ± 0.296; p= 0.032). There was no support for a difference in seroprevalence between males
325 and females for RVFV (Est. $_{males}$ ± SE= 0.097 ± 0.381; p= 0.798), YFV (Est. $_{males}$ ± SE= 0.425 ± 0.413; p= 0.304),
326 DENV1 (Est. $_{males}$ ± SE= -0.377 ± 0.248; p= 0.129), DENV3 (Est. $_{males}$ ± SE= -17.43 ± 2021.76; p= 0.993), WNV

327 (Est. $_{males}$ ± SE= -0.009 ± 0.397; p= 0.982), MAYV (Est. $_{males}$ ± SE= -1.222 ± 1.080; p= 0.258) and ONNV (Est. $_{males}$

328 ± SE= -17.75 ± 1663.70; p= 0.991).

329 The analysis of the age variable showed a strong statistical support for a higher

330 seroprevalence in subadults than in juveniles for DENV1 and DENV2, a moderate support for

331 CHIKV and a weak support for YFV, ZIKV, TBEV, WSLV and CCHFV. There was no support for a

332 difference in subadult and juvenile seroprevalence in the other tested arboviruses. A

333 significantly higher seroprevalence in adults compared to juveniles was shown for ZIKV,

334 DENV1, DENV2, WSLV and CHIKV with a strong support. A moderate support for a higher

335 seroprevalence in adults than in juveniles was detected for YFV and CCHFV. Adults showed a

336 weak statistical support for a higher seroprevalence in contrast to juveniles for WNV and

337 TBEV. All other tested arboviruses showed no support for a statistical difference between

338 adults and juveniles. The comparison between subadults and adults showed a strongly

339 supported statistical difference for DENV1 and CHIKV with a higher seroprevalence in adults.

340 A moderate support for a higher seroprevalence in adults compared to subadults was

341 detected for ZIKV and CCHFV. Yellow Fever virus, WNV, WSLV and ONNV showed a weak

342 support for a statistically higher seroprevalence in adults than in subadults. The other

343 arboviruses showed no statistically significant difference between adults and subadults. See

344 Table 3 for estimates, standard errors, and p-values.

345 **Table 3. Difference in coefficient estimate on logit scale between the age levels with standard error (SE).**

	Juvenile - Subadult		Juvenile - Adult		Subadult - Adult	
	Estimate ± SE	p-value	Estimate ± SE	p-value	Estimate ± SE	p-value
RVFV	-0.227 ± 0.480	0.637	-0.649 ± 0.446	0.146	-0.422 ± 0.421	0.316
YFV	-1.368 ± 0.794	**0.085**	-2.197 ± 0.757	**0.004**	-0.829 ± 0.449	**0.065**
ZIKV	-1.349 ± 0.656	**0.040**	-2.308 ± 0.611	**< 0.001**	-0.959 ± 0.365	**0.009**
DENV1	-1.610 ± 0.456	**< 0.001**	-2.468 ± 0.434	**< 0.001**	-0.858 ± 0.243	**< 0.001**
DENV2	-1.551 ± 0.356	**< 0.001**	-1.780 ± 0.352	**< 0.001**	-0.229 ± 0.221	0.301
DENV3	-16.47 ± 2176.65	0.994	-18.14 ± 2176.65	0.993	-1.665 ± 1.073	0.121
WNV	0.007 ± 0.582	0.991	-1.20 ± 0.477	**0.012**	-1.207 ± 0.480	**0.012**
TBEV	-1.855 ± 1.083	**0.087**	-2.566 ± 1.039	**0.014**	-0.711 ± 0.499	0.155

WSLV	-0.960 ± 0.539	**0.075**	-1.656 ± 0.492	**< 0.001**	-0.697 ± 0.357	**0.051**
CCHFV	-1.999 ± 1.072	**0.062**	-3.321 ± 1.021	**0.001**	-1.321 ± 0.434	**0.002**
CHIKV	-2.267 ± 0.749	**0.002**	-3.474 ± 0.723	**< 0.001**	-1.207 ± 0.283	**< 0.001**
MAYV	0.642 ± 1.228	0.601	-0.807 ± 0.844	0.339	-1.449 ± 1.104	0.189
ONNV	-17.05 ± 1747.82	0.992	-18.15 ± 1747.82	0.992	-1.099 ± 0.641	**0.087**

Data originates from the pairwise comparison of the age class variables of the generalized linear model. P-values marked in bold have at least a weak statistical support ($p < 0.1$).

In the case of DENV4, were there was a weak support for an interaction, the analysis showed that there was a strong statistical support for a higher seroprevalence in female adults compared to female juveniles (Est. $_{female - adult}$ ± SE= 1.844 ± 0.486; $p < 0.001$). A moderate support was shown for a higher seroprevalence in female subadults compared to female juveniles (Est. $_{female - subadult}$ ± SE= 1.379 ± 0.517; $p = 0.008$) and a weak support for a higher seroprevalence in female adults compared to male adults (Est. $_{female - adult}$ ± SE= 1.898 ± 0.736; $p = 0.010$). For USUV the model analysis with a weak interaction, showed that there was weak statistical support for a higher seroprevalence in female adults compared to female subadults (Est. $_{female - adult}$ ± SE= 0.868 ± 0.345; $p = 0.012$) and also a weak support for a higher seroprevalence in female adults compared to male adults (Est. $_{female - adult}$ ± SE= 1.515 ± 0.612; $p = 0.013$).

Fig 3 displays the seroprevalence for the six distinct levels (two levels of sex and three levels of age) for all tested arboviruses, with statistical support lines based on the log odds.

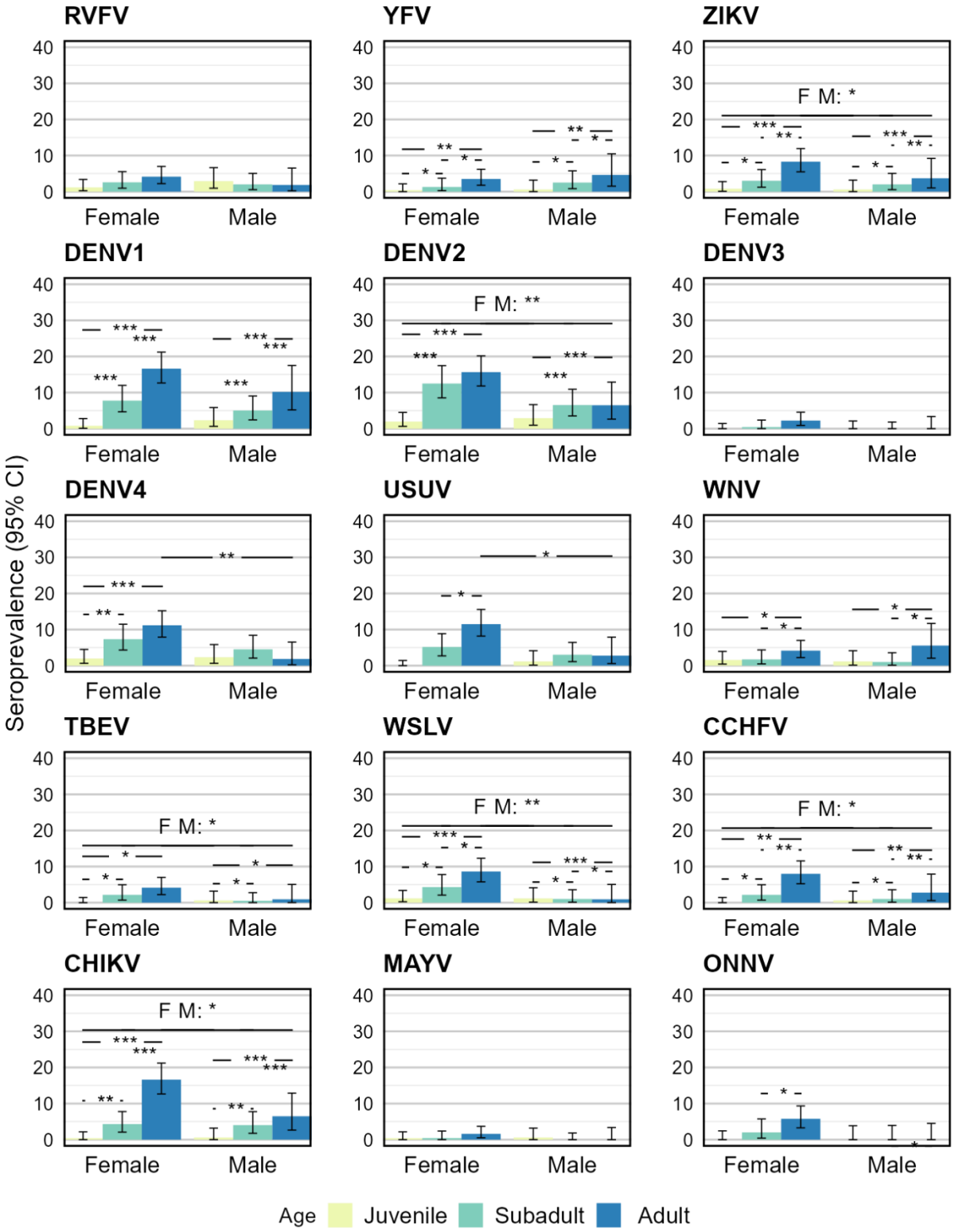

Fig 3. Seroprevalence according to sex and age combinations with 95% confidence error bars for each arbovirus. Statistical support on seroprevalence difference is indicated by asterisks in the horizontal lines. Sample size: 660 females of which 256 juveniles, 172 subadults and 232 adult and 620 males with 199 juveniles, 313 subadults and 108 adults. Sample sizes for ONNV are 560 females: 150 juveniles, 150 subadults, 260 adults and 266 males: 94 juveniles, 92 subadults and 80 adults.

366 # Discussion

367 In this study we optimized a high-throughput multiplex immunoassay for the
368 simultaneous detection of IgG antibodies against 15 medically relevant arboviruses and used
369 it to investigate the potential of *M. natalensis* to serve as a host for arboviruses. We describe
370 the screening results of a historic set of wild *M. natalensis* DBS samples. Our results revealed
371 an overall seroprevalence of 24% against the entire panel of tested antigens. Virus family-
372 specific seroprevalences were approximately 2.6%, 20%, 2.8% and 7% for respectively
373 *Bunyaviridae*, *Flaviviridae*, *Nairoviridae* and *Togaviridae*. We further found that female
374 rodents were more likely to be classified as antibody positive for eight of the 15 tested
375 arboviruses. Additionally, positivity increased significantly with age for almost all tested
376 arboviruses.

377 The lack of realistic natural positive controls limits the possibility to determine a true
378 cutoff, we therefore used recaptured seroconverted individuals to determine a cutoff value.
379 The use of antibody titers at multiple time points are a standard practice to determine
380 antibody or pathogen development and (sero)conversions in human studies [76]. However,
381 multiple samples of an individual animal across time are often impossible or very difficult in
382 wildlife studies. Our study is unique in that regard that we have measurements of individual
383 recaptured *M. natalensis*. We consider that our cutoff based on seroconverted individuals is
384 a good proxy for the natural cutoff value, since it is based on similar methods as in human
385 studies [76]. We tried to show in our analysis that the tested mathematical methods could
386 approximate this calculated cutoff and thus provide a method for future studies that do not
387 have access to recaptured seroconverted wildlife samples. Unfortunately, the tested cutoff
388 methods did not significantly approximate the seroprevalence according to the cutoff using

389 samples from recaptures. The negative control-based cutoff (i.e., the mean plus three times
390 the standard deviation of the negative control samples) gave unrealistic high seroprevalences.
391 This can be explained by the fact that the negative control samples originate from a breeding
392 colony. These animals have thus never been exposed to a natural environment and the
393 pathogens that occur in the environment. The statistical methods vary in their seroprevalence
394 with some methods approximating the estimated seroprevalence according to the recaptured
395 cutoff. This high degree of variation makes it difficult to decide on one method that works for
396 all the tested arboviruses. The cutoff value for CCHFV seems extremely high compared to the
397 other arboviruses, but the unit values for CCHFV are also much higher than for the other
398 arboviruses (see S1 Fig). The reason is that the unit values are calculated based on the positive
399 dilution series and the positive controls for CCHFV were not of the same magnitude as for the
400 other arboviruses. The value in determining a cutoff and the resulting seroprevalence is that
401 it allows the comparison of results with previous and future studies on arbovirus
402 seroprevalence in rodents or other wildlife. We are aware that the used cutoff and resulting
403 seroprevalences could be an over- or underestimation and might not reflect the natural
404 arbovirus seroprevalence. We therefore encourage future research to investigate and
405 compare different cutoff methods for arbovirus (or pathogen) antibody detection in wildlife
406 studies.

407 The detection of antibodies against each of 15 tested arbovirus antigens indicates that
408 these arboviruses, or closely related viruses, are present in *M. natalensis*. The overall
409 arbovirus seroprevalence of 24% suggests that this rodent species is commonly infected with
410 one or more arboviruses and that it could thus play a significant role in virus transmission and
411 persistence. Our results corroborate previous studies, which detected USUV and WNV RNA in
412 respectively *M. natalensis* and *M. erythroleucus*, in Senegal [24,54]. Besides in this genus,

413 arboviral RNA has also been found in other rodents in Africa, such as *Rattus rattus* for USUV
414 and WSLV and *Desmodillus auricularis* for WSLV [22,24,53]. The findings in our study thus
415 further corroborate that arboviruses are likely present in rodents, and specifically in the
416 ubiquitous *M. natalensis*. The demographic and ecological characteristics of *M. natalensis*
417 may have particularly important implications for arbovirus transmission. The population
418 densities of *M. natalensis* in Tanzania are strongly dependent on weather conditions. More
419 specifically, early rainfall and elevated temperatures lead to an exponential growth in the
420 population density, due to an increase influx of juveniles [29,30,32]. The rainfall and increased
421 temperatures are also beneficial for the breeding of mosquitoes and the multiplication of
422 arboviruses within these vectors [82]. Further, *M. natalensis* is highly abundant around
423 houses and in the crop fields at the fringes of the villages. These factors increase the likelihood
424 of arbovirus outbreaks in *M. natalensis* populations, with the possibility of spillover to
425 humans.

426 Arboviruses that show the highest seroprevalence are DENV1, DENV2, DENV4 and
427 CHIKV, with seroprevalences between five to nine percent. These seroprevalences could be
428 caused by cross-reactivity due to antibodies of other dengue virus serotypes or other
429 flaviviruses binding to the non-structural protein 1 (NS1 protein) of DENV1, DENV2 and
430 DENV4. The same effect could also be true for alphaviruses binding to the envelope protein 2
431 (E2 protein) of CHIKV. Whether these seroprevalences are indeed due to the presence of the
432 arbovirus specific antibodies or a related arbovirus remains to be investigated. Nonetheless,
433 it indicates that a part of the sampled *M. natalensis* population in Morogoro is exposed to
434 dengue virus and CHIKV or respectively to a related flavivirus and alphavirus. This hypothesis
435 is supported by the fact that flavi- and alphaviruses are the most prevalent arboviral genera

436 in humans, compared to other arbovirus genera, and potentially thus also in rodents involved
437 in the sylvatic cycle [83,84].

438 A recent health survey has shown that, in the same region as where our rodent
439 population was sampled, a high percentage of the human population is seropositive for CHIKV
440 (9.83%) [55]. Another study in the same region reported acute infection of CHIKV in 1.28% of
441 patients with fever and malaria-like symptoms [85]. Although these studies have not found
442 any indication of dengue virus in humans, a large-scale cross-sectional study in Tanzania has
443 found CHIKV and dengue virus antibodies in respectively 28.0% and 16.1% of the population
444 [56]. These studies clearly indicate that the human population in Tanzania is exposed to
445 arboviruses and then specifically to CHIKV and DENV.

446 The cross-reactivity analysis via the correlation matrix and hierarchical clustering (Fig
447 2) showed an antibody response correlation between WSLV – USUV (59%), DENV2 – DENV4
448 (56%) and DENV1 – CHIKV (50%). We expected that phylogenetically related arboviruses
449 would show elevated levels of correlation due to cross-reactivity [86]. A remarkable result in
450 this cross-reactivity analysis is that DENV1 – CHIKV cluster together with a correlation of 50%,
451 based on the serostatus of the tested samples. The branch DENV1/CHIKV clusters also closer
452 to ONNV than to the branches of WSLV/USUV and DENV2/DENV4. This is unexpected since
453 CHIKV belongs to the *Togaviridae* and DENV1 to the *Flaviviridae* [87]. The proteins used for
454 the antibody detection are also two different proteins, with the E2 protein used for the
455 *Togaviridae* and NS1 protein for the *Flaviviridae*, thus limiting the possibility of cross-
456 reactivity. Although we cannot exclude that there might be similar epitopes between the
457 different proteins, but other studies have already indicated that cross-reactivity between the
458 E2 protein of the *Togaviridae* and NS1 protein of the *Flaviviridae* is limited [88,89]. Given that
459 both *Togaviridae* and *Flaviviridae* viruses are circulating in humans in East Africa, we

460 hypothesize that these viral families may also both be present in rodents [5,10]. More
461 specifically, it is plausible that both viral families could be found in *M. natalensis,* where
462 pathogen co-infections are common [49]. This hypothesis is further supported by the fact that
463 some viruses in both families are transmitted by the same arthropod vectors, such as *Aedes*
464 *aegypti* and *Aedes albopictus* for both dengue virus and CHIKV [4,82].

465 For some of the tested arboviruses we found statistical support for a higher
466 seroprevalence in females than in males. This result is supported by previous studies where
467 it is shown that female mice have a stronger innate immune response than male mice [90].
468 Other animals (e.g., birds, fish, insects) as well as humans also display stronger immune
469 responses in females [91–95]. The major driving forces behind these immune differences are
470 genetic (i.e., X-chromosomes) and hormonal (i.e., different estrogen and testosterone levels)
471 [96]. In the case of *M. natalensis*, behavioral differences could also be the cause for this
472 divergence in seroprevalence. Previous studies have already shown that home range,
473 behavior and pathogen presence differ between male and female *M. natalensis* [48,97].
474 Besides the sex effects, we also found statistical support for a positive age effect on the
475 presence of antibodies in some of the tested arboviruses. This increased seroprevalence with
476 age corroborates previous findings for other pathogens (i.e., *Bartonella sp*., *Anaplasma sp.*,
477 helminths, and arenaviruses) [48,49,98]. This age effect further supports our hypothesis that
478 *M. natalensis* is exposed to arboviruses and that individuals develop antibodies and gain
479 immunity via repeated exposures throughout their life. To maintain the arbovirus
480 transmission among the *M. natalensis* population, there needs to be a proportion of the
481 population that is either chronically infected or immunologically naïve. Chronic infections in
482 *M. natalensis* have already been documented for mammarenaviruses [31,99]. However, as
483 far as we are aware naturally occurring chronic arbovirus infections have not been reported

484 in humans or non-human vertebrates. Therefore, the presumable driving factor in sustained
485 transmission is the presence of immunologically naïve individuals. During the breeding
486 season, which coincides with increased rainfall and temperature, there is an influx of
487 immunologically naïve juveniles. This influx can reach high proportions during population
488 outbreak periods [30,64]. We thus expect that it is mainly juveniles who are the major factor
489 in sustaining the arbovirus transmission cycle. We predict that the prevalence of arboviral
490 genetic material will be higher in juveniles than in adults, since juveniles do not possess the
491 necessary antibodies to fight of the infection.

492 We conclude from our detected antibody responses that arboviruses, or related
493 viruses, are present in *M. natalensis* in Morogoro, Tanzania. The higher seroprevalence we
494 detect in females can be explained by genetic, hormonal, ecological and/or behavioral
495 differences between sexes. Individuals are exposed to these viruses throughout their life and
496 gain immunity as they age. We hypothesize that juvenile *M. natalensis* play an essential role
497 in sustaining arbovirus transmission as they are immunologically naïve and can reach high
498 densities in favorable climate conditions that coincide with optimal vector conditions. More
499 extensive screening, such as virus neutralization tests and molecular screening of these
500 viruses within *M. natalensis* are necessary to quantify the contribution of this rodent species
501 in the arbovirus transmission cycle.

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Supporting information

S1 Fig. Histograms of wild-caught *M. natalensis* for each tested arbovirus with on the x-axis the relative antibody units in a logarithmic scale. The relative antibody units are calculated according to the positive control dilution series. The calculated cutoff values are represented by the colored vertical lines: 'CHP.m' is the changepoint mean, 'CHP.mv' is the changepoint mean-variance, 'CHP.v' is the changepoint variance, 'NegCtrl' is the mean plus three times the standard deviation of the negative control samples and 'Recap' is the maximum value of an antibody development curve based on recaptured seroconverted wild-caught *M. natalensis*.

S2 Fig. Seroprevalence, according to the calculated cutoff methods, of the wild-caught *M. natalensis* with 95% confidence interval for each of the tested arboviruses. The cutoff methods: 'CHP.m' is the changepoint mean, 'CHP.mv' is the changepoint mean-variance, 'CHP.v' is the changepoint variance, 'NegCtrl' is the mean plus three times the standard deviation of the negative control samples and 'Recap' is the maximum value of an antibody development curve based on recaptured seroconverted wild-caught *M. natalensis*. Each calculated seroprevalence was compared to the 'Recap' seroprevalence using a Chi-square test, significant difference is depicted in asterisk (*) symbols. P-values: * 0.1 - ⩾ 0.01; ** < 0.01 - ⩾ 0.001; *** < 0.001.

S1 Table. Analysis of variance from the generalized linear model (logit link function and binomial error distribution) with the response variable being the binary serostatus of each sample. Sex and age and their interaction were included as explanatory variables. P values with at least a weak statistical support are marked in bold (p< 0.1).