

Reporting Summary

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Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a Confirmed

- ☐ ☒ The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
- ☐ ☒ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- ☐ ☒ The statistical test(s) used AND whether they are one- or two-sided
Only common tests should be described solely by name; describe more complex techniques in the Methods section.
- ☐ ☒ A description of all covariates tested
- ☐ ☒ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- ☐ ☒ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- ☐ ☒ For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
Give P values as exact values whenever suitable.
- ☒ ☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- ☐ ☒ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- ☐ ☒ Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

Data collection	Sequences were curated and filtered using the OBITools bioinformatic pipeline (Boyer et al. 2016).
Data analysis	All statistical analyses were conducted in program R statistical software (version 4.2.2) . We created custom code and previously developed packages for our analyses, including gstat (Pasmada 2004), alphahull (Pateir-Lopez & Rodriguez-Casal 2022), MODISsp (Busetto and Ranghetti 2016), survival (Therneau 2020), amt (Singer et al. 2019), glmmTMB (Brooks et al. 2017), DHARMA (Hartig 2022), vegan (Oksanen et al. 2020).

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

All data, code, and materials used in our analysis will be made publicly available upon the acceptance of this manuscript for publication.

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender

Reporting on race, ethnicity, or other socially relevant groupings

Population characteristics

Recruitment

Ethics oversight

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☐ Life sciences ☐ Behavioural & social sciences ☒ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description

Research sample

Sampling strategy

We calculated NDVI from MODIS data downloaded using the MODISTsp package in R.

Movement data from GPS-collared bushbuck (n = 8), nyala (n = 4), kudu (n = 12), sable (n = 3), elephant (n = 13), wild dog (n = 1 pack), and lion (n = 8) were collected as part of ongoing, long-term studies in Gorongosa. A single pack of 14 African wild dogs was reintroduced in June 2018, and the dominant female of that pack had an active GPS collar during our study; because African wild dogs are an obligately social species that live and hunt communally and there were no other packs in the park during our study, we considered the movement data from this female to be representative of the entire wild dog population in Gorongosa.

Data on mammals' spatial distribution were from a systematic long-term camera trap grid established in 2016. Of the 48 cameras deployed at the time of the cyclone, 30 survived the flooding. We limited our analyses to data from the 30 surviving cameras across years (2017–2019) to avoid biasing our results by unbalanced sampling among cameras/years. We additionally thinned camera data to minimize repeated sightings of the same individuals (>15 minutes apart). We summed the remaining detections into month-long bins from 15 March to 15 October in each year. Five herbivore species—waterbuck, warthog, nyala, impala, and bushbuck—had sufficient data for inclusion in statistical analyses (i.e., >10 sightings in each monthly bin after March 15th in 2017, 2018, and 2019).

Data for carnivore diets were generated as part of (1) previously published observations of lion (n = 93) and wild dog (n = 71) kills in Gorongosa from 2017–2020, and (2) DNA metabarcoding of wild dog scats. To avoid pseudoreplication, we combined scat samples collected on the same date because wild dogs hunt, kill, and eat together, and more than one scat was often collected from the same

den/kill on the same day. We therefore averaged the composition of these samples, yielding a final sample count of $n = 42$ for metabarcoding analyses.

Data on herbivore diets were generated as part of a long-term study of the Gorongosa food web. The final dataset comprised 13 herbivore species, 1470 fecal samples, and 332 mOTUs. To minimize sample-size imbalance among seasons and species (mean = 16.9, min = 6, max = 40) in our evaluation of dietary turnover, we randomly rarefied a species' samples from a given collection period (season and year) to $n = 8$ (when $n > 8$) and calculated average population-level diets and dissimilarity based on this subset. We followed a similar approach in our evaluation of dietary differentiation using the R2 value from pairwise perMANOVAs among each pair of species in each season/year. Because the results of perMANOVAs can be influenced by sample size and sample sizes differed among sampling periods, we randomly rarefied species' samples to reduce inter-annual differences between sample sizes. Species represented by $n > 8$ samples in a sampling period were randomly rarefied to $n = 8$ samples, this procedure was repeated 1000 times, and the mean R2 value across iterations was used in analyses.

Data on nutritional condition were collected during capture and collaring as part of an ongoing study of spiral-horned antelopes in Gorongosa. We compared mean nutritional condition of randomly sampled bushbuck ($n = 14$), nyala ($n = 7$), and kudu ($n = 12$) after Cyclone Idai's landfall (June–July 2019) with mean condition of these species in years prior to the cyclone (June–July 2014, 2015, 2016, and 2018; yearly sample sizes, respectively: bushbuck: $n = 11, 11, 7, 13$; nyala: $n = 10, 6, 0, 4$; kudu: $n = 12, 9, 0, 18$).

Data from aerial wildlife counts were collected as part of Gorongosa's monitoring program.

Data collection

JHD and JD provided flood depth data. Flood sensors were deployed inside slotted PVC pipes set vertically into the ground and capped with PVC to reduce disturbance by wildlife; pipes were lashed with stainless steel zip ties to rebar stakes driven 60–100 cm into the ground. We measured the depth from ground level to the bottom of each hole in which a sensor was deployed for later corrections of measured water depths above ground.

RHW, JAB, RMP and RAL provided antelope movement data, collected as part of previous and ongoing studies (Atkins et al. 2019, Daskin et al. 2022, Walker et al. 2023). DDG and RAL provided elephant movement data, collected as part of previous and ongoing studies (Branco et al. 2019, Campbell-Staton et al. 2021). NA, FP, and JM provided sable movement data, collected as part of previous studies (Mamugy 2016, Arumogum 2022). MA, AP, and PB provided predator movement and kill site data, previously published as part of a prior study (Bouley et al. 2022). All animal handling procedures were in accordance with guidelines established by the American Society of Mammalogists and were approved by relevant ethical and permitting agencies (see: Ethics oversight).

KMG and MSP provided camera trap data. Cameras were mounted on a suitable tree at a height of 1 m, angled slightly downward and facing towards open areas or small game trails to maximize animal detections and minimize false triggers. Each camera was within 2 km of a road, but no cameras were placed directly alongside or facing roads.

RHW, JAB, RMP, and RAL provided antelope nutritional condition data, which were collected during capture and collaring as part of an ongoing study of spiral-horned antelopes in Gorongosa. While antelope were immobilized, we measured body dimensions (body and hind-foot length, chest girth), collected ultrasonography data (maximum rump-fat depth, thickness of biceps femoris and longissimus dorsi muscles), and conducted standardized palpation scoring of the sacroscopic ligament, lumbar vertebrae, sacrum, base of the tail, and caudal vertebrae [based on protocols developed for North American ungulates].

ABP, MCH and RMP provided herbivore diet data and carnivore DNA metabarcoding data, which were collected as part of a long-term study of the Gorongosa food web. Fecal samples were collected by driving Gorongosa's road network and opportunistically collecting samples from defecating ungulates. Occasionally, samples were collected from animals immobilized for GPS-collaring. For each sample, we recorded the GPS coordinates of the defecation site and a classification of the surrounding habitat type. We collected samples with unused nitrile gloves and deposited them in labeled, unused zip-lock bags, which we immediately placed on ice in a cooler until we returned to Gorongosa's field laboratory for processing later the same day. There, we homogenized samples within the collection bag, transferred pea-sized subsamples into labeled tubes containing silica bashing beads and DNA conservation and lysis buffer (Xpediton Lysis/Stabilization Solution; Zymo Research, CA), vortexed the tubes for 30 seconds to break up the sample and expose the DNA to the buffer, and stored them at -20°C pending transport to Princeton University for sequencing.

MES provided aerial survey data. Counts were conducted by an experienced pilot with three concurrent observers from a Bell JetRanger helicopter with all four doors removed to enhance visibility. Surveys were conducted at a constant height of 50–55 m above the ground at 96 km hr⁻¹ along a series of parallel, 500-m wide transects. All animals within 250 m on either side of the center line were individually counted and their location recorded using a GPS; when a large herd was observed, the pilot circled to enable an accurate count, and when necessary, photographs were used to count all individuals. MES participated in all aerial surveys, and all surveys were flown by the same pilot (M. Pingo, Sunrise Aviation).

Timing and spatial scale

We tracked flood depths throughout the main road network in Gorongosa before and after Cyclone Idai using loggers deployed in 2018. Between 18 August and 16 November 2018, we installed 46 automated water-level loggers (HOBO U20L-01; Onset Corp., Bourne, MA, USA) in a regular grid with 1.8-km spacing between locations, covering a 120-km² minimum convex polygon. An additional logger was deployed indoors in the park's research headquarters to record atmospheric pressure, which we later used to correct raw pressure readings from the other sensors (i.e., to obtain pressure of water, independent of air pressure). All sensors were set to record water levels every 4 h. Between June and September 2019, as floodwaters receded and deployment sites became accessible, we retrieved logger data.

We restricted spatial extent of NDVI analyses to within the remotely sensed area of Idai-induced flooding within the Gorongosa Rift Valley and a 748-km² polygon defined by the movements of GPS-collared antelopes in 2014–2019 that encompassed the floodplain margin and adjacent higher-elevation savanna-woodland habitats. To evaluate how the increased extent and duration of flooding after Cyclone Idai impacted vegetation productivity, and hence the availability of green forage for herbivores, we compared the mean monthly normalized difference vegetation index (NDVI) curves from 2019 with those from 20 bracketing years (2000–2018, 2020).

Cameras (Bushnell TrophyCamTM) were deployed over a 300-km² area south of Lake Urema in the center of 5-km² hexagonal cells, such that each camera was ~2.4 km from six nearest neighbors. We summed detections in to monthly bins after March 15th in 2017,

2018, and 2019.

We partitioned carnivore diet data into three periods—before cyclone, 1–3 mo. after landfall, and 4–9 mo. after landfall—to explore how prey selection changed after Cyclone Idai.

Herbivore diet samples were collected within Gorongosa's road network before (2016, 2018) and after (2019) the cyclone in three seasons: the late wet season (April–May), early dry season (June–July, 2016 only), and late dry season (October–November).

We sampled antelope nutritional condition in three months after Cyclone Idai's landfall (June–July 2019), when flood waters had receded to an extent comparable to the days before Idai's landfall but forage had not yet recovered in the flood zone, and in the same period in years prior to the cyclone (June–July 2014, 2015, 2016, and 2018).

Aerial surveys were conducted in 2014, 2016, 2018, and 2020 (the four years in which a total count was conducted within a standardized 193,500-ha block at the core of the park) to evaluate population trends before versus after Idai.

Data exclusions

We truncated flood sensor data from 16 November 2018 at 04:00 to 21 June 2019 at 08:00.

In our NDVI analyses, we retained only pixels with quality labels 0 or 1 (indicating unobscured pixels), usefulness labels <3 (highest quality estimates), and land labels of 1 (indicating pixel values did not represent water); other pixels were assigned 'NA'.

We rarified GPS data to include only individuals in separate herds or prides to ensure movement behaviors were independently sampled. We limited all observed and random steps to the extent of the LiDAR-derived products from which we extracted environmental covariates; one kudu was thus excluded from SSF analysis because its home range did not overlap with the extent of environmental covariates. Only two of eight GPS collars on lions in the weeks before and after Idai collected data at regular intervals and were appropriate for SSF analysis.

For carnivore diet analyses, one outlier sample (for which 96% of RRA came from the African civet, *Civetticivettia civetta*) was excluded from this analysis because this sample may have been civet feces misidentified as a wild-dog scat.

In our evaluation of herbivore dietary turnover, we excluded bushbuck and hartebeest owing to low sample sizes in the 2019 late-wet season.

Reproducibility

Not relevant with our study design.

Randomization

Not relevant with our study design.

Blinding

Not relevant with our study design.

Did the study involve field work? ☒ Yes ☐ No

Field work, collection and transport

Field conditions

Gorongosa National Park is located at the southern end of the Great Rift Valley (18.96°, 34.36°) approximately 100 km from the Mozambique Channel. The Rift Valley runs through the center of the Gorongosa National Park and encompasses Lake Urema, a large (dry season extent: 18 km²), shallow (dry season depth: 1.5 m) body of water fed by multiple rivers within the 9300-km² Urema catchment. Most annual rainfall (mean: 850 mm, IQR 650–1080 mm between 1957 and 2018) occurs during a single wet season from November–April; in that period, Lake Urema expands and floods a large portion of the Rift Valley floor (up to 780 km²)^{36,37}. When floodwaters recede as the dry season progresses (May–October), water becomes increasingly scarce and Lake Urema persists as a critical perennial water source.

Location

Our study area encompassed the region south and west of Lake Urema, an area that is largely accessible by dirt roads and supports dense concentrations of wildlife. Within this area, vegetation structure and hydrology distinguish three habitat types: (1) floodplain-grassland (8–20 m above sea level), a seasonally flooded, highly productive lawn of grasses and forbs that supports a large portion of Gorongosa's ungulate biomass, (2) floodplain-savanna transition (20–25 m above sea level), characterized by intermittent, short-duration flooding and stands of water-tolerant trees (e.g., fever trees, *Vachellia xanthophoea*; white acacia, *Faidherbia albida*; and palms, *Hyphaene* spp.), and (3) savanna woodland (> 25 m above sea level), an infrequently flooded region with a diverse community of tree species and a full continuum of canopy cover.

Access & import/export

Field work was conducted with permission from the Republic of Mozambique and Gorongosa National Park. Before import into the United States, each herbivore diet sample was subjected to an antiviral treatment (72°C for 30 minutes) as mandated by US Department of Agriculture AHPIS permits to RMP (122489, 123156, 130123).

Disturbance

Flood sensors, camera traps, diet sampling, and aerial wild life surveys induced minimal disturbance in our study system. All animal capture and collaring was conducted in accordance with guidelines established by the American Society of Mammalogists to minimize disturbance to sampled individuals.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☐	☒ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☐	☒ Plants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Animals and other research organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research, and [Sex and Gender in Research](#)

Laboratory animals	The study did not involve laboratory animals.
Wild animals	All study individuals were chemically immobilized for capture and collaring and subsequently released to range freely. GPS collars were removed within a year or upon low battery status.
Reporting on sex	We did not conduct sex-specific analyses because our hypotheses were at the species-scale.
Field-collected samples	The study did not involve animal samples collected from the field.
Ethics oversight	All animal handling procedures were in accordance with guidelines established by the American Society of Mammalogists. Bushbuck, nyala, and kudu handling procedures were approved by the Animal Care and Use Committees at the University of Idaho (protocol # IACUC-2019-32) and Princeton University (protocol #2075F-16). Sable handling procedures were approved by the animal ethics committee at the University of Witwatersrand (animal ethics number #2013/47/2A). Elephant handling procedures were approved by the Animal Care and Use Committee at the University of Idaho (protocol #2015-39) and by the Gorongosa Conservation Department. Lion and African wild dog handling procedures were approved by the Gorongosa Conservation Department.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Dual use research of concern

Policy information about [dual use research of concern](#)

Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

No	Yes
☒	☐ Public health
☒	☐ National security
☒	☐ Crops and/or livestock
☒	☐ Ecosystems
☒	☐ Any other significant area

Experiments of concern

Does the work involve any of these experiments of concern:

No	Yes
☒	☐ Demonstrate how to render a vaccine ineffective
☒	☐ Confer resistance to therapeutically useful antibiotics or antiviral agents
☒	☐ Enhance the virulence of a pathogen or render a nonpathogen virulent
☒	☐ Increase transmissibility of a pathogen
☒	☐ Alter the host range of a pathogen
☒	☐ Enable evasion of diagnostic/detection modalities
☒	☐ Enable the weaponization of a biological agent or toxin
☒	☐ Any other potentially harmful combination of experiments and agents