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Carbon finance initiatives can provide biodiversity benefits

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Abstract

Carbon finance initiatives such as Reducing Deforestation and Forest Degradation (REDD+), designed to mitigate climate change, offer an opportunity to also protect biodiversity. However, managing forests to store and sequester carbon does not necessarily conserve biodiversity. We evaluated the biodiversity co-benefits of the Gola-REDD+ initiative in the tropical forests of Sierra Leone, using bioacoustics and DNA metabarcoding under a quasi-experimental study design. We used soundscape saturation (SS) as a measure of vocalizing diversity, and e-DNA arthropod community as a complementary measure of biodiversity to examine whether a Gola-REDD+ financed protected area (Treatment-PA) conserved biodiversity more than (1) a multiuse community land (Control-CL) and (2) a PA without REDD+ finance (Control-PA). We found that REDD+ financing is associated with additional biodiversity co-benefits in the Treatment-PA compared to both control areas. Our study makes three key contributions. First, we provide concrete evidence on a carbon finance (REDD+) project's effectiveness in conserving faunal diversity while sequestering carbon. Second, we present a gold-standard causal inference study design for evaluating biodiversity co-benefits of conservation strategies. Third, we highlight the role of conservation technologies like bioacoustics and DNA metabarcoding in informing conservation policy.

KEYWORDS

bioacoustics, biodiversity conservation benefits, carbon finance, quasi-experimental design, REDD+, regression discontinuity, tropical forest

1 | INTRODUCTION

Global biodiversity is threatened due to the synergistic pressures of habitat loss and degradation, overexploitation, invasive species, and climate change (IPBES, 2019). Various strategies have been proposed to protect biodiversity while mitigating climate change (Hilty et al., 2020; Naidoo et al., 2019; Watson et al., 2014). Protected areas (PAs) combined with market-based strategies, such as carbon financing through Reducing Emissions from Deforestation and Forest Degradation (REDD+), provide an opportunity to protect tropical forest biodiversity as a co-benefit to climate mitigation (Buřivalová et al., 2023; Koh et al., 2021; Sreekar et al., 2022; UNFCCC, 2005). However, such potential biodiversity co-benefits remain rarely studied (Buřivalová et al., 2023; Hyde et al., 2022; UNFCCC, 2010, 2011, 2012).

REDD+ is a global initiative that aims to mitigate climate change by financially incentivizing the preservation and sustainable management of forests, thereby maintaining or creating biological carbon sinks to offset emissions, particularly in developing countries (UNFCCC, 2005, 2011, 2012). While curbing deforestation and forest degradation, REDD+ also aims to promote biodiversity conservation and the rights of indigenous communities, attempting to mitigate the unequal responsibility for biodiversity and climate protection placed on developing nations by the international community (Buřivalová et al., 2023; Koh et al., 2021; Sreekar et al., 2022; UNFCCC, 2014, 2016). Since its inception during the Third Conference of the Parties (COP3) in 1997, REDD+ has spread worldwide with over 350 projects in 50 countries and has seen a surge in financial investments (>US $20 billion from public and private funds) (Guizar-Coutiño et al., 2022; Simonet et al., 2020; UNFCCC, 2021, 2022).

Habitat loss from land-use change is currently the greatest global threat to tropical forests, where, despite having much of the world's remaining biodiversity, deforestation and degradation are widespread (Harfoot et al., 2021; Jaureguiberry et al., 2022). In West African rainforests (where REDD+ is relatively rare), deforestation and forest degradation for timber and agriculture, along with wildlife trade, are the primary threats to biodiversity (Buchanan et al., 2021; Norris et al., 2010; RSPB, 2015; Simonet et al., 2020). Therefore, bolstering protected areas with strong financial support for conservation and alternative livelihoods for local communities (e.g., through REDD+) could directly aid species survival and recovery. Our operating assumption is that REDD+ finance pays for more effective patrolling and alternative livelihood programs to adjacent local communities dependent on forest resource use, and thus reduces hunting and habitat degradation that would otherwise occur through logging, swidden agriculture, and small-scale artisanal mining, leading to biodiversity conservation (RSPB, 2015).

A recent systematic global study of 40 verified REDD+ projects found widespread environmental benefits (Guizar-Coutiño et al., 2022). It is, however, unlikely that any conservation strategy is uniformly effective (Burivalova, Allnutt, et al., 2019; Burivalova, Game, & Butler, 2019). In the case of REDD+, discrepancies in its effectiveness are widespread, often due to non-rigorous evaluation methods and dissimilarities in outcomes being assessed (Duchelle et al., 2018; Guizar-Coutiño et al., 2022; West et al., 2020). Additionally, the co-benefits of REDD+ for biodiversity conservation beyond habitat are still uncertain and understudied even for charismatic and keystone species (Buřivalová et al., 2023; Duchelle et al., 2018; Hyde et al., 2022). Therefore, it is important to understand its effectiveness in a broad variety of contexts and in terms of various outcomes, beyond carbon (Correa et al., 2020; Ellis et al., 2020).

The existing rigorous assessment of most conservation strategies, including REDD+, typically measures the impact of interventions on deforestation and forest degradation by using satellite imagery (Buřivalová et al., 2023; Guizar-Coutiño et al., 2022). Some studies also use remotely sensed habitat metrics as proxies for faunal biodiversity, but as yet, no satellite images can measure faunal biodiversity directly (Buřivalová et al., 2023; Burivalova, Allnutt, et al., 2019; Guizar-Coutiño et al., 2022; Jayachandran et al., 2017; Roopsind et al., 2019; Wilebore et al., 2019). A major limitation of using such proxies for biodiversity outcomes is that habitat alone does not fully drive conservation outcomes for fauna. Factors including climate change, invasive species, and, in West Africa especially, past and present hunting, also drive biodiversity outcomes in ways that we cannot yet fully predict—dampening the biodiversity co-benefits of REDD+ (Ferreiro-Arias et al., 2024; Harrison et al., 2016; Sagar et al., 2023; Scheffers et al., 2019; Wilkie et al., 2011). As a result, direct measurement of biodiversity is warranted. For evidence-based conservation of wildlife and to incentivize the flow of funds into ‘high-quality’ carbon projects (Ecosystem Marketplace, 2024), we need to quantify the true impact of REDD+ on biodiversity with field-based methods.

We fill the above research gap by using direct, on-the-ground measurements of fauna using bioacoustics and e-DNA metabarcoding to evaluate the biodiversity co-benefits of REDD+. Bioacoustics and metabarcoding are fairly new technologies, which have increased our capacity to measure biodiversity at broad spatial and taxonomic scales (Bradfer-Lawrence et al., 2023; Burivalova, Game, & Butler, 2019; Hartig et al., 2024; Rodríguez-Ezpeleta et al., 2021). We sampled continuous soundscapes (all the sounds in a landscape) using passive acoustic monitors (PAMs, see Section 2), and we calculated soundscape saturation (SS) as a proxy for biodiversity. SS is a summary metric developed to operationalize the Acoustic Niche Hypothesis, which proposes that a richer vocalizing fauna should fill up more of the available frequency range with sounds (Burivalova et al., 2018, 2021; Burivalova, Wahyudi, et al., 2019; Zwerts et al., 2022). In our case, we used PAMs to record the human-audible frequency range (0–22 kHz) for a continuous 5-day period at 133 sites (Table S1; see Section 2) (Burivalova et al., 2018, 2022; Krause, 1987; Pijanowski et al., 2011). We also sampled arthropod diversity at a subset of the same sampling sites, using Townes-style Malaise traps (Skvarla et al., 2021), which we characterized by using DNA metabarcoding (Yang et al., 2021) to measure compositional variation in Operational Taxonomic Units (OTUs, see Section 2).

We evaluate biodiversity outcomes of the Gola-REDD+ initiative in Sierra Leone as a case study of REDD+ projects, and the wider carbon financing initiative in tropical forests (Butsic et al., 2017; Pearl, 2009; RSPB, 2015). Gola-REDD+ started in 2012, as a partnership with multiple Non-Governmental Organizations (NGOs) and Government agencies. The purpose of the initiative was to create the Gola Rainforest National Park (GRNP) in Sierra Leone, and manage it to reduce deforestation and degradation, while explicitly including socio-economic and biodiversity co-benefits (RSPB, 2015). This case study is of global interest, because it represents a scenario common to many forest conservation projects: it was established to protect the largest remaining contiguous forest ecosystem within Sierra Leone—a country with a very limited budget for large-scale biodiversity conservation (RSPB, 2015). At the same time, GRNP and the neighboring Gola Forest National Park (GFNP) are also politically and ecologically important as they are part of the Greater Gola Landscape—a ‘transboundary peace park’ between Sierra Leone and Liberia (RSPB, 2015).

We collected biodiversity data from 133 field sites in three regions. Our treatment region is the GRNP (Treatment-PA). Our first control region is a landscape mosaic of community-owned forest patches and agroforestry adjacent and sometimes bordering the GRNP (Control-CL) (Figure 1, see Section 2) (Malan et al., 2024; RSPB, 2015). Our second control region is the GFNP (Control-PA), a protected area in Liberia that is contiguous with the Treatment-PA and has similar bio-geo-climatic conditions. The Treatment-PA receives REDD+ finance, whereas the Control-PA does not. The Control-CL is not officially protected in any way; however, it does receive substantial REDD+ funding towards developing deforestation-free livelihood activities to reduce the pressure on the Treatment-PA and ‘leakage’—increase in forest loss rate after REDD+ project inception due to the displacement of human activity from GRNP (Treatment-PA), into the Control-CL.

A particular challenge to evaluating PA effectiveness in any context, including ours, is that governments

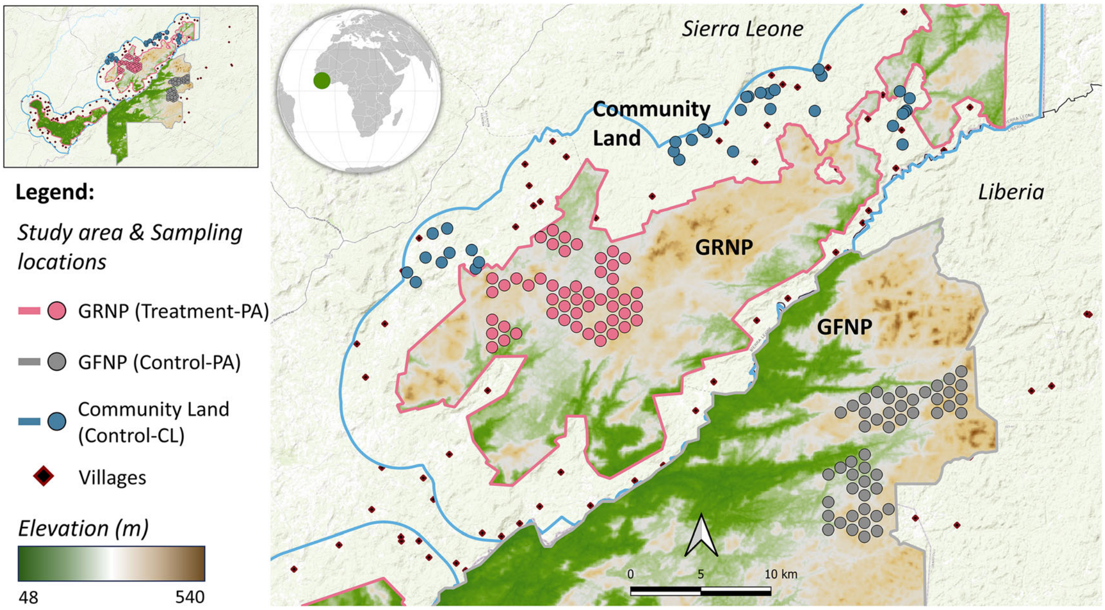

FIGURE 1 Map of the study area in the Greater Gola Landscape, with two adjacent national parks and a surrounding community forest. The Gola Rainforest National Park (GRNP) in Sierra Leone receives REDD+ finance (Treatment-PA), whereas the Gola Forest National Park (GFNP) in Liberia does not (Control-PA). The community landscape (CL) forest mosaic just outside the GRNP is not officially protected in any way but receives REDD+ funds towards alternative livelihood activities (Control-CL).

generally do not assign protection to areas randomly (e.g., focusing on areas that are too high in elevation, too steep, or too remote to be useful for agriculture, or areas that already have higher biodiversity). Therefore, naively comparing outcomes inside and outside the protected area can be misleading, capturing pre-existing differences in the landscape rather than the effect of protection itself (Coetzee et al., 2014). Matching approaches have been widely used to mitigate this bias by balancing observed covariates (Börner et al., 2020); however, these methods cannot control for unobservable drivers of differences in biodiversity (e.g., enforcement capacity, hunting pressure, and other unmeasured human uses) between the treatment and control areas (Butsic et al., 2017). A spatial regression discontinuity design (RDD) addresses this weakness of matching methods by using the PA boundary as a quasi-experimental treatment cutoff (Neal, 2024). It assumes that, in the absence of protection, biodiversity levels change smoothly over space, and sites arbitrarily close to the PA boundary are therefore comparable in both observed and unobserved characteristics—assumptions we later test (see Section 4). Thus, any discontinuous change in biodiversity levels at the border can be causally attributed to protection. Because Control-CL and Treatment-PA are spatially adjacent, we are able to apply a spatial RDD to estimate the local average treatment effect of protection at the border (Figures 1 and S1).

In contrast, while Treatment-PA and Control-PA is contiguous, the sampling locations are not spatially adjacent due to the presence of villages and, and low-elevation areas (Figure 1). Therefore, we could not apply an RDD and instead relied on matching methods to select comparable sampling sites ex ante (Figure S1). Specifically, we used covariates identified through a directed acyclic graph (DAG) to balance observed confounders prior to field sampling and thereby reduce bias arising from non-random PA placement (Elwert & Morgan, 2013; Pearl, 2009) (see Section 2). Briefly, we first generated gridded treatment and control areas and the centroid of each grid represents the universe of potential sampling sites. Then, we restricted potential sites to areas with similar historical logging pressure, elevation, slope, and remoteness, which are key observable factors that could bias comparisons of biodiversity. Finally, we stratified potential sites into remoteness categories and randomly selected matched pairs with similar elevation and slope values across the two PAs. These variables were also included in our statistical models to further adjust for any residual differences (see Section 2).

We hypothesized that (i) designating the forest as a national park with REDD+ financing (Treatment-PA) protected it from the biodiversity loss that would have followed from forest degradation, habitat loss, and hunting, which all occur in the surrounding community forest (Control-CL), and that (ii) protecting and managing the Treatment-PA with the financial support from Gola-REDD+ conserved biodiversity more effectively than protected area designation alone (Control-PA).

2 | METHODS

2.1 | Study area

Our main study area is the Gola Rainforest National Park (GRNP) in south-eastern Sierra Leone (Figure 1). It harbors the country's largest remaining forest areas belonging to the Upper Guinea Tropical Forests Biome, recognized as a Key Biodiversity Area (Key Biodiversity Areas Partnership, 2020a). Dominated by lowland evergreen forest, the landscape is home to >300 species of birds, 163 of which are restricted to the Guinea-Congolian forest (Klop et al., 2010), and 49 species of large mammals, of which 20 species are threatened (Lindsell et al., 2011). With an annual rainfall of c. 3000 mm, these forests give rise to important rivers such as the Moa, Mano, and Moru (Lindsell & Klop, 2013). With the support of financial aid from a REDD+ initiative, the forest reserves within the current day GRNP were designated as a National Park in 2012 (RSPB, 2015). The same year, the Gola-REDD+ initiative was started as a partnership between the Royal Society for Protection of Birds, the Government of Sierra Leone represented by the Ministry of Agriculture, Forests and Food Security, and the Conservation Society of Sierra Leone. The initiative's focus has been to reduce deforestation and forest degradation within GRNP (Treatment-PA) and the surrounding community lands (Control-CL) to offset carbon emissions, while explicitly including socio-economic and biodiversity co-benefits (RSPB, 2015).

The mechanisms to achieve these co-benefits include promoting alternative livelihood activities in the Control-CL, such as production of shade-grown cocoa, marketing support, access to (co-managed) financial services, and encouraging protection and community use of forests for hunting and non-timber forest products. The collection of non-timber forest products and fishing is permitted within GRNP, whereas hunting and agriculture is not (Malan et al., 2024). While a reduction in deforestation rate in the Control-CL relative to other nearby communities has been seen since the inception of Gola-REDD+, deforestation has not completely ceased (Malan et al., 2024; Wunder et al., 2020). The Control-CL is a mosaic of multiple-use forest patches, of various ages and structures, interspersed with villages, ground crops, fallow farmland and some shade-grown cocoa.

We chose Gola Forest National Park (GFNP), in Liberia, at the border with Sierra Leone, as the second control site (Control-PA). The Control-PA is contiguous with the Treatment-PA, with similar biodiversity, biogeography, climate, historical anthropogenic disturbance, resource usage and forest habitat type. Despite being a protected area formally since 2013 and a Key Biodiversity Area, due to insufficient financial resources, there was a notable absence of effective on-the-ground forest protection and management during our study (Key Biodiversity Areas Partnership, 2020b). The presence of similar pressures and a large expanse of old-growth forests similar to the Treatment-PA makes it a suitable control site.

2.2 | Study design

Within the Treatment-PA and Control-PA, we selected our sampling sites using matching of potential confounding variables (variable matching) followed by a stratified random sampling method. We used variable matching during the study design phase to minimize the effect of confounding factors for three reasons: (1) to increase our efficiency during field data collection, (2) to take maximum advantage of all the data collected, and (3) to design a field survey with a specific motive to evaluate treatment effects using a casual inference framework. We first used Directed Acyclic Graph (DAG) to visualize the most relevant causal relationships within our system (see Section 2, Appendix S1), following the Structural Causal Model framework, where variables (nodes) are connected to each other via directed arrows, pointing from cause to effect (Arif & MacNeil, 2022; Cronin & Schoolmaster, 2018; Elwert & Morgan, 2013). We then used the R package daggity (Textor et al., 2016) to apply the 'backdoor criterion' to determine the covariates that must be controlled to evaluate the effect of REDD+ on biodiversity (Appendix S1) (Pearl, 2009). We found that elevation, slope, and historical logging intensity are the three most important matching criteria.

To select sampling sites matched for their confounding factors, we first divided the entire Treatment-PA and Control-PA into hexagons, the centroids of which were 1 km apart from each other. The centroids were our potential sampling sites. We then limited our potential sampling sites to regions with similar historical pressure. While we were unable to directly measure and control for a full suite of historical logging pressures, due to a lack of historical land-use data; we collected information of logging pressure data using (Lindsell & Klop, 2013; RSPB, 2015) and through personal communication with local partners and coauthors (MET, ZN, SJ). For the selected region, we then estimated the elevation and slope for each potential sampling site (see "Section 2.3 " within Section 2), which were the variables selected from the DAGs. First, we limited our potential sampling sites to those with elevations between 250 and 450 m to reduce the effects of stream noise and to take advantage of the availability of the elevation range within both PA (Figure 1). Next, as a proxy for human forest use, both legal and illegal, which can confound our treatment effect, we estimated the remoteness of each of these potential sampling sites (see "Section 2.3.3" within Section 2). Then, we stratified all the potential sampling sites across both the PAs into five remoteness categories. Within each PA, we then randomly selected 10 paired sampling sites in each of the five remoteness categories, with similar values of confounding variables: elevation (mean = 320 m; CV = 12%) and slope (mean = 47, and CV = 17%). To further minimize the influence of elevation and slope on our results, we explicitly included these confounding variables in our statistical models (see Section 2.4).

Given the heterogeneous nature of the forest-agroforestry mosaic of the Control-CL area, we identified potential sampling sites, focusing on areas with tree cover, which included both forested land and agroforestry areas. This approach provided us with potential sites with a gradient of forest quality, from mature old-growth forest patches to disturbed forest areas, with a proportion of sampling sites also including sites with a small percentage of shade-grown cocoa plantations with native tree canopies. If we found that a selected site was in a newly cleared area for swidden agriculture when we visited the field, we relocated it to the nearest forest patch. This process yielded 133 sampling sites at a gradient of distances from Treatment-PA boundary: 50 in the Treatment-PA, 49 in the Control-PA, and 34 in Control-CL. We then selected analytical frameworks designed to minimize potential biases arising from differences in the number of treatment and control sites (see Section 2.4).

2.3 | Biodiversity data from field

2.3.1 | Bioacoustics sampling

We conducted bioacoustics sampling at our selected sites between November 2021 and February 2022 using passive acoustic monitors, scheduled for autonomous recording. Recordings were collected in the dry season to reduce the effect of rain on the acoustic recordings. While some rainy-season activity of species was not captured, our dry-season sampling provides a robust and comparable basis for assessing treatment effects across sites—with reduced acoustic disturbance from the sound of rain. At each sampling site (Figure 1) we collected continuous, 24 h recordings for five consecutive days (Bradfer-Lawrence et al., 2019; Burivalova et al., 2021). All the devices were attached to a tree trunk that was clear from any leaves to reduce noise and placed approximately 1.5 m from the ground facing magnetic South. We sampled 133 sites across the Treatment-PA (50 sites), Control-CL (34 sites) and Control-PA (49 sites) using 12 BAR-LT (Frontier Labs) and 20 AudioMoths (Open Acoustic Devices) (Frontier Labs, 2023; Hill et al., 2018). We used a block-sampling method, where the same set of devices was rotated after each sampling block for five consecutive days. Within the Treatment-PA and Control-PA, each block had sampling sites along a gradient of accessibility from villages to reduce potential biases from device rotation. We sampled Treatment-PA and Control-PA sites using BAR-LT (Frontier Labs) recorders (Frontier Labs, 2023), separated by a minimum of 1 km to maintain acoustic independence. We sampled Control-CL sites using a combination of AudioMoths and BAR-LT devices (Frontier Labs, 2023; Hill et al., 2018), and the possible biases from using two types of PAMs were reduced by (a) sampling a subset of sites with both AudioMoths and BAR-LT, and (b) statistically controlling this effect within the model.

We processed the bioacoustics recordings and estimated the acoustic index SS, following the methods described by Truskinger et al. (2014), which are briefly summarized here. We first calculated the acoustic index, Power Minus Noise (PMN), which yields a matrix with 1440 columns, representing minutes of the day, and 256 rows, representing frequency bins (~43 Hz each). From PMN, we then calculated SS, which reduces the PMN matrix to a single row (1 value per minute), indicating the percentage of frequency bins that exceeded a threshold of 2 dB (see supplementary figures from Burivalova et al., 2022), for a given minute. This threshold was determined to yield the closest-to-normal distribution of the resulting SS data. Thus, we converted a 24 h continuous raw bioacoustics recording into a per-minute SS value (0%–100%), which can be plotted as a 24 h time series (Table S1) (Burivalova et al., 2018). We calculated the acoustic index separately for recordings obtained through BAR-LT and AudioMoth devices to check for their optimum threshold value. We found that the threshold value was the same for both devices—2 dB. We calculated multiple measures of SS based on the frequency segments: (a) Total SS estimated using all frequency bins between 0 and 11,025 Hz, and (b) very low SS (0–1 kHz), (c) low SS (1–2.2 kHz), (d) medium (2.8–3.8 kHz) and high (3.8–4.8 kHz) (see Appendix S1 for ecological justification of the frequency segments).

2.3.2 | Arthropod diversity using eDNA sampling

We used Townes-style Malaise traps (Skvarla et al., 2021) to collect and quantify arthropod diversity at all the sampling sites within the Control-CL, and 12 sites within Treatment-PA, all paired with bioacoustics recorders. The 12 sites were chosen based on a gradient of forest remoteness. We allocated more DNA metabarcoding effort in Control-CL due to the relatively homogeneous forest within Treatment-PA, in contrast to the varying disturbance regimes across the Control-CL landscape. We sampled arthropods only in Control-CL and Treatment-PA, to test whether Gola-REDD+ protected Treatment-PA from the biodiversity loss associated with habitat degradation and hunting, all of which occurred Control-CL. We prioritized this comparison because arthropods are highly sensitive to habitat change, and this matched most appropriately to our logistical and financial constraints. We deployed the Malaise traps for five continuous days at each sampling site. We used 95% alcohol to collect all the arthropods using a collection container attached to the trap (Skvarla et al., 2021). We then extracted the information on arthropod diversity by identifying Operational Taxonomic Unit (OTU) using DNA metabarcoding (see Appendix S1 for details). The DNA extraction and metabarcoding were done in collaboration with the company NatureMetrics (NatureMetrics, 2024).

2.3.3 | Environmental data

To support our matching procedure for the Treatment-PA and Control-PA sites (see “Section 2.2” in Section 2), we collected data on forest remoteness, elevation, and slope for each sample location. We also extracted remotely sensed data on mean tree height and precipitation to conduct placebo tests for the RDD comparing Treatment-PA and Control-CL (in addition to elevation and slope). We selected mean tree height and precipitation because the landscape experienced selective logging prior to protection—areas with lower tree height likely reflect heavier logging—and because changes in precipitation can strongly influence tropical forest land use and biodiversity; both factors could therefore have affected the placement of the protected area boundary. Details of the placebo tests are provided below (see “Section 3.1” in Section 3). All these data were gridded and resampled to have similar spatial resolution.

Forest remoteness: We estimated the remoteness of sampling site as a proxy for the human forest use pressure it likely was under, with greater remoteness representing weaker human forest use pressure (Ferreiro-

Arias et al., 2024; Sagar et al., 2023). The use of this proxy was necessary due to the difficulty of quantifying activities such as hunting, fishing and non-timber forest produce (NTFP) collection, across large landscapes during the study design phase (Sagar et al., 2023). Within the Treatment-PA and Control-PA, there were no roads that could be accessed using a motorized vehicle from the settlements; within the Control-CL, despite the presence of forest roads, the low availability of motorized vehicles or bicycles forces the community to reach places by walking, making the presence of roads largely irrelevant. Therefore, given that these settlements were observed to be trade hubs for bush meat, fish, and NTFP products (personal observation and communication with Gola-REDD+ staff), we assumed that the primary determinant of human accessibility to a given sampling site would be the effort needed to access it on foot. Thus, the most conservative estimate of human accessibility is the distance from the center of the village settlements. For each sampling site, we calculated the Euclidean distance from the nearest village settlement as a measure of human accessibility, thus its remoteness, using the package 'FNN' (Beygelzimer et al., 2019) in R (R Development Core Team, 2022). All our sampling sites had similar habitat and terrain, so these factors do not significantly influence remoteness across sampling sites.

Elevation: We used the Shuttle Radar Topography Mission (SRTM) 1 Arc-Second global digital elevation model (DEM) to estimate the elevation for each of our sampling sites. We downloaded the DEM data for the entire study region from the United States Geological Survey Earth Resources Observation and Science (EROS) archives (USGS, 2024). We estimated the elevation as the mean elevation within the 100 m radius from the sampling sites, using QGIS version 3.34 Prizren (QGIS, 2023).

Slope: We used SRTM 1 Arc-Second (30 m) DEM data to calculate the slope for the entire study region. We used QGIS version 3.34 Prizren to process the data (QGIS, 2023). We estimated the slope as the average value of slope within the 100 m radius from the sampling sites.

Tree height: We used the global tree height data from Lang et al. (2023) to estimate the average tree heights within each of the sampling sites. The tree height data is a 10 m resolution global tree height data for the year 2020 that was developed by using a combination of Global Ecosystem Dynamics Investigation (GEDI) space-borne LiDAR mission with satellite images from Sentinel-2, using deep learning models (Lang et al., 2023). We estimated the tree height as the average tree height within the 100 m radius of the sampling sites using GQIS version 3.34 Prizren (QGIS, 2023).

Precipitation: We downloaded the 1-km spatial resolution surface precipitation data from WorldClim 2 using worldclim.org (Fick & Hijmans, 2017).

2.4 | Statistical analysis

We conducted all statistical analyses using the R programming language version 4.3.2 (R Development Core Team, 2022).

2.5 | Difference in SS between control-CL and treatment-PA

As a motivating visualization, we show every minute SS patterns for the Control-CL versus Treatment-PA (Figure 2a), using generalized additive mixed effect models using the *bam*() function (Wood, 2017) (Equation (1)). The response variable, soundscape saturation (SS), was modeled as a function minute of day (*m*)—continuous variable with 1440 units representing every minute of the 24 h period for every site (*i*). The effect of the minutes (m) modeled using a cyclic cubic regression spline to account for the dial nature of time. This smooth term was further stratified by treatment effect to allow the daily pattern of the soundscape to differ across Treatment-PA and Control-CL. Treatment was also included as a fixed effect to capture overall differences between categories. To account for the hierarchical nature of the dataset, we included: (i) replicates—representing the number of days sampled at each site, and (ii) sampling month, random variables. We then additionally included the device used (BAR, AudioMoth, or both) as a random variable in the model to statistically control for the bias from the device type. The model was fitted with a Gaussian distribution and an identity link function, using restricted maximum likelihood (fREML) for estimation. Knots were specified for time of day to ensure proper cyclicity, and the model was optimized for computational efficiency by enabling discrete smoothing and parallelization (Wood, 2017). We used gam.check within the mgcv to check for the model fit and to choose the optimum value of *k*, which determines the number of basis functions (the flexibility allowed to explain the temporal variation, while avoiding overfitting), and also checked for the concurvity—non-linear equivalent of collinearity, occurring when one smooth term can be approximated by a combination of other smooth terms, making their individual effects hard to separate (Wood, 2017).

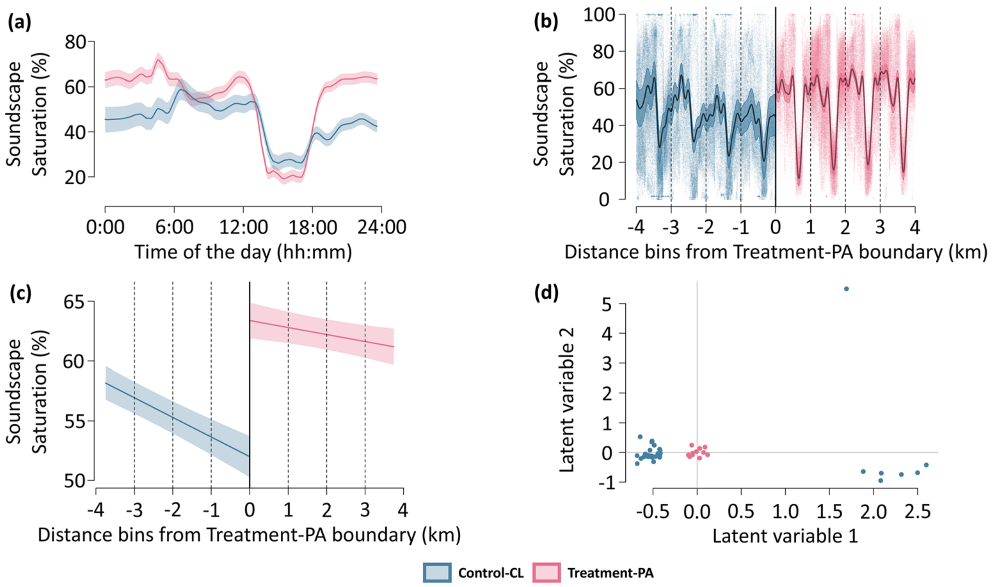

FIGURE 2 Effect of Treatment-PA (Gola Rainforest National Park receiving REDD+ financing) on faunal diversity, relative to Control-CL (multiple-use community forest). Panel (a) presents the modeled daily soundscape saturation over 24 h, showing the mean prediction (line) over all sampling sites, with a 95% confidence interval (shaded region). Panel (b) shows the discontinuity in daily soundscape saturation at the Treatment-PA geographic boundary, by 1 km bins. The vertical dashed lines show distances of sampling sites from the Treatment-PA border, for example, the −2 to −1 km bin represents samples 1–2 km outside of the PA. Excluded are sites within 0200 m to reduce bias from boundary demarcation (see Section 2). Panel (c) shows discontinuity in the dawn soundscape saturation. In panels (a–c), lines represent regression coefficients and shaded areas represent 95% confidence intervals. Panel (d) depicts differences in the total arthropod community structure between Treatment-PA and Control-CL, using an ordination plot. The dots represent each sampling site.

$$SS_{m,t} = \beta 0 + f(\text{minute of day}_m, \text{treatment}_i) + \beta 1^{*}\,\text{treatment}_i + \varepsilon \tag{1}$$

As a causal test of the observed differences between the temporal daily pattern of the SS of Treatment-PA and Control-CL, we use a spatial regression discontinuity design (Butsic et al., 2017) where the running variable is the distance to the Treatment-PA boundary and the treatment status equals 1 for distance ≥0 (inside the PA) and 0 otherwise (outside the PA) (Figure 1). To reduce the effect of non-random placement of the management boundary, we created a 200 m buffer within the PA, where we did not sample. This 200 m buffer was also used to account for uncertainty that resource users on the ground may have around the precise location of the PA boundary. We modeled the daily (temporal) pattern of SS across the spatial discontinuity in treatment status at the PA boundary in two ways:

Regression within 1 km bandwidth: Here we modeled the change in the SS between Treatment-PA and Control-CL for every hour of the day (*h*), for every sampling site (*i*), using a 1 km bandwidth (Equation (2)). Here we modeled each hour as a categorical variable interacting with the treatment variable. We used generalized mixed effect models using lmer package to conduct the analysis. We estimated the 95% Confidence Interval by performing a parametric bootstrapping with 2000 simulations, using the R package 'lme4'. The output from this model was then represented in Table 1.

$$SS(\text{bin}1)_{i,h} \sim \beta 0 + \beta 1\,\text{treatment}_i + \beta 2\,\text{Hour of the day}_h + \beta 3(\text{Hour of the day}_h{}^{*}\,\text{treatment}_i) + \varepsilon \tag{2}$$

Spatio-temporal non-linear RDD: We modeled the change in the continuous daily pattern of SS between Treatment-PA and Control-CL, relative to the distance of the field site from the PA boundary (Equation (3)). The time of the day (*t*) was a continuous variable with 1440 units representing every minute of the 24 h period, for every 1 km bin, scaled to the treatment-PA boundary, which forms the break in management. We used five pairs of 1 km bins (0–1, 1–2, 2–3, 4–5, and 5–6 km) on either side of the break (total 10 bins). We ran this model using generalized additive mixed effect models using the mgcv package, by keeping sampling site (*i*) as a random variable (Butsic et al., 2017). The output from this model was used to represent the graphical representation of the discontinuity (Figure 2b).

TABLE 1 Difference in predicted soundscape saturation (SS) for each hour of the day between Control-CL and Treatment-PA.

	Treatment-PA versus Control-CL		
Hour	**Difference**	**95% CI**	***p* value**
0	20.78	19.28, 22.27	<.01
1	19.04	17.55, 20.53	<.01
2	16.93	15.41, 18.46	<.01
3	15.49	14.02, 16.95	<.01
4	20.43	18.96, 21.90	<.01
5	16.14	14.69, 17.60	<.01
6	9.55	8.02, 11.09	<.01
7	2.90	1.43, 4.36	<.01
8	8.22	6.73, 9.71	<.01
9	13.44	11.94, 14.94	<.01
10	16.12	14.52, 17.72	<.01
11	20.45	18.90, 21.99	<.01
12	23.23	21.69, 24.77	<.01
13	3.42	1.91, 4.94	<.01
14	−3.20	−4.51, −1.89	<.01
15	−3.11	−4.42, −1.79	<.01
16	−3.58	−4.91, −2.26	<.01
17	−4.21	−5.53, −2.90	<.01
18	8.37	6.91, 9.83	<.01
19	24.86	23.37, 26.35	<.01
20	18.87	17.38, 20.37	<.01
21	19.44	17.94, 20.94	<.01
22	15.06	13.59, 16.53	<.01
23	19.62	18.13, 21.10	<.01

Note: The difference in SS is within the 1 km bin (bandwidth) on either side of the treatment break (as visualized within Figure 2b). The positive value in the difference represents a higher value within Treatment-PA.

$$
\begin{aligned}
\mathrm{SS}_{i,t} \sim \beta 0 + \beta 1\ \mathrm{treatment}_i + f1\ \mathrm{Time\ of\ day}_t \\
+ f2(\mathrm{Time\ of\ the\ day}_t{}^{*}\ \mathrm{treatment}_i) + \varepsilon
\end{aligned}
\tag{3}
$$

2.6 | Difference in SS between Control-PA and Treatment-PA using back-door criteria

To study the effect of management between Treatment-PA and Control-PA, we used a similar approach to that as the difference between Control-CL and Treatment-PA (Equation (1)). We used non-linear models using generalized additive mixed effect models (Wood, 2017), with a separate intercept and slope model for each of the treatments. Based on the back-door criteria, in addition to the variable matching, we also statistically controlled for the possible effect of elevation and slope. Please refer to the Difference in SS between Control-CL and Treatment-PA section for the details on the model structure. We used our above model to first predict the SS (mean and 95% CI) for every minute for the day (m) for Treatment-PA and Control-PA. We used this model prediction to calculate the difference in mean SS, and to statistically test for the treatment effect.

2.7 | Arthropod community

To compare arthropod diversity between Treatment-PA and Control-CL sites, we used the iNEXT package in R (Hsieh et al., 2016), which applies rarefaction and extrapolation methods based on Hill numbers to standardize diversity comparisons across sampling efforts (34 vs. 12 sites between Control-CL and Treatment-PA, respectively). Presence-absence data was analyzed using the iNEXT() function with $q = 0$, 1, and 2, representing species richness, Shannon diversity, and Simpson diversity, respectively (Hsieh et al., 2016).

We modeled the difference in arthropod OTU community composition between Treatment-PA and Control-CL, under a model-based analysis of multivariate abundance data framework, using *mvabund* package in R (Wang et al., 2012). We used *manyglm ()* function to run generalized linear models to our high-dimensional relative-abundance data, and we checked if our model assumptions were met using the approached suggested in Wang et al. (2012). We then used *anova.manyglm()* function to test our hypothesis whether community composition was statistically different between the treatment and control. We used ecoCopula package in R (Popovic et al., 2019) to visualize the difference in community composition by using the output from mvabund.

3 | RESULTS

3.1 | Gola-REDD+ protected area compared to the community forest

Soundscape saturation (SS) was significantly higher during most of the day in the Treatment-PA than in the Control-CL mosaic community landscape (Figure 2a). There was a sharp discontinuity in SS at the boundary between Treatment-PA and Control-CL across most of the day (Figure 2b, Table 1). Averaging over the whole day, the Control-CL had significantly lower soundscape saturation (−12.8 percentage points, 95% CI: −2.0 and −23.7, $p = 0.021$) at the PA border compared to

Treatment-PA (Figure 2b). The discontinuity in SS was particularly significant during dawn and at night, with SS within Control-CL significantly lower compared to Treatment-PA (Figure 2c, Table 1). We found Control-CL to have higher soundscape saturation during afternoon, compared to Treatment-PA (Table 1).

We analyzed the eDNA meta-barcoding data in terms of arthropod community composition and OTU diversity. We found that the total arthropod OTU community composition was different between Treatment-PA and Control-CL (Deviance = 669.8, $p = 0.01$; Figure 2d). At the Order level, we found that Coleoptera and Lepidoptera OTU community composition differed between Treatment-PA and Control-CL, but Diptera and Hymenoptera OTU community did not (Table S2, Figure S2). We found that the total arthropod OTU diversity to be significantly higher within Control-CL than Treatment-PA (Table S3). We found Diptera and Lepidoptera orders to have higher species diversity measures within Control-CL than Treatment-PA, but we did not find a significant difference among Coleoptera and Hymenoptera orders in terms of diversity metrics (Table S3).

The main assumption required for our spatial RDD model to recover causal effects of REDD+ financing with area protection is that biodiversity outcomes would be smooth around the border of the Treatment-PA, in the absence of protection. This assumption could be violated if the government established the Treatment-PA boundary based on the pre-existing biodiversity level, which was in turn determined by another pre-existing variable (e.g., precipitation, elevation, or tree height). We conducted two placebo tests to evaluate the validity of this identifying assumption; in both cases, discontinuities at the border could indicate a potential violation. The first placebo test examines discontinuities in variables that could influence biodiversity at the PA boundary (Figure S3). Here we did not find a discontinuity in the placebo variables (see Section 2) elevation ($\beta = 0.011$, SE = 2.02, $p = 0.99$), slope ($\beta = -0.77$, SE = 0.38, $p = 0.05$), and precipitation ($\beta = 1.74$, SE = 3.215, $p = 0.58$); although the discontinuity in slope is statistically significant, the size of the coefficient (less than 1°) is ecologically insignificant. We also found a discontinuity in tree height of very small magnitude ($\beta = 1.04$, SE = 0.26, $p < 0.01$), with Treatment-PA having taller trees compared to the Control-CL (Figure S3). Overall, these results show that other important drivers of biodiversity differences (elevation, slope, and precipitation)—aside from those directly influenced by REDD+ financing (tree height)—do not vary sharply at the boundary; therefore, these covariates cannot be driving our results. The second placebo test evaluates discontinuities in biodiversity outcomes at an arbitrarily chosen distance cutoff from the PA boundary (Figure S4). Following (Imbens & Lemieux, 2008), we use the median distance of sites outside the PA as the treatment discontinuity; then, we repeat this analysis using the median distance for sites inside the PA (see Section 2). Using such arbitrarily chosen cutoff, we did not find a sharp discontinuity in SS across most time periods, within both Control-CL and Treatment-PA (Figure S4), except for the low acoustic activity afternoon period (Table 1) within the Treatment-PA.

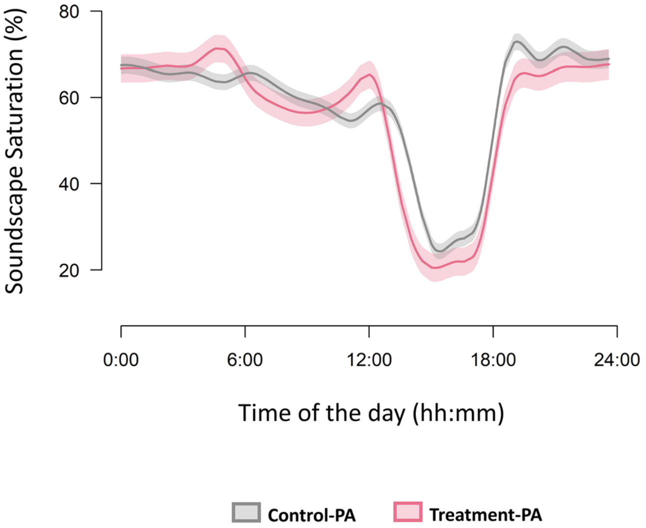

FIGURE 3 Effect of Treatment-PA (Gola Rainforest National Park receiving REDD+ financing) on vocalizing diversity, compared to the counterfactual, Control-PA (Gola Forest National Park not receiving REDD+ financing). Figure shows the modeled soundscape saturation over a 24-h period, with the line indicating the mean prediction and the shaded region representing the 95% confidence interval.

3.2 | Gola-REDD+ protected area compared to the non-REDD+ protected area

The total SS was on average similar in the Treatment-PA relative to the Control-PA (Figure 3, −4.3 percentage points, 95% CI: −3.9 and −4.5, $p = 0.041$). However, we observed two significantly higher peaks in SS in the Treatment-PA, indicating sharp increases in vocalizing species, before dawn (04:00–06:00 h) and during mid-day (11:00–13:00 h; Figures 3 and S5). During the afternoon and after dusk, the Control-PA had significantly higher SS (Figures 3 and S5).

Next, we analyzed specific frequency segments of the soundscape (see Section 2) following a similar method to Yoh et al. (2024), which signify different communities of vocalizing species based on their ecological and

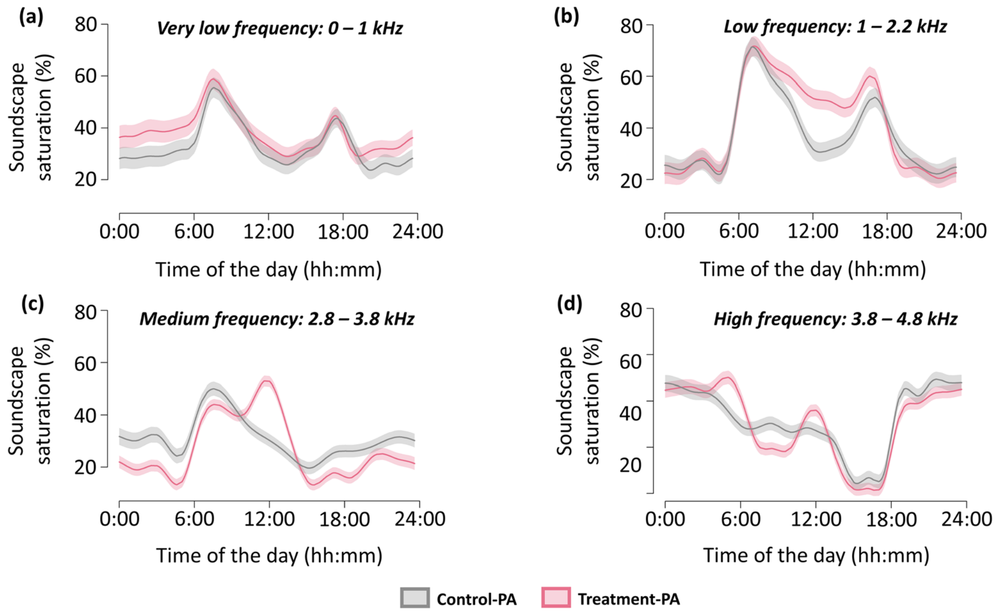

FIGURE 4 Modeled soundscape saturation for Treatment-PA and Control-PA within frequency segments over a 24-h period. The lines indicate the mean predictions and the shaded regions indicate the 95% confidence intervals.

evolutionary traits (Sagar et al., 2024). We found that the daily pattern of SS of these categories differed between Treatment-PA and Control-PA (Figure 4). Treatment-PA had a significantly higher SS for lower frequency categories (very low and low frequencies, Figure S6), and during mid-day (10:00–13:00 h) across most frequency categories (Figure S6). Additionally, in general we found Control-PA to have a significantly higher SS for medium and high frequency categories during early morning and dawn period (Figure S6c,d). When validating this finding through sonotypes analysis, we found that this difference in SS corresponded to a significantly higher number of sonotypes (unique sound types) of birds and arthropods (Figure S7).

4 | DISCUSSION

We evaluated the effectiveness of REDD+, one of the most widely used carbon financing strategies, in protecting tropical biodiversity beyond preventing deforestation using a quasi-experimental study design. We used soundscape saturation as a measure of vocalizing diversity, and e-DNA arthropod community diversity and composition as a complementary measure of biodiversity to examine whether a REDD+ financed PA (Treatment-PA) protected biodiversity more than (1) an unprotected community land (Control-CL) and (2) a PA without REDD+ finance (Control-PA). We find that REDD+ financing is associated with additional biodiversity co-benefits in the Treatment-PA compared to both control areas. Most studies that evaluate the effectiveness and biodiversity co-benefits of REDD+ use remote sensing data, focusing mainly on habitat-level measures, such as deforestation and forest degradation, with assumed co-benefits to the wider faunal community (Guizar-Coutiño et al., 2022; Malan et al., 2024; West et al., 2020). Our study provides crucial evidence on the impact of REDD+ financing on biodiversity that cannot be sensed remotely.

We find higher SS in the Treatment-PA compared to both control areas, although there were some differences in the magnitude and timing of these effects. First, we find that SS was higher on average in the Treatment-PA compared to the Control-CL (Figure 2). This effect is likely driven by habitat degradation and deforestation in the Control-CL area, which is associated with lower SS in tropical forests in prior studies, through changes in faunal communities such as birds (Burivalova et al., 2021, 2022). Bird communities have been documented to alter significantly, becoming simpler with less phylogenetic and functional diversity, even with slight levels of disturbance to forests (Burivalova et al., 2014; Şekercioğlu et al., 2002). Additionally, habitats disturbed through logging and agriculture also play a significant role in filtering the tropical faunal species towards a subset of more generalist species (Edwards et al., 2019; Hua et al., 2024; Srinivasan, 2013), which is then reflected within the saturation measure (Burivalova et al., 2021, 2022).

Second, we find that REDD+ has a positive effect on species that are acoustically active during pre-dawn and mid-day, by comparing the Treatment-PA to Control-PA (Figures 3 and S5). Segmenting the soundscape by frequency can yield insights into which taxonomic groups likely drive the differences in SS between the two protected areas (Figures 4 and S6). The pre-dawn peak in the Treatment-PA (and its absence in the Control-PA) is driven largely by differences in the high frequency sounds, and the midday peak is driven by medium and high frequency sounds. These medium and high frequency sounds are typically emitted by birds and invertebrates, respectively (Burivalova et al., 2022). Low and very low frequency categories, which had generally similar or slightly higher SS in the Treatment-PA (Figures 4 and S6), are typically emitted by larger-bodied birds and mammals (e.g. hornbills, turacos, owls, and monkeys) (Sagar et al., 2024). The biggest positive effect of REDD+ on these frequency categories was at night for the very low frequency (Figure S6a), and during the midday and afternoon for the low frequency (Figure S6b). Based on our results, REDD+ might have a negative effect on medium frequency species active during the afternoon and after dusk (Figure S6c). This could be driven by changes in arthropods and nocturnal mammals and birds such as the Western Tree Hyrax (*Dendrohyrax dorsalis*) and owl species.

During our limited manual, post hoc examination of whether the observed differences in SS between Treatment-PA and Control-PA, accurately reflected the differences in biodiversity between the two (Appendix S1), we found that the soundscapes of Treatment-PA had a higher number of unique bird and arthropod sounds—which could mean a higher number of species or higher abundance of species (Figure S7). With advances in machine learning and growing wildlife sound libraries, future analyses of our soundscapes data may be able to reveal which species contribute most to the difference in soundscapes through, for example, occupancy analysis (Brunk et al., 2023; Kahl et al., 2021). The possibility of such re-analyses highlights the advantage of collected soundscapes as a permanent record of vocalizing biodiversity (Burivalova, Game, & Butler, 2019).

Importantly, SS alone (or indeed any acoustic index), despite the measures taken during the PAM deployment (e.g. during the dry season; away from streams) and analysis (e.g., estimation of signal-to-noise ratio), can still be influenced by the environmental and human-made noise. Additionally, it does not capture less vocal species, such as certain large-bodied mammals (Zwerts et al., 2022). This limitation of bioacoustic data is particularly important in places that experience significant hunting of mammals. Although hunting pressure is correlated with reduced SS in Gabon (Yoh et al., 2024), the effects on less vocal species may be inadequately captured. The widespread demand for bushmeat within Sierra Leone and Liberia (Gray et al., 2018; Jones et al., 2017, 2019; Noss, 1998) and anecdotal field evidence from the study area—including observations of live snares (some containing trapped monkeys and duikers), encounters with spent shotgun shells, and recorded gunshots (personal observation, H.S.S.C.S.)—attest to hunting pressure in the Greater Gola landscape, despite anti-poaching patrols. Although our study demonstrates biodiversity benefits for vocalizing species, we did not explicitly measure potential effects of REDD+ on less vocal species, and so we cannot conclude whether REDD+ impacts wildlife via reduced hunting or not. We recommend future research to quantify hunting pressure and assess the effects of REDD+ on hunted species to understand its broader implications for biodiversity. Given the extensive baseline soundscape data collected under our quasi-experimental study design, such analyses could be conducted using targeted, machine-learning–based sound recognizers developed to detect gunshots and to identify acoustically active, commonly hunted species—such as Western Red Colobus (*Piliocolobus badius*)—within the Treatment-PA and Control-PA sites, thereby quantifying both hunting pressure and the responses of hunted faunal communities (Wood et al., 2023; Yoh et al., 2024).

In contrast to the SS results, our e-DNA analysis shows lower diversity and richness of arthropods in the Treatment-PA compared to the Control-CL, particularly among Coleoptera (beetles) and Diptera (flies) and Lepidoptera (winged insects, e.g., butterflies) communities, but not among Hymenoptera (e.g., bees, ants, and wasps) (Figures 2d and S2; Tables S2 and S3). This could be related to the higher habitat heterogeneity in the community landscape. Such heterogeneity commonly results from periodic forest disturbance and regeneration after logging, swidden agriculture, and agroforestry (Malan et al., 2024); the microclimatic heterogeneity that emerges through such disturbances can increase arthropod diversity (Marta et al., 2021). Research in other tropical forest landscapes such as Panama and Kenya has also linked change in vegetation structure and patch size of tropical forest to a change in arthropod diversity (Basset et al., 2015; Kung'u et al., 2023). Such situations—where one taxonomic group shows a positive response while another shows the opposite—are likely to become increasingly common as technological advances allow us to survey multiple groups simultaneously. As these heterogeneous patterns emerge more frequently, conservation decision-makers will need to develop approaches that can reconcile divergent responses across taxa and guide landscape-level management accordingly.

Causal interpretation of the results relies on several identifying assumptions. The matching methods we use to compare the Treatment-PA to the Control-PA require that no unobservable variable is driving differences in biodiversity between the treated and untreated areas, aside from REDD+ financing. We used Directed Acyclic Graphs (see Section 2) to identity these matching variables and rule out the non-confounding variables. The

RDD methods we use to compare the Treatment-PA to the Control-CL require that biodiversity levels would have been smooth across the PA boundary, in the absence of protection, as noted previously. Although the exact boundary of the protected area was not randomly assigned (RSPB, 2015), we use two placebo tests to show that the strategic placement likely does not violate this assumption. This method also requires that there is no spillover effect of treatment on untreated areas. If deforestation, hunting, or other downward pressures on biodiversity divert from the protected area to nearby unprotected areas, then our measured treatment effect would be biased upward (i.e., the PA looks better than it otherwise would because it is causing harmful outcomes in the control area). However, we see no evidence that this is happening. Deforestation rates in the Control-CL area are lower than in other community land areas in the region, not higher (Malan et al., 2024). These positive outcomes may be partially related to the fact that some REDD+ money flows into the Control-CL area (see Section 2), so it is not a perfect control. However, this spending would tend to bias our effects downward (i.e., in our case PA looks worse than it otherwise would because REDD+ is also benefiting the control area); therefore, our measured effect is likely a lower bound.

Finally, it is critical to contextualize what treatment effect we are measuring. First, the Treatment-PA comparison to the Control-PA captures the effect of REDD+ in isolation, whereas comparison to the Control-CL captures the effect of REDD+ combined with other potential benefits of protected area status. The former comparison addresses our research question more directly, but we argue that the latter comparison is also interesting and policy relevant, since most REDD+ schemes involve area protection. We conclude that protected area management coupled with REDD+ effectively protects biodiversity in addition to preventing deforestation; the additionality of REDD+ beyond protecting area alone was significant, but smaller. Our work shows that, in addition to delivering socio-economic benefits, the Gola-REDD+ project has been effective in protecting vocalizing biodiversity that might have otherwise been depleted or lost. This highlights its potential for broader landscape-scale conservation. Building on its success, similar initiatives could be replicated in the Gola Forest National Park (GFNP), our control protected area, and across the Greater Gola Landscape—expanding Gola-REDD+ into a multinational, transboundary effort to safeguard one of the largest remaining tracts of old-growth forest in the Upper Guinea region. Furthermore, the baseline data from our research provide a foundation to evaluate the effectiveness of such an expansion using a Before-After-Control-Impact (BACI) design. Additionally, we emphasize that each project must be monitored using targeted counterfactuals, rather than assuming that REDD+ is universally effective, as project-specific evidence is essential for informed management and adaptive decision-making.

Studies that evaluate the causal effects of conservation strategies on fauna in tropical forests are still rare (Buřivalová et al., 2023; Burivalova, Allnutt, et al., 2019; Zhang et al., 2023). The methods we develop here offer a generalizable framework for causal impact analysis of space-based conservation interventions, using increasingly adopted methods of biodiversity monitoring—soundscape and environmental DNA analyses. Our baseline biodiversity data can be repeated to study the efficacy of future management strategies. This paves the way towards an evidence-based approach to motivate and direct carbon finances towards projects that are committed to be not only good for the climate but also for biodiversity.

AUTHOR CONTRIBUTIONS

Conceptualization: HSSCS, ZB. Methodology: HSSCS, ZB, JR, DWY, AB, SJ. Investigation: HSSCS, BG, MEP, TB, MET, MAF, MN. Visualization: HSSCS. Funding acquisition: HSSCS, ZB, Project administration: FAE, FJS, SJ, TB, MET. Supervision: ZB, FAE, FJS. Writing – original draft: HSSCS. Writing – review & editing: HSSCS, JR, FAE, FJS, SJ, DWY, AB, MEP, TB, MET, BG, MAF, ZB.

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CONFLICT OF INTEREST STATEMENT

Several co-authors are employed by the organization that implements the intervention evaluated in this manuscript.

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DATA AVAILABILITY STATEMENT

All data and code will be made available upon request to the corresponding authors.

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SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

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