# Effects of Local- and Landscape-level Drivers in Influencing Bird Diversity and Persistence in Cashew Plantations of the Northern Western Ghats

by

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**in**
**Wildlife Science**

Under the supervision of

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# DECLARATION

I hereby declare that the work conducted under the thesis entitled **“Effects of Local- and Landscape-level Drivers in Influencing Bird Diversity and Persistence in Cashew Plantations of the Northern Western Ghats”,** is a record of original and independent research work done by me and subsequently submitted for the award of the degree of **Master’s in Wildlife Science** at the **Academy of Scientific and Innovative Research**. This research work has been carried out under the guidance and supervision of **Dr. Rajah Jayapal**, **Scientist (SACON),** and co-supervision of **Dr. Navendu Page**, **Scientist (WII)**, and **Dr. Rohit Naniwadekar, Scientist (NCF)**. The work has not formed the basis for the award of any other degree, diploma, or any other qualification. I also declare that the thesis embodies my own work, analysis, observation, understanding and the particulars given in it are true to the best of my knowledge.

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# CERTIFICATE

This is to certify that the thesis by **Nandita Madhu** entitled "**Effects of Local- and Landscape-level Drivers in Influencing Bird Diversity and Persistence in Cashew Plantations of the Northern Western Ghats"** is an original and independent research work submitted to the **Academy of Scientific and Innovative Research**, for the award of the degree of **Master's in Wildlife Science**.

**Nandita Madhu** has put one semester of research work embodied in this thesis under my guidance and supervision. The work presented in this thesis has not been submitted to any other University or Institute for the award of any degree, diploma or distinction.

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**Dr. Ruchi Badola**
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# CERTIFICATE OF PLAGIARISM CHECK

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It is the end of June 2024. The weather seems to be hitting the sweet spot when it is not as blistering hot as the summer and not as biting as the winter. Some days, it showers like there is no tomorrow. Today looks like such a day with the morning adorned with grey clouds. It is the perfect weather to write, the perfect time to put down in words whatever one must be feeling. Yet, here I am, utterly clueless on how to properly express my gratitude.

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## SUMMARY

Agricultural expansion is a significant driver of deforestation and biodiversity loss, particularly in the tropics. The Western Ghats-Sri Lanka biodiversity hotspot is no exception. Most forest patches in the northern Western Ghats are being cleared for cashew cultivation. However, here, cashew plantations host varying proportions of cashew and native trees and have varying extents of ambient forest cover. Investigating the effects of such local and landscape-level drivers across land use types on taxonomic, functional, and phylogenetic diversities, as well as species- and trait-specific responses of birds, as implemented in this study, can give comprehensive insights on the impacts of forest conversion. I conducted this study in the low-elevation forests and cashew plantation landscape of Tillari, Maharashtra. I compared tree species diversity and vegetation structural attributes across land use types using Hill-Shannon diversity and linear models (LMs). To assess how land use type affects bird species composition and taxonomic diversity, I used non-metric multidimensional sampling (NMDS) and Hill-Shannon diversity. To compare functional and phylogenetic impacts across land use types, I used SES (Standardised Effect Size) values of fMPD (functional Mean Pairwise Distance) and pMPD (phylogenetic Mean Pairwise Distance) for LMs and Tukey's post-hoc analysis. Using Hierarchical Modelling of Species Communities (HMSC), I looked for 1) bird species responses, 2) trait responses, and 3) a phylogenetic signal in the residuals. I collected bird and vegetation data from 100 points distributed across forest, mixed cashew plantations, and pure cashew plantations. My field collaborator (Vishal Sadekar) and I sampled vegetation within a 10 m radius of circular plots around all points. We sampled birds, implementing 10-minute point counts at a point, replicated 5 times across 4 months between January to May 2024. Vegetation differed significantly across all three land use types in terms of tree species diversity and tree height, where the forest had the highest estimates followed by mixed cashew. NMDS showed that the community in mixed cashew plantations overlapped with that of pure cashew plantations. There was no significant effect of land use type on functional diversity. But taxonomic and phylogenetic diversities were lowest in pure cashew. The HMSC model revealed a low explained variation (Tjur $R^2 = 0.1372$), but I found land use type, a site-level variable, to exhibit the highest explained variation of 58% compared to the landscape-level variables. Forest species like Malabar Trogon (*Harpactes fasciatus*) and Black-naped Monarch (*Hypothymis azurea*) responded negatively to mixed and pure cashew plantations. Species like Golden-fronted Leafbird (*Chloropsis auriforns*) and Tickell's Blue Flycatcher (*Cyornis tickelliae*) benefitted from mixed cashew and open country species like Indian Peafowl (*Pavo cristatus*) and Plain Prinia (*Prinia inornata*) responded positively to pure cashew. Trait response analysis revealed that evergreen species responded positively to the forest and negatively to both cashew habitats. Sedentary species responded positively to forest cover in 800 m. No evidence of a phylogenetic signal was found in the residuals ($\rho = 0.23$, 95% CI: 0 - 0.68). This study highlights the value of mixed cashew plantations which are more habitable than pure cashew plantations due to native tree prevalence. However, this study also emphasises that even mixed cashew plantations cannot replace forests as habitats for evergreen forest species. This message is now more crucial than ever in the light of ongoing forest clearance in the northern Western Ghats.

## INTRODUCTION

Habitat conversion to agriculture is one of the biggest threats affecting terrestrial biodiversity (Birch et al., 2024; Fischer et al., 2008). Production landscapes, taking up about 40% of the earth's landmass, are currently the single most significant land use in the world (Cannon et al., 2019), fast taking over the tropics. Demands are projected to increase by 30–62% by 2050 to meet the production needs of the growing human population (Rader et al., 2024; Van Dijk et al., 2021). Protected areas cover less than 12% of the Earth's surface, have limited geographic cover (Baldwin & Beazley, 2019), are often isolated,  are unevenly distributed, and often concentrated in the temperate and montane zones (Hoekstra et al., 2005). They, by themselves, are insufficient to conserve tropical wildlife in the long term (Anand et al., 2010). Therefore, in the face of ongoing agricultural expansion, it is imperative to determine factors that enable biodiversity to persist within production landscapes.

The expansion of monocultures and their intensification is known to impact biodiversity negatively (Castaño-Villa et al., 2019; Foley et al., 2005). Compared to conventional farming, agroforests that partially retain tree structure in hitherto tropical forest areas are often promoted to maintain species diversity and ecosystem function (e.g. carbon sequestration). However, high-intensity management of these agroforests by removing native trees may make these agroforests less suitable for harbouring bird diversity. For example, reducing native tree diversity has been documented to impact animal persistence in coffee plantations negatively (Ong'ondo et al., 2022). Along with site-level factors (e.g. structure and diversity of native plants at the site), landscape-level features may also influence retention of biodiversity (Ranganathan et al., 2010; Turner, 2005). Remnant habitats in predominantly agricultural landscapes can be critical for retaining biodiversity (Anand et al., 2010). Therefore, it is essential to determine the relative influence of local- and landscape-level features in helping sustain biodiversity in predominantly agricultural landscapes.

Traditionally, responses of anthropogenic activities on biodiversity have been examined from a taxonomic diversity lens. However, examining responses of functional and phylogenetic diversity to anthropogenic perturbations, which provide information on ecosystem function and evolutionary uniqueness, is increasingly being acknowledged (Chapman et al., 2017; Hanz et al., 2019). While the responses of taxonomic, functional and phylogenetic diversity to anthropogenic perturbations may be congruent, they have also been found to be differing, indicating differential impacts of anthropogenic perturbations on taxonomic (which considers all species equal), functional and phylogenetic diversity (Spasojevic & Suding, 2012). Moreover, while studies typically focus only on community measures like diversity metrics, it is critical to simultaneously examine species-specific responses. This can provide deeper insights on differing responses of community metrics. For example, forest specialist species may be replaced by open habitat species (e.g., ecological replacement of Crimson-backed Sunbird *Leptocoma minima*, a forest specialist, with Purple-rumped Sunbird *Leptocoma zeylonica* and Purple Sunbird *Cinnyris asiaticus* which are open habitat species), which may compensate for lost function leading to differing patterns in taxonomic and functional diversity. Similarly, replacement of endemic and forest specialist species of bulbuls belonging to different genera, like Grey-headed Bulbul *Microtarsus priocephalus* and Yellow-browed Bulbul *Acritillas indica* with Red-vented and Red-whiskered Bulbuls *Pycnonotus* spp. in open habitats may result in no change in taxonomic diversity but changes in phylogenetic diversity as two unique genera are filtered out from the community. Thus, examining species-level responses along with community metrics can help disentangle differential responses of community metrics to land use change.

The Western Ghats-Sri Lanka biodiversity hotspot is home to several endemic and threatened species (Myers et al., 2000). It is one of the eight hottest biodiversity hotspots as well as one of the most densely populated (Cincotta et al., 2000). The Western Ghats, in particular, constitutes less than 6% of India’s landmass but harbours more than 30% of floral and faunal species in the country (Das et al., 2006). However, forest loss has been so rapid here that only about 6.8% of its primary vegetation exists currently (Myers et al., 2000). This region has been cultivated for well over 2000 years (Ranganathan et al., 2008) and much of this forest loss has been attributed to agroforestry plantations. While tea, coffee and rubber are predominant agroforestry crops in central and southern Western Ghats, mango and cashew are dominant agroforestry crops in the more seasonal northern Western Ghats. The impacts of conversion to coffee and tea are relatively well-studied (Anand et al., 2008; Chettri et al., 2018; Karanth et al., 2016; Pawar & Sadekar, 2023; Raman, 2006; Raman et al., 2021; Ranganathan et al., 2010; Sidhu et al., 2010; Sreekar et al., 2013), but our understanding of the impacts of agroforestry plantations like cashew have received relatively less attention (but see (Munje & Kumar, 2022; Rege et al., 2020). This is particularly important since the impacts of different forms of agroforestry plantations on biodiversity can vary, depending on the nature of their impact. For example, conversion to coffee may entail retaining native tree cover, while conversion to tea, at least of conventional variety, results in very sparse tree cover, often monospecific and composed of non-native shade trees like *Grevillea robusta* (Raman et al., 2021; Sidhu et al., 2010).

The more seasonal northern Western Ghats (Das et al., 2006) are home to several endemic and threatened fauna (Biswas et al., 2024). Unlike the central and southern Western Ghats, where Protected Areas cover low-elevation sites, most of the Protected Areas in the northern Western Ghats are in high elevations (Sahyadri Tiger Reserve and Radhanagari and Bhimashankar Wildlife

Sanctuaries) with most low-elevation areas being privately-owned. While 10% of Sindhudurg District is under Reserved Forests, less than 1% of forested area of the Ratnagiri District is under the Forest Department. These low-elevation forests are critical for threatened and endemic birds as shown by recent studies (Biswas et al., 2023; Mudappa & Raman, 2009; Pawar & Sadekar, 2023). Such private forests are vulnerable to degradation, habitat conversion and loss (Kulkarni & Mehta, n.d.). Forest conversion to cashew is happening here at an alarming rate and on a large scale. A recent study reported that close to one-third of the geographical area of two taluks in Sindhudurg district has been converted to cashew (Rege & Lee, 2023). Given that most land in the northern Western Ghats is privately owned and government policies encourage conversion to cashew and mango (Rege & Lee, 2022), an increasing amount of area will be covered by cashew plantations in the near future. Therefore, it is critical to identify measures that can make these monocultures more biodiversity friendly.

Cashew is a perennial, globally dominant, drought-resistant, tree-based crop that can fully mature within 7–10 years. The cultivar varieties can grow fully and provide fruit within 3–4 years. Due to its high yield, high profit, low maintenance, tolerance of nutrient-deficient soils and ability to grow across wide elevational gradients, it is widely grown in 33 countries of the tropics (Rege & Lee, 2023). India is the second largest cashew producer, with Maharashtra, Goa, Andhra Pradesh and Orissa as the primary states for cultivation. Recent studies have documented the negative impacts of cashew plantations on wildlife such as mammals, birds, and anurans (Biswas et al., 2023; Komanduri et al., 2023; Lad et al., 2024; Munje & Kumar, 2022; Rege et al., 2020). However, in Sindhudurg district of Maharashtra, it is not uncommon to find native varieties of cashew being grown among native trees. Moreover, there are still patches of forest that continue to harbour large mammals (e.g., tiger *Panthera tigris*, elephants *Elephas maximus*) and threatened and/or endemic birds (e.g., Great Hornbill *Buceros bicornis*, Malabar Imperial-pigeons *Ducula cuprea*, Nilgiri Wood-pigeon *Columba elphinstonii*). This provides an interesting opportunity to explore the role of native trees and landscape level features in harbouring bird diversity in cashew agroforestry plantations. This information can feed in conservation planning and management and ongoing restoration efforts in the region.

Birds are a suitable taxon as they have broad niche ranges, are good ecological indicators (M. L. Rurangwa et al., 2022), provide ecosystem services such as pollination, seed dispersal, pest control, and nutrient deposition (Sekercioglu, 2006, 2012), and are relatively easy to spot, identify and study due to their close and strong associations with their niches and ecological functions (Pigot et al., 2020). Moreover, there is excellent data available on functional traits and phylogenetic relationships of birds allowing reliable examination of functional and phylogenetic responses to anthropogenic perturbations.

Given this background, I asked the following questions in predominantly cashew agroforestry dominated landscape with remnant forest patches: 1) How does taxonomic, functional and phylogenetic diversity and composition of birds differ between forests, mixed-cashew plantations and pure-cashew plantations? 2) What are the species- and trait-specific responses to local and landscape-level factors and do phylogenetic relationships influence these species responses? To this end, I used point count sampling method to collect data on birds from pure and mixed cashew plantations (plantations where cashew is planted with native trees) and forests. I did vegetation sampling at the point to understand local or site-level characteristics and used a land use land cover map based on a recent study (Rege & Lee, 2022) to determine the influence of landscape-level characteristics. I used different diversity metrics and a joint species distribution modelling approach to determine responses of birds to local- and landscape-level predictors.

## METHODS

### Study Area

I conducted the study from January to May 2024 in the low-elevation forests and cashew plantations in Dodamarg tehsil of Sindhudurg district of Maharashtra. This area forms the northern part of the Western Ghats-Sri Lanka Biodiversity Hotspot, known for high levels of species endemism. This area is at an important biogeographic boundary (Goa Gap) as range limits of several species of endemic vertebrates (e.g. *Micrixalus uttaraghati*, *Draco dussumieri*, *Hypnale hynale*), including birds (*Tephrodornis sylvicola*, *Microtarsus priocephalus*) lie in this region. The average annual rainfall of this region is about 3500 mm, and the annual temperature ranges between 12–40°C (Munje & Kumar, 2022). The dominant vegetation type in these lower elevations is moist deciduous forest with patches of semi-evergreen and evergreen forests. Historically, these forests likely harboured evergreen forests that have now been converted to deciduous to repeated clear felling (Biswas et al., 2024). The evergreen forest patches harbour trees like *Beilschmiedia dalzellii*, *Dysoxylum gotadhora*, *Knema attenuata*, *Elaeocarpus variabilis*, *Garcinia gummi-gutta*, *Hydnocarpus pentandrus*, *Saraca asoca* among others, while the disturbed forest patches harbour trees like *Tectona grandis*, *Terminalia elliptica*, *Terminalia paniculata*, *Terminalia bellirica*, *Syzygium cumini*, *Schleichera oleosa*, and *Careya arborea* (Biswas et al., 2024). The area harbours the northernmost patches of *Myristica* swamps (Sreedharan & Indulkar, 2018), one of which was discovered recently (Desai et al., 2024). The Reserved and Private Forests in the region serve as an important wildlife corridor between three protected areas: Radhanagari Wildlife Sanctuary of Maharashtra, Mhadei Wildlife Sanctuary of Goa, and Kali Tiger Reserve of Karnataka. The Reserved Forests are part of the Sawantwadi Forest Division, and some portions of these Reserved Forests have been declared as Conservation

Reserves, thereby giving them additional protection (Pawar & Sadekar, 2023; Punjabi & Rao, 2017). Past studies in the region have highlighted the critical role of these low-elevation forests in harbouring bird biodiversity (Biswas et al., 2023; Munje & Kumar, 2022).

Only 10% of the geographic area is under the Protected Area network in the Western Ghats. Moreover, the distribution of the Protected Area network is biased towards high elevations, especially in the northern portion of the Western Ghats. Most of the Protected Areas in northern Western Ghats (Sahyadri Tiger Reserve, Radhanagari Wildlife Sanctuary, Bhimashankar Wildlife Sanctuary) are in the high elevations. The low-elevation forests are being degraded or converted to agroforestry plantations at an alarming rate. About a third of the geographic area of Sawantwadi and Dodamarg Tehsil is under cashew cultivation, highlighting the need to determine local and landscape-level effects of cashew on biodiversity (Rege & Lee, 2022). The pure cashew plantations using hybrid cultivars are increasingly replacing the traditional method of growing cashew trees amidst native trees. Unlike local cashew trees, the cultivar cashew does not grow tall but instead spreads, making it easier for cashew picking. Given that the area will experience an expansion of cashew plantations, it is critical to determine the role of native trees within cashew plantations (local-level factors) and the presence of forest patches (landscape-level factors) in helping retain bird biodiversity in this region.

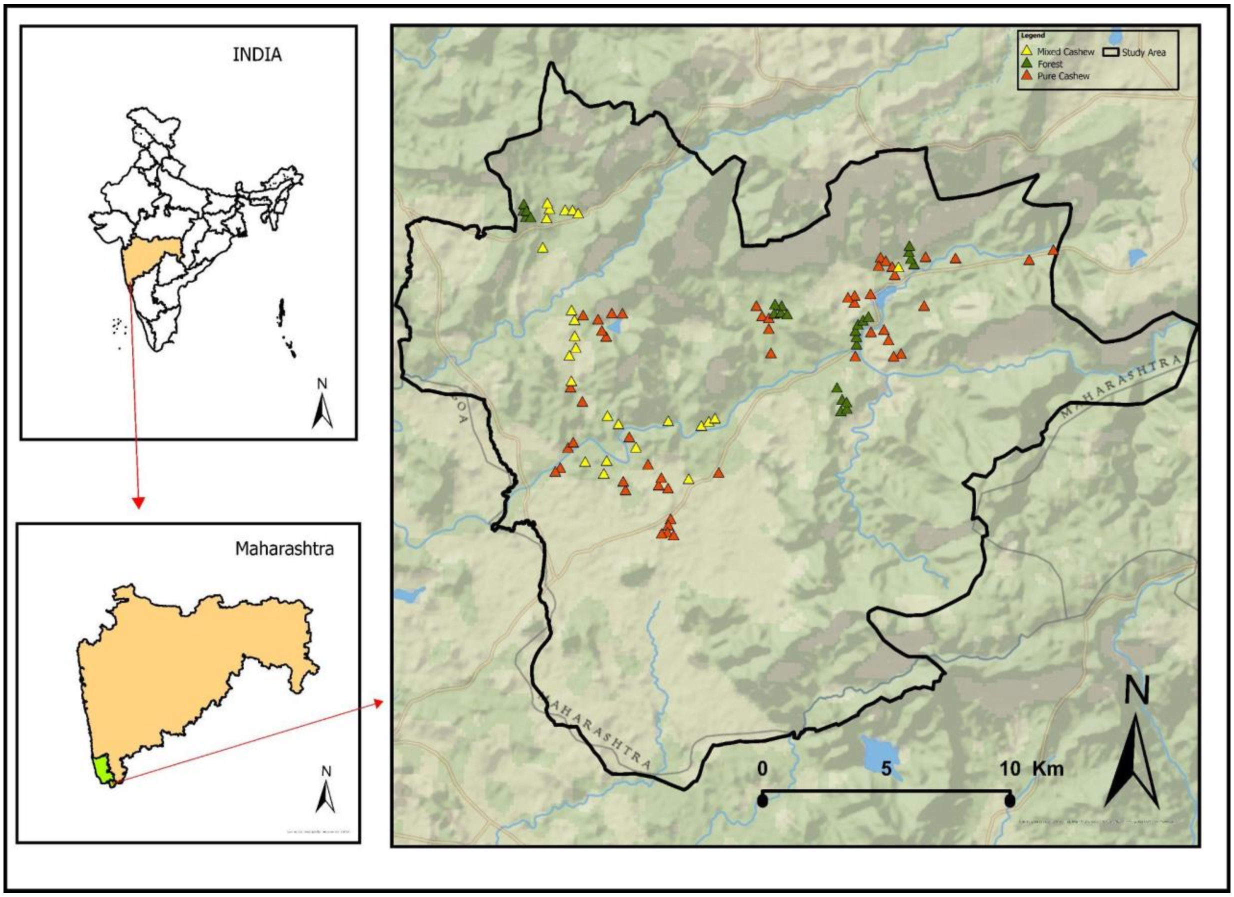


**Figure 1.** Map of my study area in Dodamarg, Maharashtra, displaying all 100 sampling point locations.

## Sampling design

### Bird sampling

To determine the diversity and abundance of birds, my field collaborator (Vishal Sadekar) and I conducted variable-width point count surveys at 100 points (spatial replicates = 100). We sampled each of the 100 points five times (temporal replicates = 5) between January and April 2024. The 100 points were distributed across pure cashew plantations (50 points), mixed-cashew plantations (25 points) and forests (25 points). Sampling was carried out in the mornings between 0645–1000 hr. Two points were separated by at least 250 m. We recorded species identity, number of individuals, sighting distance if seen, and sighting distance class if heard. I only included birds detected within 100 m of the point for analysis.

### Vegetation sampling

At each of the 100 points where we conducted bird sampling, we established 10-m radius circular plots to determine the influence of site-level factors on bird diversity and prevalence. In each plot, we recorded the number of woody plants (≥ 30 cm girth at breast height), species identity, girth, tree height, canopy cover, and shrub cover. Using this information, we estimated structural attributes of the site like tree density per ha, basal area ($m^2$ $ha^{-1}$), tree height (m), canopy cover (%), and tree species richness across the three land-use categories (forest, mixed-cashew and pure cashew plantations).

### Functional trait data

I obtained functional trait data from three sources. The morphological trait data was obtained from AVONET (Tobias et al., 2022), the dietary trait data from Elton Traits (Wilman et al., 2014), and habitat preferences of birds from (Ali & Ripley, 1999). I checked for correlation between bird traits using Pearson's correlation (Figure 6). Bird traits like beak width, tarsus length and hand-wing index are associated with diet and locomotion in birds (Pigot et al., 2020). Similarly, insectivorous, frugivorous and forest-specialist birds are known to be negatively impacted by habitat modification. In contrast, habitat modification positively affects granivorous birds (Biswas et al., 2023).

### Phylogenetic data

I obtained 100 Bayesian phylogenetic trees from birdtree.org (Jetz et al., 2012), following the Ericson backbone (Ericson All Species: a set of 10,000 trees with 9993 OTUs each). Using these trees, I obtained a maximum clade credibility tree for further analysis, i.e. estimating the mean pairwise phylogenetic diversity and joint species distribution modelling.

### Landuse Landcover Data

Apart from site-level factors, the amount of habitat at the landscape level also impacts bird prevalence (Fahrig, 2013). A recent study used RS-GIS to estimate the amount of forest and cashew cover in Dodamarg and Sawantwadi Tehsils (Rege et al., 2022). I obtained the amounts of forest and cashew cover around each sampling point within a pre-defined buffer radius (see below for methodological details of the choice of buffer radius) using the land use landcover raster as generated by (Rege et al., 2022) (Fig. S1).

### Analytical methods

I conducted all the analyses in R version 4.4.0 (R Core Team, 2024).

### Tree species richness and vegetation structure attributes

To determine differences in tree species richness across land-use categories, I used the Hill-Shannon diversity measure (q=1), employing the sample-coverage-based-rarefaction method, using the *‘estimateD’* function of the ‘iNEXT’ package (Roswell et al., 2021). (Roswell et al., 2021) recommend the Hill-Shannon diversity measure that focuses on the diversity of common species likely to be using the habitat to compare diversity across multiple categories. I bootstrapped the data 1000 times to estimate 95% confidence intervals (CIs). I inferred statistical differences between categories if the 95% CI did not overlap following (Cumming et al., 2007).

To determine differences between site-level vegetation structural attributes like tree density, basal area, tree height, and canopy cover across land-use categories, I used general linear models (Gaussian error distribution). I tested for normality of each attribute using Shapiro-Wilk's test and log-transformed non-normal attributes to approximate normality. I estimated marginal means and assessed pairwise contrasts using Analysis of Variance (ANOVA) and Tukey's post-hoc tests. I estimated bootstrapped 95% CI using 'boot' and 'confint' functions of R-packages 'boot' and 'car' (Fox et al., 2001).

### Bird composition and diversity

For the analysis of bird diversity and composition, I only included terrestrial birds detected within 100 m of the point. I excluded wetland birds from the analysis as my study focused on understanding the impacts of land use change on terrestrial and forest-dwelling birds.

### Selection of landscape variables

The landscape-level predictors we selected for the study were the amounts of forest and cashew cover around a point within a buffer radius. I extracted the percentages of forest and cashew cover around the 100 points in different buffer radii (from 100 to 3000 m at 100 m intervals) using R. I examined the best scale of effect by using an approach outlined by (Fahrig, 2013) and implemented by (Bonfim et al., 2024). This method estimates the relationship between a diversity metric (species richness, in this case) and habitat amount (amount of forest cover, in this case) using $R^2$ values. The buffer radius at which the relationship between species richness and habitat amount was strongest was selected as the buffer to estimate forest and cashew cover (Figure 3).

### Bird composition

I used the function *metaMDS* from the R package 'vegan' on bird abundance data (Oksanen et al., 2001). I pooled data across the temporal replicates for each point for this analysis. I examined differences in bird composition across land-use types (forest, mixed cashew, and pure cashew) by using non-metric multidimensional scaling (NMDS) with the Bray-Curtis dissimilarity index. I used three-dimensional ordination due to the high-stress score (>0.2) generated by the two-dimensional ordination.

### Taxonomic, functional, and phylogenetic bird diversities

I used the sample-coverage-based rarefaction method to compare the taxonomic diversity of birds across land use types. I estimated the sample coverage of each land use type.The sample coverage was very high (> 0.99), indicating adequate sampling. Equal sample coverage is increasingly advocated for comparing diversity across different communities rather than sample sizes (Chiu, 2023). Therefore, I used sample coverage of 0.9919 (the sample coverage for the forest habitat which was the least among the three categories) to compare diversity using the *'estimateD'* function from R package iNEXT. I bootstrapped the data 1000 times to obtain 95% CIs. I inferred statistical differences between the three land use categories if the 95% CI did not overlap, following (Cumming et al., 2007). For this analysis, data across all temporal replicates was pooled.

I checked for correlations between bird traits using Pearson's correlation, and used uncorrelated traits for further analysis. Correlated traits should be avoided to avoid inflating their influence on functional diversity metrics. I used the maximum clade credibility tree (as described above) to estimate phylogenetic diversity.

To ensure that I estimate functional and phylogenetic diversity using similar methods, I used Mean Pairwise Distance (MPD). This tree-based metric averages the functional or phylogenetic distances between all possible species pairs to estimate the observed value of functional or phylogenetic diversity for each sampling point. I used the unweighted pair group method for constructing a tree based on functional traits. To account for the influence of varying species richness on functional and phylogenetic MPD values, I estimated standardised effect sizes of the MPD values. This also allows us to infer the role of environmental filtering (if the SES values are negative, it is evidence of environmental filtering) and competition (if the SES values are positive, it is evidence of overdispersion) in structuring communities (Chapman et al., 2017). I used functions *'vegdist'*, *'hclust'*, *'as.phylo'*, and *'ses.mpd'* from R packages 'vegan', 'ade4', and 'picante' for this analysis (Kembel et al., 2010).

To determine differences between SES-fMPD (functional diversity) and SES-pMPD (phylogenetic diversity) across land-use categories, I used general linear models (Gaussian error distribution). I tested for normality using the Shapiro-Wilk's test and square-root-transformed them to approximate normality. I estimated marginal means and assessed pairwise contrasts using ANOVAs and Tukey's post-hoc tests. I estimated bootstrapped 95% CI using 'boot' and 'confint' functions of R-packages 'boot' and 'car' (Fox et al., 2001).

## Species and trait responses

While the previous analysis allowed me to examine community-level patterns, I used the Hierarchical Modeling of Species Communities (HMSC) framework (Ovaskainen & Abrego, 2020), a Joint Species Distribution Modeling (JSDM) approach, to determine 1) species responses to local and landscape predictors, 2) trait responses to local and landscape predictors, and 3) phylogenetic signal in responses of species to predictor variables. We excluded rare species (occurring in less than 5% of the points) from the analysis since they provide little information on community assembly processes and pose problems for MCMC (Markov Chain Monte Carlo) convergence (Ovaskainen & Abrego, 2020). I used the bird trait data and phylogenetic tree for this analysis.

I used the R package 'Hmsc' to fit the model in a Bayesian framework using prior distributions (Tikhonov et al., 2019). We modelled species and trait responses as a function of local (land use type: forest, mixed cashew and pure cashew) and landscape predictors (forest cover in 800 m and cashew cover in 800 m). I incorporated the location of each sampling point as a random effect to account for spatial autocorrelation explicitly. Using a presence-absence model with a probit link, I modelled occurrence probabilities of 70 out of the 102 species (which occurred in more than 5% of sampling points). I sampled posterior distributions with three MCMC chains, thinned by 1000, to achieve 250 samples for each chain. The first 50,000 samples were removed as burn-in. I obtained the beta coefficients for all bird species across predictors. I also assessed the trait responses to predictors. I sought evidence of a phylogenetic signal in the residuals by assessing the posterior distribution and 95% credible intervals of the phylogenetic signal parameter ‘ρ’.

## RESULTS

### Tree species richness and vegetation structure attributes

I enumerated 637 trees of 56 species belonging to 29 families across our 100 (10-m circular radius) plots (Table S1). Forest had 2.3- and 18-times higher tree diversity than mixed-cashew and pure-cashew plantations, respectively (Fig. 2; Table S2). Forests had higher tree density, basal area, tree height, and canopy cover than pure-cashew plantations and higher high tree height and canopy cover than mixed-cashew plantations (Fig. 2; Table S3 and S4).

| Structural attribute | Df | F value | Pr (>F) |
|---|---|---|---|
| Tree density per hectare | 2 | 17.27 | < 0.001 |
| Basal area | 2 | 28.25 | < 0.001 |
| Tree height | 2 | 93.89 | < 0.001 |
| Canopy cover | 2 | 7.539 | < 0.01 |

Table 1. ANOVA statistics of land use type for each structural attribute

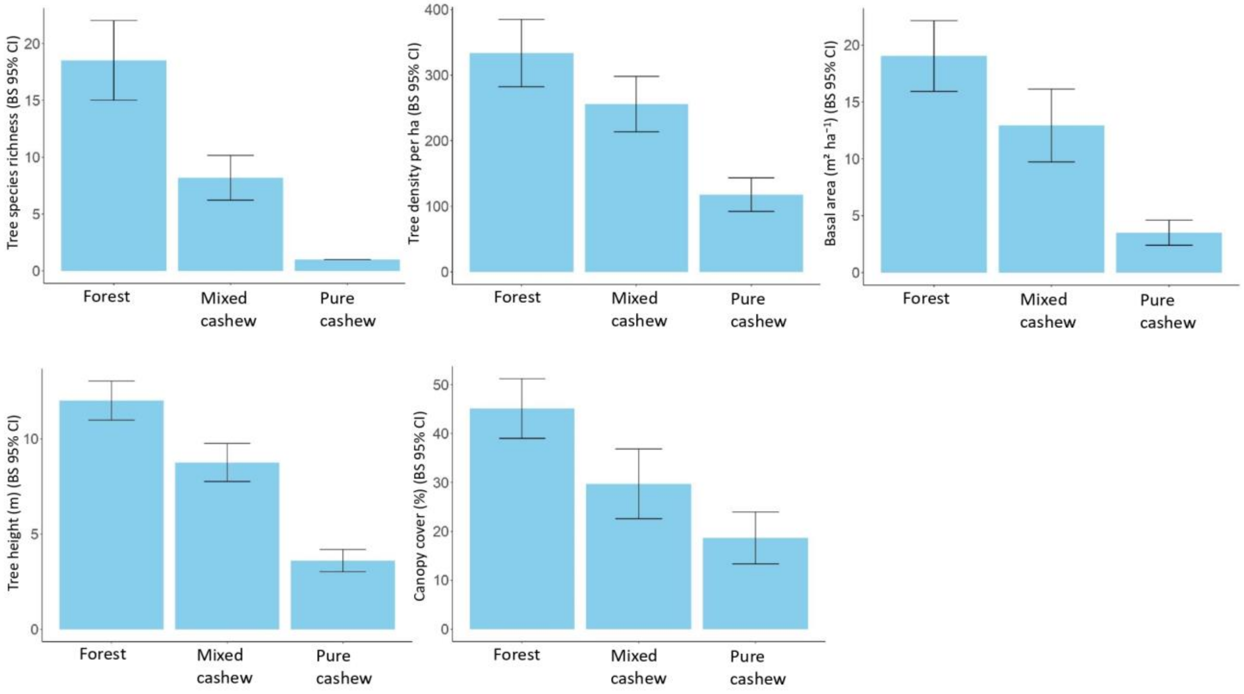


**Figure 2**. Bar plots comparing tree species richness and vegetation structural attributes across the land-use categories. Error bars represent bootstrapped (n = 1000) 95% CIs.

### Bird composition and diversity

I recorded 6735 individuals of 102 species of birds belonging to 38 families (Table S5).

### Selection of landscape variables

The relationship between the observed species richness at a point with the amount of surrounding forest cover peaked at 100, 200, and 800 m (Fig. 3). We decided to choose forest cover and cashew cover in 800 m circular radius along each sampling point as our landscape-level predictors. Since we had already sampled for vegetation diversity and structure at each point, we had relevant and finer-level information at the local scale. Therefore, we did not choose the forest and cashew cover amount at 100 or 200 m circular radii as predictor variables.

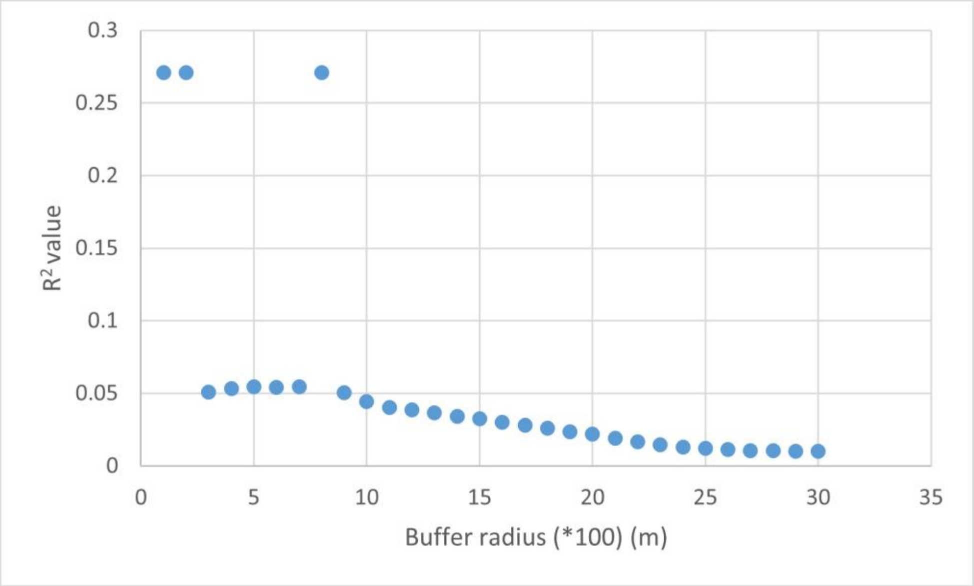


**Figure 3.** $R^2$ values for models testing for association between species richness and amount of forest cover at different buffer radii (100 m to 3500 m around each sampling point). I did this to determine the optimum buffer radius for landscape-level variables following the scale-of-effect approach suggested by (Fahrig, 2013)).

### Bird composition

The NMDS analysis showed that the composition of birds differed across land use types (ANOSIM statistic $R = 0.589$; $p = 0.001$, perMANOVA $R^2 = 0.245$, df = 2, $F = 16.081$, $p = 0.001$).

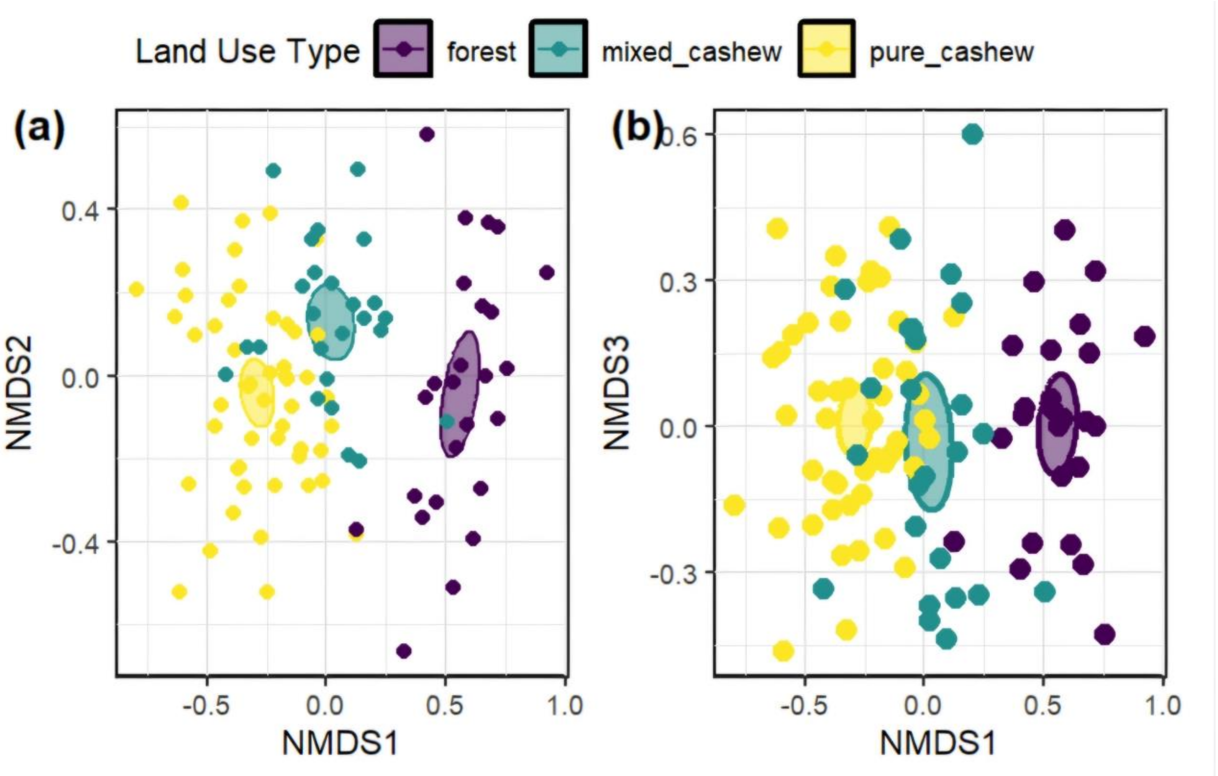


**Figure 4.** NMDS plots showing dissimilarities in species composition of birds between the three land-use types of the northern Western Ghats. Ellipses represent 95% CIs.

## Bird diversity

### Taxonomic

Mixed cashew plantations and forests had ~1.3 and ~1.2 times higher Hill-Shannon diversity than pure cashew plantations (Fig. 5a; Table S6). The mean Hill-Shannon diversity in mixed cashew was higher than in forests. However, the bootstrapped 95% CI overlapped.

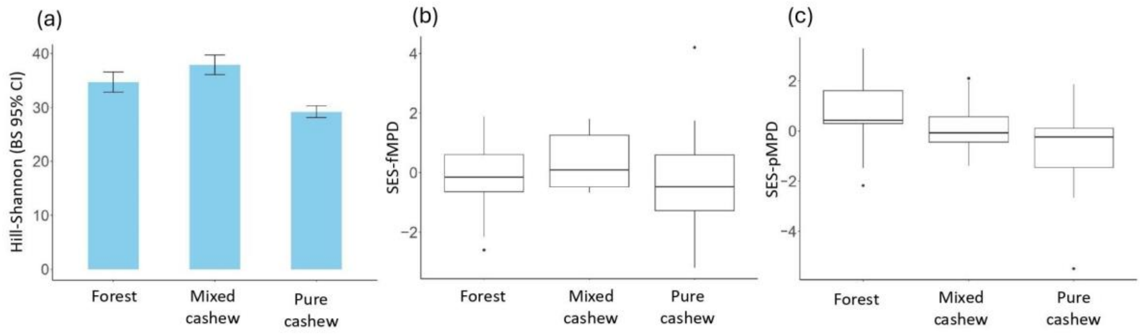
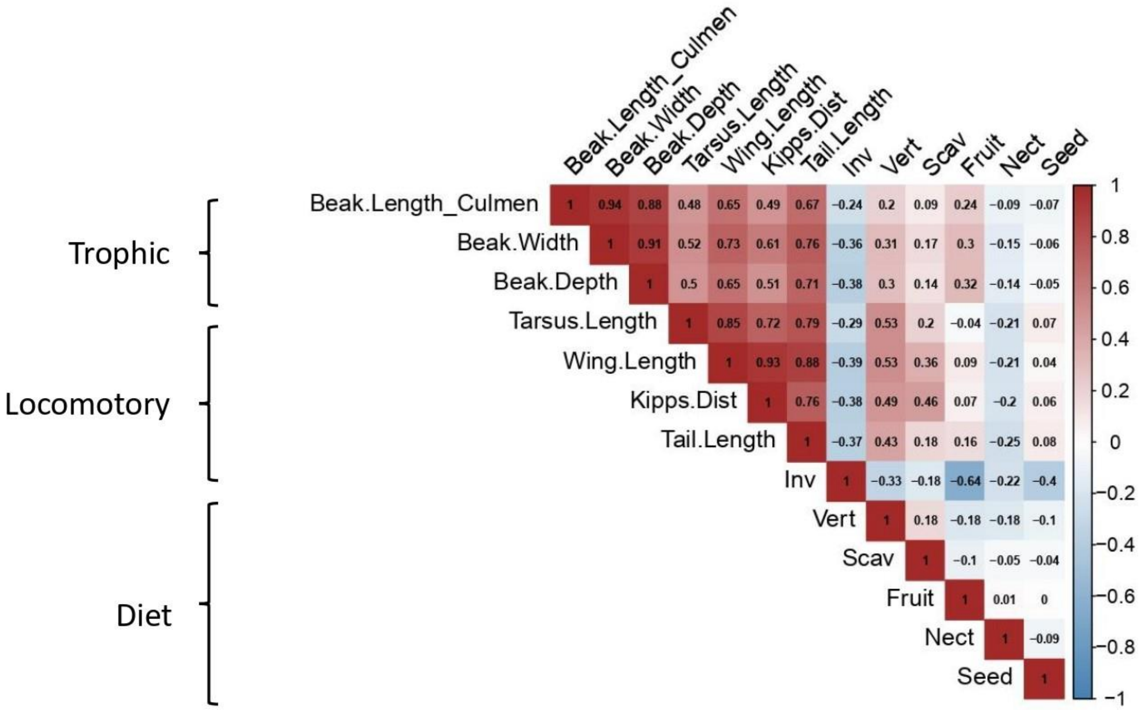


**Figure 5**.Taxonomic (Hill-Shannon) (a), functional (SES-fMPD) (b), and phylogenetic (SES-pMPD) (c) diversities across and use types. SES - Standardised Effect Size. fMPD - Functional Mean Pairwise Distance. pMPD - Phylogenetic Mean Pairwise Distance. Values above zero indicate overdispersion and values under zero indicate clustering in the community.

### Functional and phylogenetic

### Selection of traits

Beak length (culmen), beak width, and beak depth were highly correlated with each other. Tarsus length, wing length, Kipp’s distance, and tail length were highly correlated with each other (Fig. 6). We used beak width, tarsus length, Kipp’s distance, all diet-related variables, migratory status, and habitat preference (evergreen/deciduous) as traits for further analysis.



| | Beak.Length_Culmen | Beak.Width | Beak.Depth | Tarsus.Length | Wing.Length | Kipps.Dist | Tail.Length | Inv | Vert | Scav | Fruit | Nect | Seed |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Beak.Length_Culmen | 1 | 0.94 | 0.88 | 0.48 | 0.65 | 0.49 | 0.67 | −0.24 | 0.2 | 0.09 | 0.24 | −0.09 | −0.07 |
| Beak.Width | | 1 | 0.91 | 0.52 | 0.73 | 0.61 | 0.76 | −0.36 | 0.31 | 0.17 | 0.3 | −0.15 | −0.06 |
| Beak.Depth | | | 1 | 0.5 | 0.65 | 0.51 | 0.71 | −0.38 | 0.3 | 0.14 | 0.32 | −0.14 | −0.05 |
| Tarsus.Length | | | | 1 | 0.85 | 0.72 | 0.79 | −0.29 | 0.53 | 0.2 | −0.04 | −0.21 | 0.07 |
| Wing.Length | | | | | 1 | 0.93 | 0.88 | −0.39 | 0.53 | 0.36 | 0.09 | −0.21 | 0.04 |
| Kipps.Dist | | | | | | 1 | 0.76 | −0.38 | 0.49 | 0.46 | 0.07 | −0.2 | 0.06 |
| Tail.Length | | | | | | | 1 | −0.37 | 0.43 | 0.18 | 0.16 | −0.25 | 0.08 |
| Inv | | | | | | | | 1 | −0.33 | −0.18 | −0.64 | −0.22 | −0.4 |
| Vert | | | | | | | | | 1 | 0.18 | −0.18 | −0.18 | −0.1 |
| Scav | | | | | | | | | | 1 | −0.1 | −0.05 | −0.04 |
| Fruit | | | | | | | | | | | 1 | 0.01 | 0 |
| Nect | | | | | | | | | | | | 1 | −0.09 |
| Seed | | | | | | | | | | | | | 1 |

**Figure 6.** Correlation biplot depicting correlations among traits. Values inside boxes represent Pearson's correlation coefficients. The scale indicates a positive to negative gradient in correlation coefficients. Inv: percentage invertebrates in diet, Vert: percentage vertebrates in diet, Scav: percentage scavenging, Fruit: percentage fruit in the diet, Nect: percentage nectar in the diet, Seed: percentage of seeds in the diet. The morphological traits were sourced from AVONET (Tobias et al., 2022), dietary traits were sourced from (Wilman et al., 2014).

## Functional and phylogenetic diversities

Functional diversity did not differ between the three land use types (Fig. 5b; Table S7 and S8). However, phylogenetic diversity in pure cashew plantations was significantly lower than in mixed cashew plantations and forests (Fig. 5c; Table S7 and S8). Mixed cashew and forest did not differ significantly in phylogenetic diversity. Forest and mixed cashew tended to have phylogenetically overdispersed communities, indicating high phylogenetic diversity.

| Diversity metric | Df | F value | Pr (>F) |
|---|---|---|---|

| | | | |
|---|---|---|---|
| SES-fMPD | 2 | 2.513 | 0.0863 |
| SES-pMPD | 2 | 3.918 | 0.026 |

Table 2. ANOVA statistics of land use type for functional and phylogenetic diversity metrics.

**Species and trait associations with predictors and phylogenetic signal in the residuals**

Out of the 102 species, 70 were included in the analysis since the rest of them were rare (occurring in less than 5% of samples). The potential scale reduction factor was 1.0135 (0.9972 – 1.0905), suggesting MCMC convergence. The HMSC model explained an average variation of 13.7% (*Tjur* $R^2$ = 0.1372) across the 70 species (Fig. 7; Table S9). Fixed effects explained 85.9% of the total variation while the remaining 14.1% was explained by the spatial random effect (Fig. 7). Among the fixed effects, land use type, a site-level predictor, accounted for the highest explained variation (58%) in species occurrences, followed by the landscape-level predictors - cashew cover in 800 m (mean = 15%), and forest cover in 800 m (12.9%), highlighting the greater importance of site-level characteristics on bird occurrence vis-a-vis landscape level covariates. For 56 out of the 70 species, 50% or more of the variation in their occurrences were explained by land use type alone (Table S9).

Probability of occurrence of 18 species was lower in pure cashew plantations than forests (Fig. 7 and 10). This included large-bodied and endemic species like the Malabar Grey Hornbill *Ocyceros griseus* and Grey-fronted Green-Pigeon *Treron affinis* and wide-ranging small-bodied species like the Large-billed Leaf Warbler *Phylloscopus magnirostris*. Interestingly, the probability of occurrence of 11 species was lower in mixed cashew plantations than in forests, suggesting filtering out of species even in cashew plantations with native trees. This included species like the Malabar Trogon *Harpactes fasciatus*, Malabar Flameback *Chrysocolaptes socialis*, Yellow-browed Bulbul *Acritillas indica*, Indian Paradise Flycatcher *Terpsiphone paradisi*, Black-naped Monarch *Hypothymis azurea.* On the other hand, the probabilities of occurrence of open habitat species like the Red-vented *Pycnonotus cafer* and Red-whiskered Bulbul *Pycnonotus jocosus*, *Prinia* spp., Common Tailorbird *Orthotomus sutorius* were higher in cashew plantations compared to forest habitats (Fig. 7 and 11). Interestingly, the probabilities of occurrence of certain species, including the Malabar Grey Hornbill, Jungle Owlet *Glaucidium radiatum*, Malabar Whistling Thrush *Myophonus horsfieldii*, and Small Minivet *Pericrocotus cinnamomeus* were significantly lower in pure cashew plantations as compared to forest. However, the difference in occurrence between mixed cashew plantations and forests was not statistically significant, suggesting the value of mixed cashew plantations for some forest-specialist birds.

Traits explained 13.6% of the variation in species occurrences. The probability of occurrence of evergreen forest species was significantly lower in mixed and pure cashew plantations than in forests (Fig. 8 and 9a). The probability of occurrence of resident species was positively associated with the landscape variable, forest cover in 800 m around the sampling point (Fig. 8 and 9b). I did not detect any phylogenetic signal in the residuals ($\rho$ = 0.23, 95% CI: 0 - 0.68) indicating lack of evidence for niche conservatism i.e. closely-related species differed in their responses to predictor variables (Harvey & Pagel, 1991) as is evident from the clade of bulbuls, where the Yellow-browed Bulbul *Acritillas indica*, is negatively impacted by cashew but the Red-vented and Red-whiskered Bulbuls *Pycnonotus* spp. are positively affected by cashew plantations.

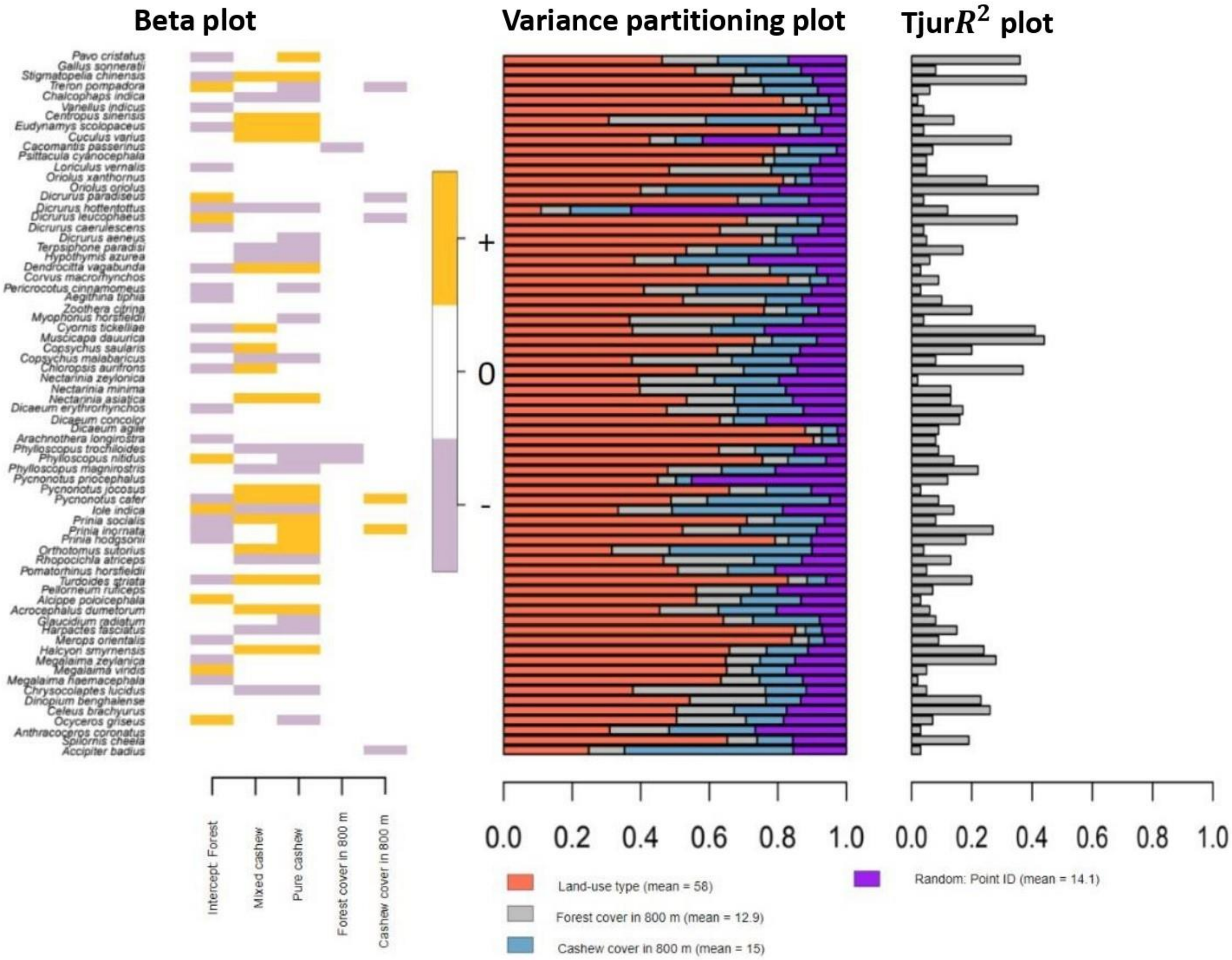


**Figure 7**. Composite figure showing beta plot, variance partitioning plot, and TjurR2 plot. Beta plot showcases the responses of the 70 species to the three covariates (land use type, forest cover in 800 m radius around the point and cashew cover in 800 m radius around the point and cashew cover in 800 m radius around the point), where species are in rows and predictors in columns. Orange and violet boxes indicate significantly positive and negative responses (where the 95% credible intervals of the beta coefficients did not overlap zero), respectively. Variance partitioning

plot shows the amount of variance in occurrence of each of the 70 species explained by different predictors, and Tjur $R^2$ plot shows the amount of variation in occurrence of each of the 70 species explained by the model.

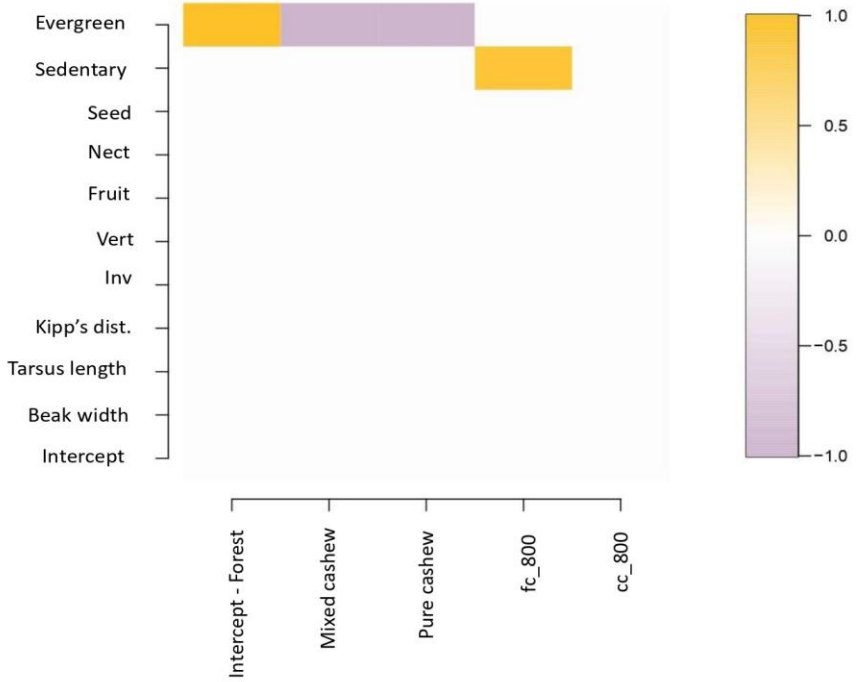


**Figure 8.** Gamma plot showcasing trait responses to local (land use type) and landscape predictors (forest and cashew cover in 800 m circular radius). The scale represents a positive to negative gradient in response.

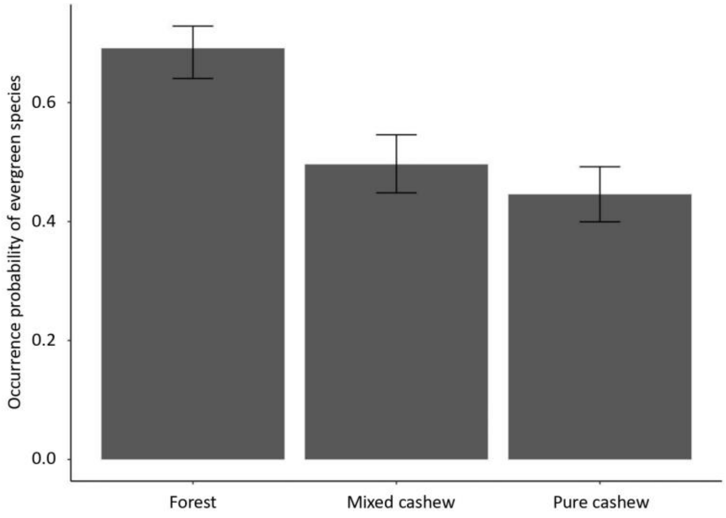


**Figure 9.** Probability of occurrence (associated 95% CI) of evergreen species across the three land use types.

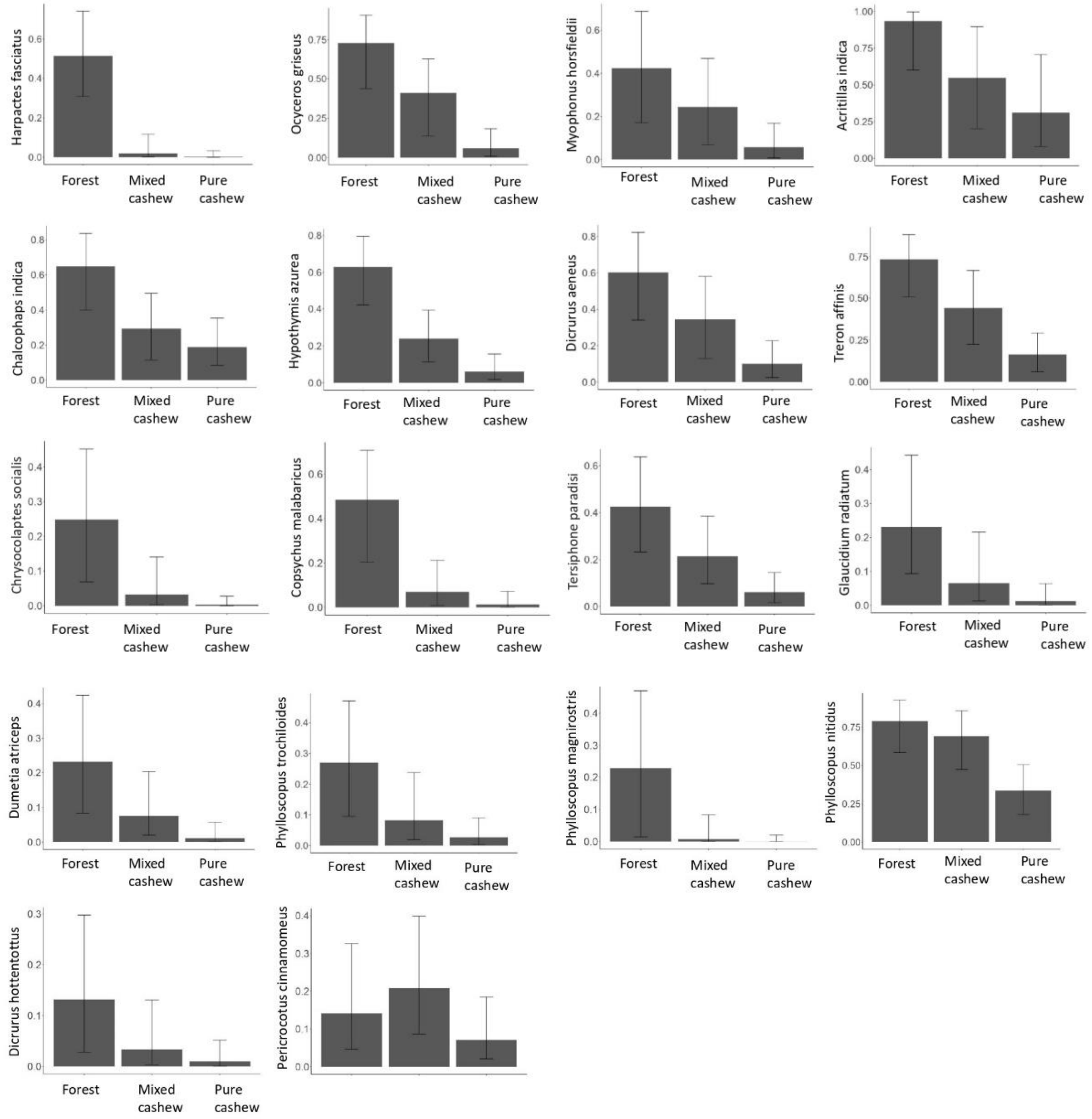


**Figure 10**. Predicted probability of occurrence of different bird species (see y-axis labels for species id) across the different land-use types. These are the species whose probability of occurrence is significantly lower in cashew plantations than forests (‘Losers).

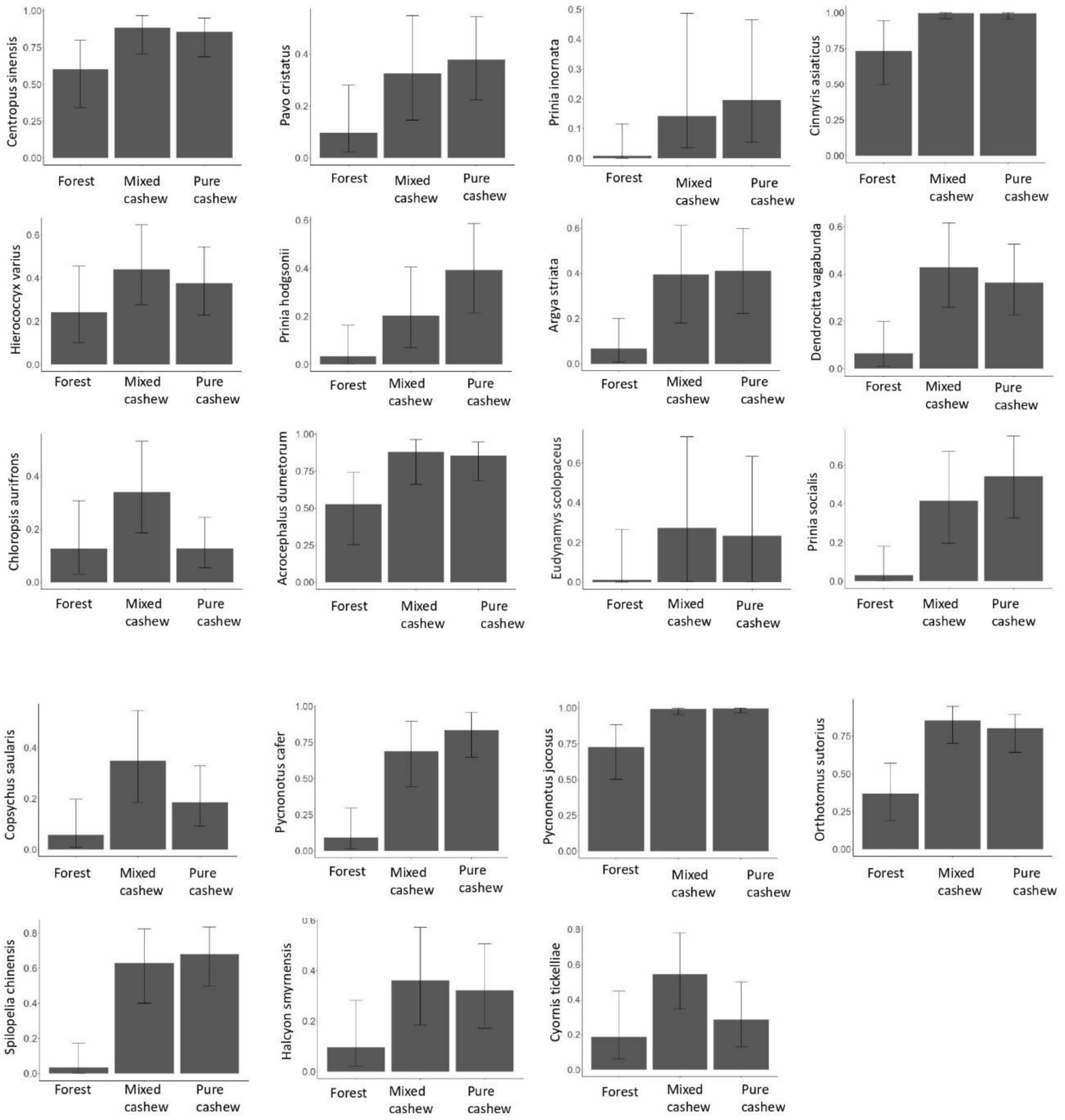


**Figure 11.** Predicted probability of occurrence of different bird species (see y-axis labels for species ID) across the different land-use types. These are the species whose probability of occurrence is significantly higher in cashew plantations ('Winners') than forests.

## DISCUSSION

This is one of the few studies in India determining the relative influence of local and landscape-level predictors on bird diversity and persistence in cashew plantations. Given the rapid expansion and promotion of cashew agroforests, particularly in northern Western Ghats, this timely study provides suggestions for retaining bird diversity in cashew agroforests. As expected, compared to forests, pure cashew plantations had lowered native tree diversity, altered forest structure, distinct bird composition, lower taxonomic and phylogenetic diversity and lower prevalence of forest specialist birds. On the other hand, compared to forests, mixed cashew plantations had comparable structural attributes and taxonomic diversity and experienced lower filtering of forest specialist species compared to pure cashew plantations. Interestingly, in contrast to literature that has found the importance of landscape-level attributes (Anand et al., 2010; Birch et al., 2024; Bonfim et al., 2024; Cannon et al., 2019; Gilroy et al., 2014), my study demonstrates that local-scale attributes explained more significant variation in bird responses than landscape-scale attributes. Also, I only found associations between habitat specialisation and land use type among the different morphological, dietary and behavioural traits I examined.

### Role of native trees in cashew plantations

Agroforests are often promoted as a sustainable form of agriculture because of improved vegetation structural integrity than other forms of agriculture (Karanth et al., 2016; Syiem et al., 2023). However, intensively managed agroforestry practices that result in almost complete loss of native tree cover can harm biodiversity (Donald et al., 2006; García-Navas et al., 2022). As this study demonstrates, pure cashew plantations had lower prevalence of forest-specialist bird species, many of which are endemic and threatened species (e.g., Malabar Grey Hornbill *Ocyceros griseus*, Grey-fronted Green-pigeon *Treron affinis*). Unfortunately, mixed-cashew plantations that retain some native tree cover and structure are on their way out, as revealed by local cashew farmers and challenges when finding mixed-cashew plantations during the reconnaissance period of this study. Pure cashew plantations are increasingly replacing them as farmers have improved access to technology that quickly allows transforming forests into tabled cashew plantations. Earthmovers can transform a forest patch to levelled land in a couple of days if not hours. Moreover, while there are legal restrictions on the felling of certain species of native trees on private lands (e.g. Maharashtra Felling of Trees (Regulation) Act, 1964) that mandate seeking permissions from the relevant Tree Officer before tree felling, these may be poorly implemented, resulting in progressive degradation of habitats. Given that this study has demonstrated the greater importance of local-scale attributes for retaining bird diversity, retaining native tree cover for forest-specialist birds is critical. Therefore, it is vital that the local tree officer implements existing laws effectively and agroforestry farmers are encouraged to retain native tree cover. In cases where the native tree cover has been lost, ecological restoration practitioners and agroforestry farmers can work together to restore native tree cover on private lands.

While the bulk of the variation in bird prevalence was explained by local-scale attributes, landscape-level attributes, particularly increased cashew cover, negatively impacted several forest-dwelling bird species, like the Grey-fronted Green-pigeon *Treron affinis*, and Racket-tailed Drongo *Dicrurus paradiseus* and positively affected open habitat species (e.g. Plain Prinia *Prinia inornata* and Red-vented Bulbul *Pycnonotus cafer*). Since a third of the focal region is now under cashew cultivation (Rege & Lee, 2022), ensuring this landscape does not become wholly homogenised is a severe challenge. While there is little control over the future of private forest lands, the existing Reserved Forests in the landscape can ensure that the landscape retains some landscape diversity. Therefore, these Reserved Forests should not be de-notified or diverted for non-forestry purposes. Moreover, with the support of local communities, the existing Reserve Forests, which still need to be notified as conservation reserves, should be done as soon as possible. This will ensure the maintenance of habitat diversity in the region. For Ratnagiri District, where most forests are privately owned, it will be a greater challenge to retain natural habitats. Community-conserved areas, such as sacred groves, have progressively degraded over the years (Gunawardene et al., 2007; Patwardhan et al., 2021) and need to be protected and restored with the support of the local communities.

In the context of production landscapes or agroforestry mosaics, two land allocation strategies compete to incorporate conservation into agriculture (Green et al., 2005) – land sharing, where less intensive management practices are followed to ensure wildlife-friendly farming, and land-sparing, where biodiversity and agriculture are exclusive to each other (Birch et al., 2024). Given the greater influence of site-level characteristics, this study provides evidence for land-sharing approaches to retain bird diversity in the landscape.

## Need for examining community- and species-level responses in tandem

Many recent studies have only examined community-level metrics, i.e., taxonomic, functional and phylogenetic responses to environmental and anthropogenic drivers (Chapman et al., 2017; Hanz et al., 2019; Liu et al., 2024; Monnet et al., 2014; F. Montaño-Centellas et al., 2023; F. A. Montaño-Centellas et al., 2020; Penjor, Cushman, et al., 2022; Penjor, Jamtsho, et al., 2022; M. Rurangwa et al., 2021; M. L. Rurangwa et al., 2022; Sreekar et al., 2021). This study demonstrates the need to examine both community- and species-level responses. We found varying taxonomic, functional and phylogenetic diversity responses across the three land-use types. Variable responses of functional and phylogenetic diversities to drivers have been reported earlier

(Chapman et al., 2017; Craven et al., 2018; De Bello et al., 2021). While taxonomic diversity was highest in mixed-cashew plantations, functional diversity was similar across the three land-use types, and phylogenetic diversity was highest in forests.

The greater taxonomic diversity in mixed cashew plantations can be understood on closer examination of the beta and gamma plots. They reveal that while certain forest-specialist bird species are filtered in mixed-cashew plantations, many open-habitat specialists are added to the community, resulting in greater taxonomic diversity in mixed-cashew plantations. On the other hand, more forest-specialist species are filtered from cashew plantations, which is not necessarily compensated by open-habitat species. Habitat modification results in winners and losers (Penjor, Cushman, et al., 2022; M. L. Rurangwa et al., 2022; Sreekar et al., 2021), in mixed cashew plantations, there are fewer losers than winners, resulting in the observed taxonomic patterns.

The absence of trends in functional diversity can be explained by the gamma plot, where I did not find any relationship for the different dietary guilds (e.g., frugivores, invertivores) or morphological traits with land-use type or landscape variables. This points towards the functional replacement of losers with winners. For example, there is a lowered prevalence of Yellow-browed Bulbul *Acritillas indica* but an increased prevalence of Red-vented and Red-whiskered Bulbul *Pycnonotus spp.* in cashew plantations. ‘Winners’ compensate for the loss of functional diversity due to the filtering of ‘losers’ in cashew plantations. Thus, while functional diversity metrics examined the overall patterns, species- and trait-level analyses allowed determining how individual species and traits respond to anthropogenic drivers thereby providing an improved understanding of observed patterns in functional diversity.

The progressive decline in phylogenetic diversity with the intensification of cashew farming demonstrates the loss of distinct evolutionary lineages from the community, i.e., phylogenetic clustering, a potential outcome of environmental filtering (Fukami et al., 2005; Watkins & Wilson, 2003; Webb et al., 2002; Weiher et al., 1998). Genera like *Ocyceros*, *Treron*, *Harpactes*, and *Hypothymis* across different bird families were filtered in cashew plantations. However, their replacement happens with multiple species within the same families, as is evident with positive responses of *Prinia* spp. to cashew plantations or of the Asian Koel *Eudynamys scolopacea*, Greater Coucal *Centropus sinensis* and the Common Hawk-Cuckoo *Hierococcyx varius*, all of which belong to the family Cuculidae. This highlights the importance of retaining distinct evolutionary lineages and examining species-specific responses that allow determining lineages vulnerable to agroforestry intensification.

## Conclusions and conservation implications

This study builds upon previous work in the landscape that demonstrated negative impacts of agroforestry plantations on birds (Biswas et al., 2023; Munje & Kumar, 2022). By closely examining habitat characteristics, this study has provided evidence for a land-sharing approach for bird conservation in a predominantly cashew production landscape where there are no protected areas. Given that these low-elevation areas are critical for many threatened and endemic species, there is a need for greater engagement with agroforestry farmers on behalf of conservation and restoration practitioners and enforcement of existing laws that can help retain and restore native tree cover. This is one of the few studies from the Western Ghats that has compared responses of multiple dimensions of bird diversity across different land-use types. By integrating community- and species-level analysis, this study provides a nuanced understanding of bird responses to agroforestry plantations.

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## APPENDIX MATERIAL

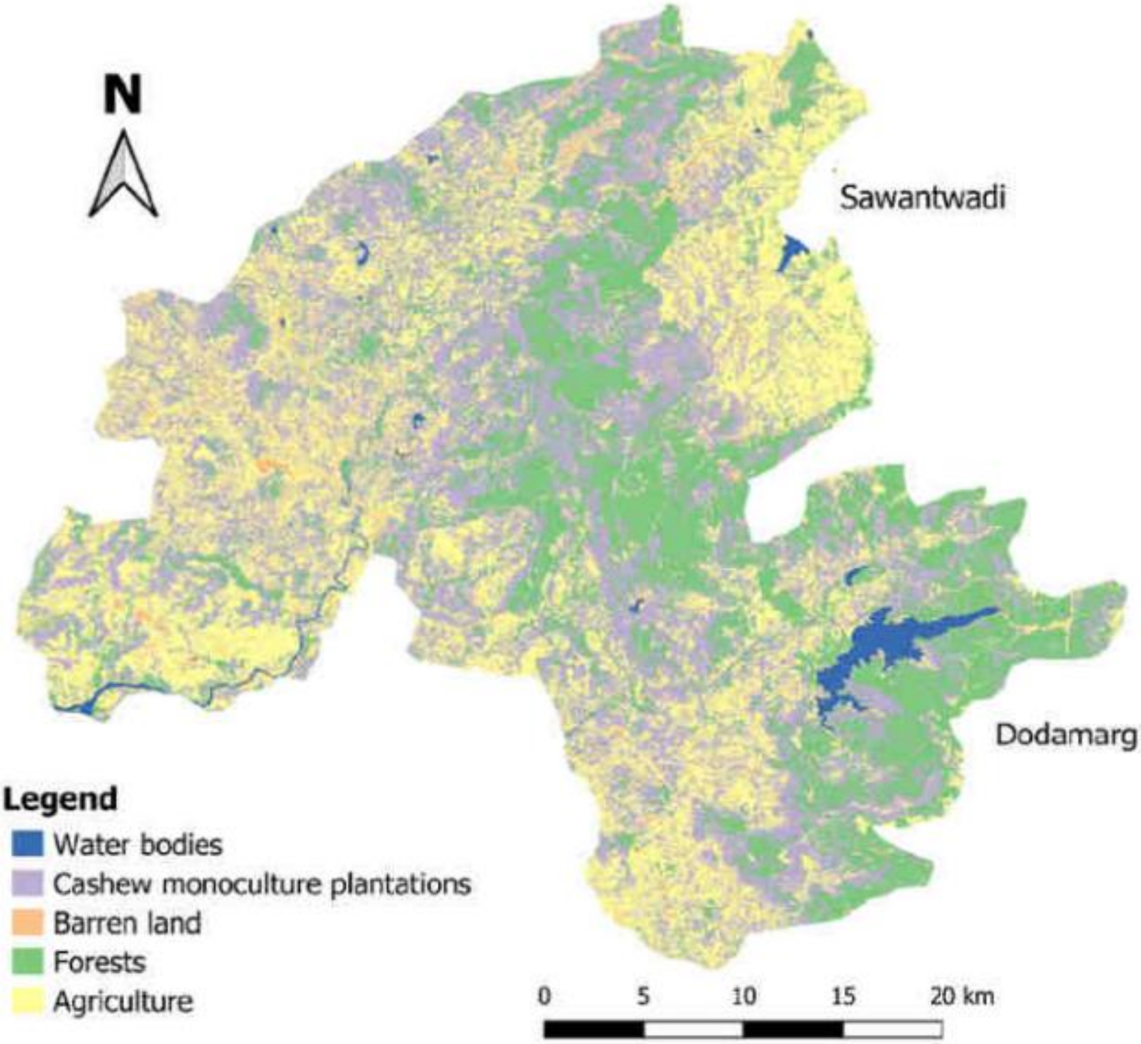

**Figure 12.** Land cover map of the Sawantwadi-Dodamarg landscape. Source: Rege et al., 2022

**Table S1.** Checklist of tree species detected in 100 (10 m circular radius) plots, the number of plots in which the species was detected, and the total number of individuals detected.

| Sr. No. | Species | Family | Number of individuals | Number of plots in which the species was detected |
|---|---|---|---|---|
| 1 | *Anacardium occidentale* | Anacardiaceae | 272 | 66 |
| 2 | *Holigarna arnottiana* | Anacardiaceae | 16 | 5 |
| 3 | *Holigarna grahamii* | Anacardiaceae | 1 | 1 |
| 4 | *Mangifera indica* | Anacardiaceae | 2 | 2 |
| 5 | *Nothopegia castaneifolia* | Anacardiaceae | 1 | 1 |
| 6 | *Miliusa tomentosa* | Annonaceae | 4 | 4 |
| 7 | *Monoon fragrans* | Annonaceae | 1 | 1 |
| 8 | *Alstonia scholaris* | Apocynaceae | 2 | 2 |
| 9 | *Tabernaemontana alternifolia* | Apocynaceae | 8 | 6 |
| 10 | *Caryota urens* | Arecaceae | 1 | 1 |
| 11 | *Cocos nucifera* | Arecaceae | 2 | 1 |
| 12 | *Stereospermum angustifolium* | Bignoniaceae | 1 | 1 |
| 13 | *Lophopetalum wightianum* | Celastraceae | 1 | 1 |
| 14 | *Garcinia indica* | Clusiaceae | 3 | 3 |
| 15 | *Terminalia bellirica* | Combretaceae | 4 | 4 |

| | | | | |
|---|---|---|---|---|
| 16 | *Terminalia elliptica* | Combretaceae | 21 | 12 |
| 17 | *Terminalia paniculata* | Combretaceae | 80 | 33 |
| 18 | *Dillenia pentagyna* | Dilleniaceae | 5 | 5 |
| 19 | *Diospyros candolleana* | Ebenaceae | 7 | 3 |
| 20 | *Elaeocarpus tuberculatus* | Elaeocarpaceae | 1 | 1 |
| 21 | *Macaranga peltata* | Euphorbiaceae | 1 | 1 |
| 22 | *Mallotus philippensis* | Euphorbiaceae | 3 | 2 |
| 23 | *Acacia auriculiformis* | Fabaceae | 11 | 4 |
| 24 | *Dalbergia sissoo* | Fabaceae | 1 | 1 |
| 25 | *Saraca asoca* | Fabaceae | 1 | 1 |
| 26 | *Xylia xylocarpa* | Fabaceae | 22 | 12 |
| 27 | *Tectona grandis* | Lamiaceae | 10 | 4 |
| 28 | *Vitex altissima* | Lamiaceae | 2 | 2 |
| 29 | *Machilus glaucescens* | Lauraceae | 1 | 1 |
| 30 | *Careya arborea* | Lecythidaceae | 14 | 9 |
| 31 | *Strychnos nux-vomica* | Loganiaceae | 2 | 2 |
| 32 | *Lagerstroemia microcarpa* | Lythraceae | 4 | 3 |
| 33 | *Lagerstroemia parviflora* | Lythraceae | 2 | 2 |

| | | | | |
|---|---|---|---|---|
| 34 | *Bombax ceiba* | Malvaceae | 1 | 1 |
| 35 | *Grewia tiliifolia* | Malvaceae | 2 | 2 |
| 36 | *Pterospermum angustifolium* | Malvaceae | 1 | 1 |
| 37 | *Pterospermum diversifolium* | Malvaceae | 1 | 1 |
| 38 | *Sterculia guttata* | Malvaceae | 1 | 1 |
| 39 | *Artocarpus heterophyllus* | Moraceae | 4 | 3 |
| 40 | *Artocarpus hirsutus* | Moraceae | 1 | 1 |
| 41 | *Syzygium cumini* | Myrtaceae | 16 | 10 |
| 42 | *Chionanthus mala-elengi* | Oleaceae | 1 | 1 |
| 43 | *Tetrapilus dioicus* | Oleaceae | 5 | 4 |
| 44 | *Aporosa cardiosperma* | Phyllanthaceae | 39 | 13 |
| 45 | *Bridelia retusa* | Phyllanthaceae | 4 | 4 |
| 46 | *Phyllanthus emblica* | Phyllanthaceae | 1 | 1 |
| 47 | *Carallia brachiata* | Rhizophoraceae | 5 | 4 |
| 48 | *Adina cordifolia* | Rubiaceae | 1 | 1 |
| 49 | *Ixora brachiata* | Rubiaceae | 16 | 8 |
| 50 | *Meyna laxiflora* | Rubiaceae | 1 | 1 |
| 51 | *Mitragyna parvifolia* | Rubiaceae | 1 | 1 |

| | | | | |
|---|---|---|---|---|
| 52 | *Glycosmis cochinchinensis* | Rutaceae | 4 | 2 |
| 53 | *Zanthoxylum rhetsa* | Rutaceae | 2 | 2 |
| 54 | *Flacourtia montana* | Salicaceae | 5 | 4 |
| 55 | *Schleichera oleosa* | Sapindaceae | 9 | 6 |
| 56 | *Xantolis tomentosa* | Sapotaceae | 9 | 4 |

**Table S2.** Sample coverage and Hill-Shannon diversity numbers and the associated bootstrapped 95% CI for the three land use types.

| Land use type | Sample coverage | Hill-Shannon Diversity | 95% LCL | 95% UCL |
|---|---|---|---|---|
| Forest | 0.9 | 18.5 | 15.1 | 22.0 |
| Mixed cashew | 0.9 | 8.2 | 6.2 | 10.2 |
| Pure cashew | 1 | 1 | 1 | 1 |

**Table S3.** Treatment contrast table comparing different site-level structural attributes across the three land use categories (forest, mixed cashew and pure cashew plantations).

| **Structural attribute** | **Land use type** | **Estimate** | **95% CI** | ***p*** |
|---|---|---|---|---|
| Tree density per hectare | Intercept: Forest | 5.7305 | 5.527 – 5.933 | < 0.001 |
| | Mixed cashew | -0.2915 | -0.575 – -0.007 | 0.0574 |
| | Pure cashew | -0.7713 | -1.041 – -0.501 | < 0.001 |
| Basal area ($m^2$ $ha^{-1}$) | Intercept: Forest | 2.8395 | 2.475 – 3.203 | < 0.001 |
| | Mixed cashew | -0.6025 | -1.111 – -0.093 | 0.0209 |
| | Pure cashew | -1.7363 | -2.220 – -1.252 | < 0.001 |
| Tree height (m) | Intercept: Forest | 2.46789 | 2.350 – 2.585 | < 0.001 |
| | Mixed cashew | -0.34782 | -0.512 – -0.183 | < 0.001 |
| | Pure cashew | -1.03301 | -1.189 – -0.876 | < 0.001 |
| Canopy cover (%) | Intercept: Forest | 3.7594 | 3.481 – 4.038 | < 0.001 |
| | Mixed cashew | -0.6104 | -1.001 – -0.220 | 0.003 |
| | Pure cashew | -0.6754 | -1.046 – -0.304 | < 0.001 |

**Table S4.** Tukey’s post-hoc results for vegetation structural attributes across land-use types.

| Structural attribute | Contrast | Difference | 95% LCI | 95% UCI | p-adjusted |
|---|---|---|---|---|---|

| | | | | | |
|---|---|---|---|---|---|
| Tree density per hectare | Mixed cashew - Forest | -0.292 | -0.632 | 0.049 | 0.109 |
| | Pure cashew - Forest | -0.771 | -1.096 | -0.447 | <0.001 |
| | Pure cashew - Mixed cashew | -0.4980 | -0.800 | -0.159 | 0.002 |
| Basal area ($m^2$ $ha^{-1}$) | Mixed cashew - Forest | -0.603 | -1.213 | 0.008 | 0.054 |
| | Pure cashew - Forest | -1.736 | -2.318 | -1.155 | <0.001 |
| | Pure cashew - Mixed cashew | -1.134 | -1.708 | -0.559 | <0.001 |
| Tree height (m) | Mixed cashew - Forest | -0.348 | -0.546 | -0.150 | <0.001 |
| | Pure cashew - Forest | -1.033 | -1.221 | -0.845 | <0.001 |
| | Pure cashew - Mixed cashew | -0.685 | -0.871 | -0.499 | <0.001 |
| Canopy cover (%) | Mixed cashew - Forest | -0.610 | -1.079 | -0.142 | 0.007 |
| | Pure cashew - Forest | -0.675 | -1.121 | -0.230 | 0.002 |
| | Pure cashew - Mixed cashew | -0.06492075 | -0.5053854 | 0.3755439 | 0.933954 |

**Table S5.** List of avian species detected during the sampling period

| No | Species | Family | No. detected in Forest | No. detected in Mixed cashew | No. detected in Pure cashew |
|---|---|---|---|---|---|
| 1 | *Accipiter badius* | Accipitridae | 4 | 3 | 8 |
| 2 | *Accipiter virgatus* | Accipitridae | 1 | 0 | 0 |
| 3 | *Haliastur indus* | Accipitridae | 0 | 1 | 0 |
| 4 | *Nisaetus cirrhatus* | Accipitridae | 4 | 0 | 0 |
| 5 | *Pernis ptilorhyncus* | Accipitridae | 0 | 1 | 0 |
| 6 | *Spilornis cheela* | Accipitridae | 9 | 4 | 10 |
| 7 | *Acrocephalus dumetorum* | Acrocephalidae | 46 | 71 | 118 |
| 8 | *Aegithina tiphia* | Aegithinidae | 12 | 23 | 37 |

| | | | | | |
|---|---|---|---|---|---|
| 9 | *Ceyx erithaca* | Alcedinidae | 1 | 0 | 0 |
| 10 | *Halcyon smyrnensis* | Alcedinidae | 4 | 9 | 24 |
| 11 | *Anthracoceros coronatus* | Bucerotidae | 14 | 14 | 9 |
| 12 | *Buceros bicornis* | Bucerotidae | 3 | 1 | 0 |
| 13 | *Ocyceros birostris* | Bucerotidae | 3 | 0 | 0 |
| 14 | *Ocyceros griseus* | Bucerotidae | 52 | 18 | 4 |
| 15 | *Pericrocotus cinnamomeus* | Campephagidae | 7 | 11 | 9 |
| 16 | *Pericrocotus flammeus* | Campephagidae | 0 | 6 | 0 |
| 17 | *Vanellus indicus* | Charadriidae | 0 | 5 | 3 |
| 18 | *Chloropsis aurifrons* | Chloropseidae | 2 | 15 | 12 |
| 19 | *Chloropsis jerdoni* | Chloropseidae | 0 | 3 | 0 |
| 20 | *Orthotomus sutorius* | Cisticolidae | 12 | 61 | 102 |
| 21 | *Prinia hodgsonii* | Cisticolidae | 1 | 2 | 44 |
| 22 | *Prinia inornata* | Cisticolidae | 0 | 9 | 20 |
| 23 | *Prinia socialis* | Cisticolidae | 0 | 17 | 65 |
| 24 | *Chalcophaps indica* | Columbidae | 52 | 6 | 15 |
| 25 | *Ducula cuprea* | Columbidae | 2 | 0 | 0 |
| 26 | *Spilopelia chinensis* | Columbidae | 0 | 39 | 61 |
| 27 | *Treron affinis* | Columbidae | 62 | 16 | 9 |
| 28 | *Corvus macrorhynchos* | Corvidae | 26 | 35 | 58 |
| 29 | *Corvus splendens* | Corvidae | 0 | 0 | 2 |
| 30 | *Dendrocitta vagabunda* | Corvidae | 1 | 16 | 23 |
| 31 | *Cacomantis passerinus* | Cuculidae | 1 | 3 | 7 |

| | | | | | |
|---|---|---|---|---|---|
| 32 | *Centropus sinensis* | Cuculidae | 22 | 56 | 102 |
| 33 | *Hierococcyx varius* | Cuculidae | 9 | 17 | 30 |
| 34 | *Eudynamys scolopaceus* | Cuculidae | 0 | 11 | 18 |
| 35 | *Dicaeum agile* | Dicaeidae | 13 | 24 | 45 |
| 36 | *Dicaeum concolor* | Dicaeidae | 57 | 50 | 69 |
| 37 | *Dicaeum erythrorhynchos* | Dicaeidae | 1 | 2 | 4 |
| 38 | *Dicrurus aeneus* | Dicruridae | 29 | 17 | 6 |
| 39 | *Dicrurus caerulescens* | Dicruridae | 0 | 0 | 6 |
| 40 | *Dicrurus hottentottus* | Dicruridae | 6 | 0 | 1 |
| 41 | *Dicrurus leucophaeus* | Dicruridae | 44 | 45 | 67 |
| 42 | *Dicrurus paradiseus* | Dicruridae | 104 | 87 | 121 |
| 43 | *Lonchura striata* | Estrildidae | 0 | 2 | 1 |
| 44 | *Carpodacus erythrinus* | Fringillidae | 1 | 0 | 2 |
| 45 | *Irena puella* | Irenidae | 2 | 0 | 0 |
| 46 | *Alcippe poioicephala* | Leiothrichidae | 88 | 99 | 132 |
| 47 | *Dumetia atriceps* | Leiothrichidae | 13 | 4 | 0 |
| 48 | *Argya striata* | Leiothrichidae | 3 | 20 | 58 |
| 49 | *Argya subrufa* | Leiothrichidae | 0 | 2 | 0 |
| 50 | *Psilopogon haemacephalus* | Megalaimidae | 9 | 8 | 11 |
| 51 | *Psilopogon malabaricus* | Megalaimidae | 3 | 0 | 3 |
| 52 | *Psilopogon viridis* | Megalaimidae | 77 | 115 | 135 |
| 53 | *Psilopogon zeylanicus* | Megalaimidae | 1 | 3 | 4 |
| 54 | *Merops leschenaulti* | Meropidae | 0 | 4 | 0 |

| | | | | | |
|---|---|---|---|---|---|
| 55 | *Merops orientalis* | Meropidae | 2 | 4 | 21 |
| 56 | *Hypothymis azurea* | Monarchidae | 29 | 11 | 4 |
| 57 | *Terpsiphone paradisi* | Monarchidae | 16 | 7 | 3 |
| 58 | *Copsychus malabaricus* | Muscicapidae | 20 | 2 | 1 |
| 59 | *Copsychus saularis* | Muscicapidae | 1 | 16 | 17 |
| 60 | *Cyornis pallidipes* | Muscicapidae | 3 | 0 | 0 |
| 61 | *Cyornis rubeculoides* | Muscicapidae | 0 | 2 | 0 |
| 62 | *Cyornis tickelliae* | Muscicapidae | 4 | 25 | 18 |
| 63 | *Eumyias thalassinus* | Muscicapidae | 0 | 1 | 0 |
| 64 | *Muscicapa dauurica* | Muscicapidae | 1 | 2 | 2 |
| 65 | *Muscicapa muttui* | Muscicapidae | 1 | 1 | 0 |
| 66 | *Myophonus horsfieldii* | Muscicapidae | 23 | 11 | 3 |
| 67 | *Saxicola caprata* | Muscicapidae | 0 | 0 | 1 |
| 68 | *Arachnothera longirostra* | Nectariniidae | 3 | 7 | 1 |
| 69 | *Cinnyris asiaticus* | Nectariniidae | 56 | 105 | 378 |
| 70 | *Leptocoma minima* | Nectariniidae | 196 | 172 | 208 |
| 71 | *Leptocoma zeylonica* | Nectariniidae | 7 | 15 | 14 |
| 72 | *Oriolus kundoo* | Oriolidae | 4 | 13 | 6 |
| 73 | *Oriolus xanthornus* | Oriolidae | 68 | 111 | 187 |
| 74 | *Gymnoris xanthocollis* | Passeridae | 0 | 0 | 1 |
| 75 | *Pellorneum ruficeps* | Pellorneidae | 18 | 9 | 19 |
| 76 | *Gallus sonneratii* | Phasianidae | 34 | 26 | 62 |
| 77 | *Pavo cristatus* | Phasianidae | 3 | 11 | 29 |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| 78 | *Phylloscopus magnirostris* | Phylloscopidae | 17 | 0 | 0 |
| 79 | *Phylloscopus nitidus* | Phylloscopidae | 36 | 31 | 25 |
| 80 | *Phylloscopus trochiloides* | Phylloscopidae | 9 | 3 | 2 |
| 81 | *Micropternus brachyurus* | Picidae | 9 | 6 | 6 |
| 82 | *Chrysocolaptes socialis* | Picidae | 13 | 2 | 0 |
| 83 | *Yungipicus nanus* | Picidae | 0 | 0 | 1 |
| 84 | *Dinopium benghalense* | Picidae | 26 | 31 | 19 |
| 85 | *Hemicircus canente* | Picidae | 2 | 1 | 0 |
| 86 | *Loriculus vernalis* | Psittaculidae | 3 | 4 | 2 |
| 87 | *Psittacula cyanocephala* | Psittaculidae | 2 | 7 | 6 |
| 88 | *Psittacula krameri* | Psittaculidae | 1 | 0 | 0 |
| 89 | *Acritillas indica* | Pycnonotidae | 187 | 31 | 26 |
| 90 | *Pycnonotus cafer* | Pycnonotidae | 2 | 32 | 119 |
| 91 | *Pycnonotus jocosus* | Pycnonotidae | 37 | 165 | 399 |
| 92 | *Rubigula gularis* | Pycnonotidae | 0 | 2 | 0 |
| 93 | *Microtarsus priocephalus* | Pycnonotidae | 16 | 11 | 6 |
| 94 | *Rhipidura albogularis* | Rhipiduridae | 1 | 0 | 0 |
| 95 | *Sitta frontalis* | Sittidae | 1 | 0 | 0 |
| 96 | *Glaucidium radiatum* | Strigidae | 9 | 3 | 0 |
| 97 | *Pomatorhinus horsfieldii* | Timaliidae | 39 | 30 | 45 |
| 98 | *Harpactes fasciatus* | Trogonidae | 32 | 0 | 0 |
| 99 | *Turdus simillimus* | Turdidae | 0 | 1 | 1 |
| 100 | *Geokichla citrina* | Turdidae | 3 | 19 | 21 |

| | | | | | |
|---|---|---|---|---|---|
| 101 | *Hemipus picatus* | Vangidae | 0 | 1 | 0 |
| 102 | *Tephrodornis pondicerianus* | Vangidae | 0 | 2 | 4 |

**Table S6.** Hill-Shannon diversity estimates (qD) of bird species across the three land use types. qD.LCL and qD.UCL represent bootstrapped (n = 1000) lower and upper 95% confidence levels.

| Land use type | Sampling coverage | Hill-Shannon | 95% LCL | 95% UCL |
|---|---|---|---|---|
| Forest | 0.99 | 34.7 | 32.8 | 36.6 |
| Mixed cashew | 0.99 | 37.9 | 36.1 | 39.7 |
| Pure cashew | 0.99 | 29.2 | 28.1 | 30.4 |

**Table S7.** Treatment contrast table of the general linear model comparing functional diversity (SES-fMPD) and phylogenetic diversity (SES-pMPD) across the three land use types (forest, mixed cashew and pure cashew plantations).

| Diversity metric | Land use type | Estimate | 95% CI | p |
|---|---|---|---|---|
| SES-fMPD | Intercept: Forest | 1.9728 | 1.8498 – 2.0958 | < 0.001 |
| | Mixed cashew | 0.1369 | -0.037 – 0.3108 | 0.121 |
| | Pure cashew | -0.0434 | -0.1946 – 0.1077 | 0.57 |
| SES-pMPD | Intercept: Forest | 2.6662 | 2.5561 – 2.7763 | < 0.001 |
| | Mixed cashew | -0.085 | -0.2406 – 0.0707 | 0.2814 |
| | Pure cashew | -0.2558 | -0.3912 – -0.1206 | 0.0002 |

**Table S8.** Tukey's post-hoc results for pair-wise comparisons of functional and phylogenetic Mean Pairwise Distances across land-use types (forest, mixed cashew and pure cashew).

| Diversity metric | Contrast | Difference | 95% LCI | 95% UCI | p-adj. |
|---|---|---|---|---|---|
| Functional SES-MPD | Mixed cashew–Forest | 0.137 | -0.072 | 0.346 | 0.267 |
| | Pure cashew–Forest | -0.043 | -0.225 | 0.138 | 0.836 |
| | Pure cashew–Mixed cashew | -0.180 | -0.362 | 0.001 | 0.052 |
| Phylogenetic SES-MPD | Mixed cashew–Forest | -0.085 | -0.272 | 0.102 | 0.527 |
| | Pure cashew–Forest | -0.256 | -0.418 | -0.094 | 0.001 |
| | Pure cashew–Mixed cashew | -0.161 | -0.333 | -0.009 | 0.037 |

**Table S9.** Summary of species-wise *Tjur* $R^2$ and the proportion of the explained variation by each of the fixed effects (land use type, forest cover in 800 m and cashew cover in 800 m) and spatial random effect for the 70 species analysed using the Hierarchical Modelling of Species Communities.

| **Species** | ***Tjur R***$^2$ | **Land-use type** | **Forest cover in 800 m** | **Cashew cover in 800 m** | **Random: Point** |
|---|---|---|---|---|---|
| *Accipiter badius* | 0.046 | 0.249 | 0.104 | 0.492 | 0.155 |
| *Acrocephalus dumetorum* | 0.147 | 0.653 | 0.087 | 0.104 | 0.156 |
| *Aegithina tiphia* | 0.070 | 0.310 | 0.173 | 0.251 | 0.266 |
| *Alcippe poioicephala* | 0.050 | 0.504 | 0.203 | 0.110 | 0.183 |
| *Anthracoceros coronatus* | 0.036 | 0.505 | 0.168 | 0.153 | 0.174 |
| *Arachnothera longirostra* | 0.084 | 0.543 | 0.223 | 0.101 | 0.133 |
| *Cacomantis passerinus* | 0.035 | 0.377 | 0.387 | 0.119 | 0.117 |
| *Micropternus brachyurus* | 0.043 | 0.634 | 0.113 | 0.126 | 0.127 |
| *Centropus sinensis* | 0.087 | 0.651 | 0.075 | 0.099 | 0.175 |
| *Chalcophaps indica* | 0.194 | 0.649 | 0.100 | 0.102 | 0.149 |
| *Chloropsis aurifrons* | 0.082 | 0.659 | 0.108 | 0.120 | 0.112 |
| *Chrysocolaptes socialis* | 0.197 | 0.841 | 0.049 | 0.046 | 0.064 |
| *Copsychus malabaricus* | 0.384 | 0.851 | 0.030 | 0.049 | 0.071 |
| *Copsychus saularis* | 0.089 | 0.642 | 0.087 | 0.194 | 0.078 |
| *Corvus macrorhynchos* | 0.019 | 0.455 | 0.172 | 0.170 | 0.204 |
| *Hierococcyx varius* | 0.058 | 0.563 | 0.129 | 0.176 | 0.132 |
| *Cyornis tickelliae* | 0.140 | 0.562 | 0.162 | 0.075 | 0.201 |
| *Dendrocitta vagabunda* | 0.120 | 0.830 | 0.056 | 0.055 | 0.059 |
| *Dicaeum agile* | 0.039 | 0.509 | 0.145 | 0.138 | 0.208 |
| *Dicaeum concolor* | 0.102 | 0.467 | 0.264 | 0.140 | 0.129 |
| *Dicaeum erythrorhynchos* | 0.031 | 0.316 | 0.169 | 0.416 | 0.100 |
| *Dicrurus aeneus* | 0.244 | 0.792 | 0.039 | 0.066 | 0.102 |
| *Dicrurus caerulescens* | 0.025 | 0.522 | 0.167 | 0.224 | 0.086 |
| *Dicrurus hottentottus* | 0.092 | 0.710 | 0.080 | 0.147 | 0.063 |
| *Dicrurus leucophaeus* | 0.071 | 0.334 | 0.157 | 0.324 | 0.185 |
| *Dicrurus paradiseus* | 0.119 | 0.488 | 0.106 | 0.357 | 0.048 |

| | | | | | |
|---|---|---|---|---|---|
| *Dinopium benghalense* | 0.089 | 0.659 | 0.108 | 0.132 | 0.102 |
| *Eudynamys scolopaceus* | 0.263 | 0.450 | 0.053 | 0.046 | 0.451 |
| *Gallus sonneratii* | 0.028 | 0.479 | 0.158 | 0.157 | 0.207 |
| *Glaucidium radiatum* | 0.126 | 0.755 | 0.074 | 0.112 | 0.059 |
| *Halcyon smyrnensis* | 0.076 | 0.629 | 0.105 | 0.115 | 0.152 |
| *Harpactes fasciatus* | 0.437 | 0.904 | 0.025 | 0.048 | 0.023 |
| *Hypothymis azurea* | 0.284 | 0.880 | 0.049 | 0.045 | 0.026 |
| *Acritillas indica* | 0.359 | 0.631 | 0.041 | 0.095 | 0.234 |
| *Loriculus vernalis* | 0.041 | 0.476 | 0.207 | 0.191 | 0.125 |
| *Psilopogon haemacephalus* | 0.027 | 0.534 | 0.139 | 0.171 | 0.156 |
| *Psilopogon viridis* | 0.058 | 0.398 | 0.277 | 0.149 | 0.176 |
| *Psilopogon zeylanica* | 0.021 | 0.395 | 0.221 | 0.188 | 0.196 |
| *Merops orientalis* | 0.032 | 0.564 | 0.136 | 0.157 | 0.143 |
| *Muscicapa dauurica* | 0.026 | 0.374 | 0.291 | 0.173 | 0.162 |
| *Myophonus horsfieldii* | 0.205 | 0.624 | 0.103 | 0.138 | 0.135 |
| *Cinnyris asiaticus* | 0.346 | 0.732 | 0.051 | 0.130 | 0.086 |
| *Leptocoma minima* | 0.075 | 0.376 | 0.231 | 0.154 | 0.239 |
| *Leptocoma zeylonicus* | 0.054 | 0.368 | 0.304 | 0.202 | 0.126 |
| *Ocyceros griseus* | 0.414 | 0.760 | 0.065 | 0.094 | 0.081 |
| *Oriolus kundoo* | 0.076 | 0.524 | 0.241 | 0.106 | 0.129 |
| *Oriolus xanthornus* | 0.053 | 0.409 | 0.155 | 0.335 | 0.101 |
| *Orthotomus sutorius* | 0.199 | 0.830 | 0.063 | 0.052 | 0.055 |
| *Pavo cristatus* | 0.090 | 0.596 | 0.181 | 0.137 | 0.086 |
| *Pellorneum ruficeps* | 0.045 | 0.382 | 0.119 | 0.215 | 0.285 |
| *Pericrocotus cinnamomeus* | 0.075 | 0.533 | 0.088 | 0.236 | 0.142 |
| *Phylloscopus magnirostris* | 0.368 | 0.755 | 0.040 | 0.049 | 0.157 |
| *Phylloscopus nitidus* | 0.216 | 0.632 | 0.164 | 0.123 | 0.082 |

| | | | | | |
|---|---|---|---|---|---|
| *Phylloscopus trochiloides* | 0.141 | 0.710 | 0.148 | 0.074 | 0.068 |
| *Pomatorhinus horsfieldii* | 0.171 | 0.109 | 0.085 | 0.178 | 0.628 |
| *Prinia hodgsonii* | 0.184 | 0.683 | 0.069 | 0.138 | 0.110 |
| *Prinia inornata* | 0.167 | 0.400 | 0.074 | 0.330 | 0.196 |
| *Prinia socialis* | 0.229 | 0.816 | 0.035 | 0.046 | 0.102 |
| *Psittacula cyanocephala* | 0.065 | 0.483 | 0.298 | 0.114 | 0.105 |
| *Pycnonotus cafer* | 0.423 | 0.758 | 0.032 | 0.133 | 0.077 |
| *Pycnonotus jocosus* | 0.252 | 0.790 | 0.043 | 0.139 | 0.028 |
| *Microtarsus priocephalus* | 0.137 | 0.427 | 0.075 | 0.079 | 0.419 |
| *Dumetia atriceps* | 0.127 | 0.805 | 0.058 | 0.066 | 0.071 |
| *Spilornis cheela* | 0.052 | 0.307 | 0.283 | 0.318 | 0.092 |
| *Spilopelia chinensis* | 0.329 | 0.884 | 0.027 | 0.044 | 0.045 |
| *Terpsiphone paradisi* | 0.158 | 0.817 | 0.054 | 0.079 | 0.051 |
| *Treron affinis* | 0.274 | 0.665 | 0.093 | 0.159 | 0.083 |
| *Argya striata* | 0.128 | 0.671 | 0.079 | 0.152 | 0.098 |
| *Vanellus indicus* | 0.052 | 0.559 | 0.148 | 0.161 | 0.132 |
| *Geokichla citrina* | 0.029 | 0.462 | 0.163 | 0.206 | 0.169 |
| **Average** | **0.137** | **0.580** | **0.129** | **0.150** | **0.141** |