

Stochastic processes shape the functional and phylogenetic structure of bird assemblages at the mine area in southwest China

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Abstract

Understanding the mechanisms of community assembly is a key question in ecology. Metal pollution may result in significant changes in bird community structure and diversity, with implications for ecosystem processes and function. However, the relative importance of these processes in shaping the bird community at the polluted area is still not clear. Here, we explored bird species richness, functional, and phylogenetic diversity, and the assembly processes of community at the mine region of southwest China. Our results showed that the 3 dimensions of diversity at the mine area were lower than that at the reference sites. In the community assembly, the result was $0 < \text{NRI}/\text{NFRI} < 1.96$, which indicated deterministic processes (environmental filtering) might drive community clustering. The results of the neutral community model, and normalized stochasticity ratio, showed the dominant role of stochastic processes in shaping the bird community assembly. We further quantified the community-level habitat niche breadth (*Bcom*), and we found that there was no difference in *Bcom*-value between the mine area and reference sites. This indicates that the bird communities at the mine area and 3 reference sites were not subjected to extreme environmental selection (same or different resource allocation) to form a highly specialized niche. These findings provide insights into the distribution patterns and dominant ecological processes of bird communities under metal exposure, and extend the knowledge in community assembly mechanisms of bird communities living in the mine area.

Key words: clustering, community assembly, functional diversity, mine area, phylogenetic diversity, stochastic process.

Understanding the assembly mechanisms of biological communities is a key question in ecology (Graham et al. 2009; Gotzenberger et al. 2012). Niche- and neutral-based theories explain the assembly mechanisms of biotic community (Bahram et al. 2016; Chen et al. 2021). The niche-based theory considers that deterministic processes, such as environmental filtering and interspecific interactions play a dominant role in community assembly (Chesson 2000; Fargione et al. 2003). Nevertheless, the neutral theory asserts that stochastic processes (e.g. birth, death, dispersal, and ecological drift) shape the biotic community (Stegen et al. 2012; Ning et al. 2019). Some studies found that during the processes of community assembly, the assembly mechanisms (deterministic and/or stochastic processes) might act independently within a community (Chen et al. 2019), concurrently (Cadotte and Tucker 2017), or occur sequentially (Dehling et al. 2014) along environmental gradients. In community ecology, an important question is that which mechanism (deterministic and/or stochastic process) plays a dominant role (Mouchet et al. 2010; Ding et al. 2021).

In exploring the assembly processes of biological community, traditional diversity (e.g., species richness) alone is not enough to insight into a deeper mechanistic of the assembly processes (Si et al. 2016; Li et al. 2019; Zhang et al. 2020).

Thus, functional diversity (FD) and phylogenetic diversity (PD) have been increasingly advocated to quantify assemblage structures, which are deemed to better reflect the underlying ecological processes than species richness (Cadotte et al. 2011; Srivastava et al. 2012). For example, environmental pollution affects assembly processes and results in functionally and phylogenetically non-random communities (Belskii and Mikryukov 2018). Species richness, functional diversity, and phylogenetic diversity showed different patterns along the altitudinal gradient (Dehling et al. 2014). Thus, FD and PD might offer more complementary information for traditional diversity and could facilitate our understanding of the assembly mechanisms underlying biodiversity and community (Hanz et al. 2018).

Birds play an important role in ecosystem function and are strongly sensitive to the changes in their environment, which made them ideal taxa to be used in exploring the assembly processes and in assessing the effects of environmental changes on biological communities (Naithani and Bhatt 2012; Chen et al. 2019; Penjor et al. 2021). It is commonly argued that metal pollution can pose stresses for birds, such as the decline of bird density, species richness, and diversity (Eeva et al. 2012; Belskii and Mikryukov 2018). In addition, trace metals pollution might also affect the assembly process

of bird communities. Because, the contamination could cause deterioration of forest ecosystems and reduce the food supply and habitat availability (Smith et al. 2005; Belskii and Mikryukov 2018). These deterministic processes such as interspecific competition due to reduced food resources and environmental filtration caused by habitat destruction could affect the assembly process of bird communities. However, it is unlikely that communities are structured by a single process, for example, stochastic factors may be more evident when the filter is relaxed (Chase 2007). Thus, the neutral community model (NCM) and normalized stochasticity ratio (NST), proposed respectively by Sloan et al. (2006) and Ning et al. (2019), are particularly useful in quantifying the importance of neutral processes.

Southwest China is a hotspot of global biodiversity, with abundant plant and animal resources, and plays an important role in the global ecosystem (Shi et al. 2019; Lu et al. 2021). And, this region is also one of the most concentrated areas of metal mineral resources in China, and mineral mining has caused serious trace metal pollution to the environment (Shen et al. 2007). As is known to all, metal pollution has emerged as one of the most severe threats to global biodiversity (Wei et al. 2014; Chen et al. 2020; Ahmad et al. 2022). To date, most of the studies on trace metal pollution mainly focused on ecotoxicology and bioaccumulation (Bonanno and Orlando-Bonaca 2018; He et al. 2019), while the effects on biodiversity and the assembly processes of biotic communities are rarely studied (Hernandez and Pastor 2008; Belskii and Mikryukov 2018).

In this study, we conducted a 3-year investigation at the mine area and 3 reference sites in southwest China to explore the assembly processes of bird communities. We hypothesize that the taxonomic, functional, and phylogenetic diversity at the mine area was lower than at reference sites, that is, the assembly mechanism of bird communities at the mine area is a deterministic process. If deterministic process dominates the bird assembly, distinct bird community compositions would be found between the mine area and reference sites. If stochastic process dominates the bird assembly, chance events due to the restricted dispersal to nearby locations would probably produce more compositionally similar communities between the mine area and reference sites. Therefore, this study aimed to (1) quantify the relative importance of deterministic and stochastic processes of community assembly at the mine region and (2) explore the effects of assembly processes on diversity of bird community.

Materials and Methods

Study sites and transects selection

This study was performed in the Daxin county of Guangxi Zhuang Autonomous Region, southwest China. This region is characterized by subtropical marine monsoons and has an average annual precipitation of 1348.80 mm and an altitude of 385.00 m. Our experimental area included a mine area and 3 reference sites. This mine area was a mine tailing, which was started exploiting mine resources by the French over 100 years ago. Mining activities were conducted at a large scale for 40 years until the mine closure in 2001 due to environmental pollution and resource exhaustion (Liu et al. 2022). Our previous studies demonstrated that a large number of trace metals, including As, Pb, Cd, Hg, Cu, and Zn were accumulated in feathers and internal tissues of the wild birds

living at the mine area (He et al. 2019; Liu et al. 2021, 2022). In addition, some nature reserves in this area are listed as Important Bird Areas, which includes many globally threatened birds and new bird species (Jiang et al. 2014). Therefore, the current research builds on these earlier studies to understand the effects of mining activity on assembly mechanisms of bird communities.

Bird diversity data were collected during the non-breeding season in 2019–2021 at one mine area and 3 reference sites of Daxin county (Figure 1, <http://bzdt.ch.mnr.gov.cn/index.html>). The reference site 1 (22°88′N, 107°25′E, altitude: 389.00 m), site 2 (22°79′N, 107°28′E, altitude: 385.00 m), and site 3 (22°95′N, 107°48′E, altitude: 393.00 m) were located at approximately 7, 20, and 25 km, respectively from the mine region. Five 1-km transects were set at the mine area. The transects were arranged at least 250 m apart from each other. Then there were three 1-km transects at each of the 3 reference sites. The reference sites have similar habitat types to the mine area (i.e., degraded karst forests).

The assessment of trace metal levels

In this study, the concentration of trace metals in grey-cheeked fulvetta *Alcippe morrisonia* was used to assess the environmental trace metal levels. Grey-cheeked fulvettas are common passerine resident birds with complex and diverse diet that are widely distributed in the forests of southern China and Southeast Asia (Zou et al. 2007; Jiang et al. 2014). An interesting characteristic is that grey-cheeked fulvettas, a “nuclear” species in mixed-species bird flocks, tend to lead bird flocks to forage (Zou et al. 2007; Jiang et al. 2014). The number of individuals in mixed-species bird flocks led by grey-cheeked fulvettas may be over 100 individuals in the tropical and subtropical forests, of which more than two-thirds belong to the nuclear species (Chen and Hsieh 2002). Our previous studies also revealed that the grey-cheeked fulvettas accumulated higher concentrations of trace metals than other passerine birds (Liu et al. 2021, 2022). Thus, grey-cheeked fulvetta is a potentially effective model for monitoring metal pollution. Here, the trace metal concentrations of the tail feathers from grey-cheeked fulvettas were used to assess the pollution levels at all 4 study sites. Grey-cheeked fulvettas were trapped using mist nets in Jan 2021. Total 21, 21, 22, and 23 adult individuals of grey-cheeked fulvettas were captured at the mine area and reference sites 1, 2, and 3, respectively. Then, the trace metals (Cd, Pb, Cu, and Zn) in the tail feathers were detected to assess the pollution levels. The analysis methods of trace metals in tail feathers of the Grey-cheeked fulvettas were described in Liu et al. (2022).

Vegetation Structure

We also investigated vegetation data at every 250 m on the transect within 10 m radius. (1) canopy height. It refers to the vertical distance between the bottom and the top of the tree canopy (i.e., the distance from the lowest branch with leaves to the highest one). (2) canopy openness. We performed hemispheric photography using a fish-eye lens attached to a phone, and subsequent Gap Light Analyzer processing. The survey methods of canopy openness were referred to Meaux et al. (2021). (3) We also estimated the density of trees with DBH greater than 20 cm within 10 m radius.

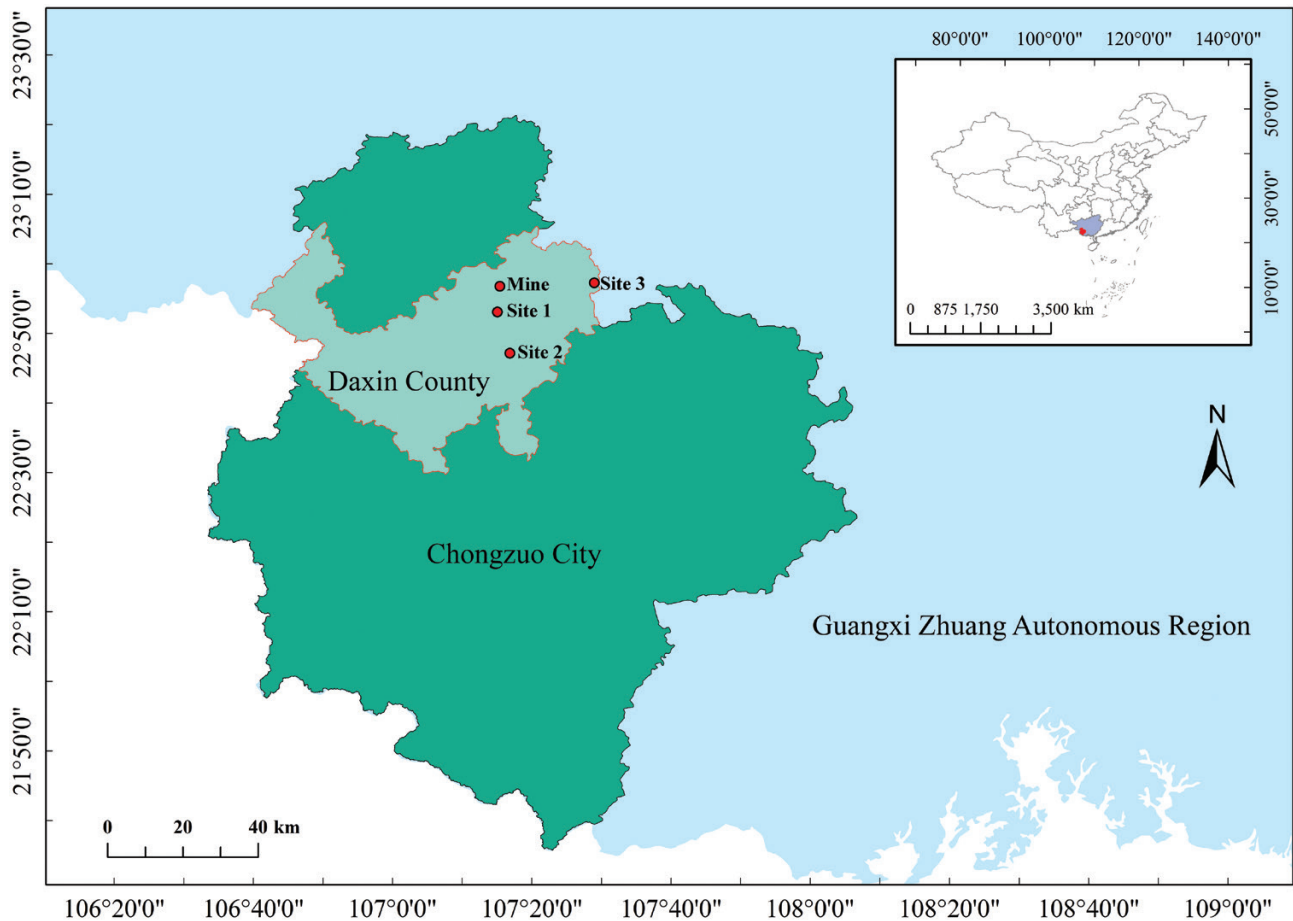


Figure 1. Map showing the study area (Daxin Lead-Zinc Mining and reference sites, Guangxi Zhuang Autonomous Region, southwest China).

Bird surveys

We censused the presence and abundance of bird species on each of the 4 study sites using standard line transect methods (Bibby et al. 2000). Data on bird species were recorded only by 2 trained observers (S. Liu and X. Tan) to reduce detection issues due to skill differences between observers. The speed of observers walking along the transects was around 1 km/h. All birds seen or heard within a unilateral 25 m distance from the observer were recorded. All transects were visited once per month during the non-breeding season (December–February) each year from 2019 to 2021, once in the morning (starting at 8 AM), and once in the afternoon (starting at 3 PM) on a different day, with the order of visits to the various transects systematically varied every month. Censuses were not conducted during inclement weather (rain or strong winds) to avoid the potential differences with the numbers of species and individuals recorded under normal weathers. We completed such visits for at least 3 months every year.

Species richness, functional, and phylogenetic diversity

We calculated species richness, functional, and phylogenetic diversity of birds at each site. Species richness was expressed as the number of recorded bird species at each sampling transect. Functional diversity quantifies the range and values of species and organismal traits that affect ecosystem functioning (Tilman 2001). Phylogenetic diversity measures the total

amount of phylogenetic distance among species in a community (Srivastava et al. 2012).

The phylogenetic tree was obtained using the Global Ornithological Phylogeny System (<http://birdtree.org>) (Jetz et al. 2012). We used all bird species and selected 5,000 random distributions on “Hackett All Species: a set of 10000 trees with 9993 OTUS each.” Then, the Bayesian method was used for phylogenetic analysis by using “TreeAnnotator” in BEAST2 software to find the maximum clade credibility tree (Bouckaert et al. 2014). Then, we calculated Faith’s phylogenetic diversity (PD) and mean pairwise distance (MPD) for each bird community.

In order to measure the extent to which traits of different species are similar on the evolutionary tree, we tested the phylogenetic signal for bird traits using Pagel’s λ (Pagel 1999). The values of λ is close to 1 correspond to traits being more similar amongst species than expected from their phylogenetic relationships; values of λ is close to 0 suggests the reverse (Ding et al. 2021).

For functional diversity metrics, we assessed functional richness (FRic) and mean pairwise functional distance (MPFD). FRic calculates the volume of the functional space occupied by the species in the community (Mason et al. 2005). Moreover, we controlled for species richness and calculated the standardized effect size (SES) of FRic using null models. Because we found species richness and FRic showed nearly identical trends, revealing FRic may be mainly driven by the variations of species richness. MPFD is the mean Euclidean distance between all species

of an assemblage that are projected in functional trait space according to their functional traits with principal coordinate analysis. To quantify functional diversity, we chose 19 traits related to the species' morphology, foraging behavior, foraging location, and diet composition (Table 1). These functional traits data were from Birds of the World (<https://birdsoftheworld.org/bow/home>).

To infer whether deterministic processes play a significant dominant role in community construction of birds on each site, we calculated the net relatedness index (NRI). It quantified the number of standard deviations of the observed MPD values and was used to test for niche or dispersal limitations (Webb 2000). To obtain NRI, we compared the observed MPD with the values from 999 sets of randomized assemblages created with the independent swap algorithm (Gotelli 2000). NRI was calculated as $NRI = -1 \times (\text{observed MPD} - \text{mean of MPD values from randomizations}) / \text{standard deviation of MPD values from randomizations}$ (Webb et al. 2002). Similar to NRI, we calculated the net functional relatedness index (NFRI), which is the MPFD standardized against null-model expectation. When NRI/NFRI values > 1.96 or < -1.96 , which indicates significant phylogenetic clustering or over-dispersion ($P < 0.05$), that is, deterministic processes dominate the communities assemble (Ding et al. 2020). Conversely, if $-1.96 < NRI/NFRI < 1.96$, it is considered that deterministic process is not important in shaping the structure of bird communities (Zeng et al. 2022).

Stochastic process of community assembly

A neutral community model (NCM) was used to estimate the effects of stochastic processes on the bird community

Table 1. Functional traits used to measure functional diversity indices and phylogenetic signal of birds at the mine area and reference sites

Trait type	Trait	Type of variable	Phylogenetic signal	
			λ	P-value
Morphology	Body mass	Quantitative, continuous	1.00	< 0.01
Diet components	Carnivorous	Binary	0.88	< 0.01
	Frugivore			
	Granivores			
	Insectivore			
	Omnivore			
Foraging behavior	Digging	Binary	0.66	0.20
	Gleaning			
	Hawking			
	Leaping			
	Probing			
	Pursuit			
	Salling			
	Scratching			
Foraging location	Air	Binary	0.59	< 0.01
	Canopy			
	Ground			
	Midstory			
	Understory			

assembly (Sloan et al. 2006). The model predicts that rich taxa are more likely to disperse by chance and become widely distributed in metacommunities, while rare taxa are lost in different local communities due to ecological drift (Sloan et al. 2006; Burns et al. 2016). The formula is as follows:

$$Frep_i = 1 - I(1/N | N * m * p_i, N * m * (1 - p_i))$$

where $Frep_i$ is the occurrence frequency of taxon i across communities; N is the number of individuals per community; m is the estimated migration rate; p_i is the average relative abundance of taxon i across communities; and $I()$ is the probability density function of beta distribution. R^2 indicates the fit of the parameter based on nonlinear least squares fitting. Calculation of 95% confidence intervals around all fitting statistics was done by bootstrapping with 1000 bootstrap replicates. The R^2 value was calculated following "Östman's method" (Ostman et al. 2010). When the R^2 value is close to 1, the community assembly is fully consistent with stochastic processes. When it does not describe the community composition, R^2 can be ≤ 0 .

To explore the relative effects of stochastic and deterministic processes on the bird communities based on our regions, we estimated Levins' niche breadth (B) index (Levins 1968) for bird community members. The Levins' niche breadth index reveals the patterns of species classification and dispersal limits. The formula is as follows:

$$B_j = 1 / \sum_{i=1}^N P_{ij}^2$$

where B_j represents the habitat niche breadth of species j in a metacommunity; N is the total number of communities in each metacommunity; P_{ij} is the proportion of species j in community i (Pandit et al. 2009). A high B -value for a species indicates its wide habitat niche breadth. The community-level B -value (B_{com}) was calculated as the average of B -values from all taxa occurring in one community (Wu et al. 2018). We expect an avian community with a wider niche breadth to be more metabolically flexible at the community level.

We further used the normalized stochasticity ratio (NST) to quantify the relative importance of deterministic and stochastic processes in community assembly with 50% as the boundary point between more deterministic (NST < 0.50) and more stochastic (NST > 0.50) assembly (Ning et al. 2019). NST is used to measure the relative position of the observed values between extreme values under purely deterministic and purely random assembly.

Statistical analysis

Statistical analysis of data was performed using R 3.6.1 software (R CoreTeam 2021). The data of trace metal concentrations and vegetation structure between sites (mine vs. reference sites) did not meet normality, so we checked the difference by nonparametric Kruskal–Wallis tests. Moreover, P -value was adjusted using a sequential Bonferroni correction to correct the increased probability of type I errors (Rice 1989). Taxonomic and phylogenetic metrics were estimated using the "Picante" package in R (Kembel et al. 2010; Morelli et al. 2021). Functional diversity was calculated using the "FD" package in R (Laliberté et al. 2014). For the differences between the mine area and reference sites in taxonomic, functional, and phylogenetic diversity, we first tested the data

normality assumption. Our data met the normal distribution, thus, we used 1-way analysis of variance test followed by Tukey's Honest Significant Difference (HSD) post hoc test. For phylogenetic signal, the λ values were calculated in the R packages "phytool" (Revell 2012). In community assembly process, the calculation of Levins' niche S_r executes through the "spaa" package (Zhang 2016), the calculation of the NCM was performed by the "picante" package (Sloan et al. 2006), and the calculation of NST is performed by the "NST" package (Ning et al. 2019).

Results

Pollution levels and vegetation data

The concentrations of Pb ($77.00 \pm 16.24 \mu\text{g g}^{-1}$) in the tail feathers of grey-cheeked fulvetta at the mine area were significantly higher than that at the reference site 1 ($w = 342.00$, $P = 0.01$), site 2 ($w = 362.50$, $P < 0.01$), and site 3 ($w = 353.00$, $P < 0.01$). The Cd levels ($26.40 \pm 4.18 \mu\text{g g}^{-1}$) of tail feathers at the mine area were also positively higher than reference site 1 ($w = 371.00$, $P < 0.01$), site 2 ($w = 376.00$, $P < 0.01$), and site 3 ($w = 379.00$, $P < 0.01$). The concentrations of Cu ($161.45 \pm 45.00 \mu\text{g g}^{-1}$) and Zn ($296.59 \pm 82.15 \mu\text{g g}^{-1}$) at the mine area were not different from the 3 reference sites. For Cd, Pb, and Cu, no remarkable differences were found at the 3 reference sites. But, the levels of Zn from the reference site 1 ($w = 362.00$, $P < 0.01$) were significantly higher than at the reference site 3 (Supplementary Table S1). Additionally, for vegetation structure, we did not find a significant difference among the 4 study sites (Supplementary Figure S1).

Species richness, functional, and phylogenetic diversity

A total of 8,608 individuals of 107 bird species were recorded across 4 sites. Among these, we recorded 54 species at the mine area, and 71, 64, and 86 species at the reference sites 1, 2, and 3, respectively (Figure 2). The species richness at the mine region were remarkably lower than at the reference sites 2 ($t = 3.99$, $P < 0.01$) and 3 ($t = 2.67$, $P = 0.04$), but no significant difference with the reference site 1 ($t = 2.02$, $P = 0.19$). There was no significant difference among the 3 reference sites for species richness (Figure 3). The λ values of body mass ($\lambda = 1.00$, $P < 0.01$), diet composition ($\lambda = 0.88$, $P < 0.01$) were close to 1, indicating a strong phylogenetic signal, that is, functional traits showed strong phylogenetic conservation. In addition, there was also significant phylogenetic signals in foraging location ($\lambda = 0.59$, $P < 0.01$), but not in foraging behavior ($\lambda = 0.66$, $P = 0.20$) (Table 1).

FRic was positively higher at 3 reference sites than that at the mine site (Figure 4A). MPFD was significantly lower at the mine site compared with the reference site 3 ($t = 2.96$, $P = 0.02$), but no difference with the reference sites 1 and 2 (Figure 4B). The Faith's PD was remarkably lower at the mine area than at the reference sites 2 ($t = 3.96$, $P < 0.01$) and 3 ($t = 3.41$, $P < 0.01$), but no significant difference with the reference site 1 (Figure 4C). Similarly, the MPD values were also significantly lower at the mine area than reference site 2 ($t = 2.81$, $P < 0.01$) and site 3 ($t = 4.31$, $P < 0.01$), but not statistically different from reference site 1 (Figure 4D). Moreover, the MPD value at the reference site 3 was higher than the reference site 1 ($t = 3.15$, $P < 0.01$) and site 2 ($t = 2.10$, $P = 0.04$).

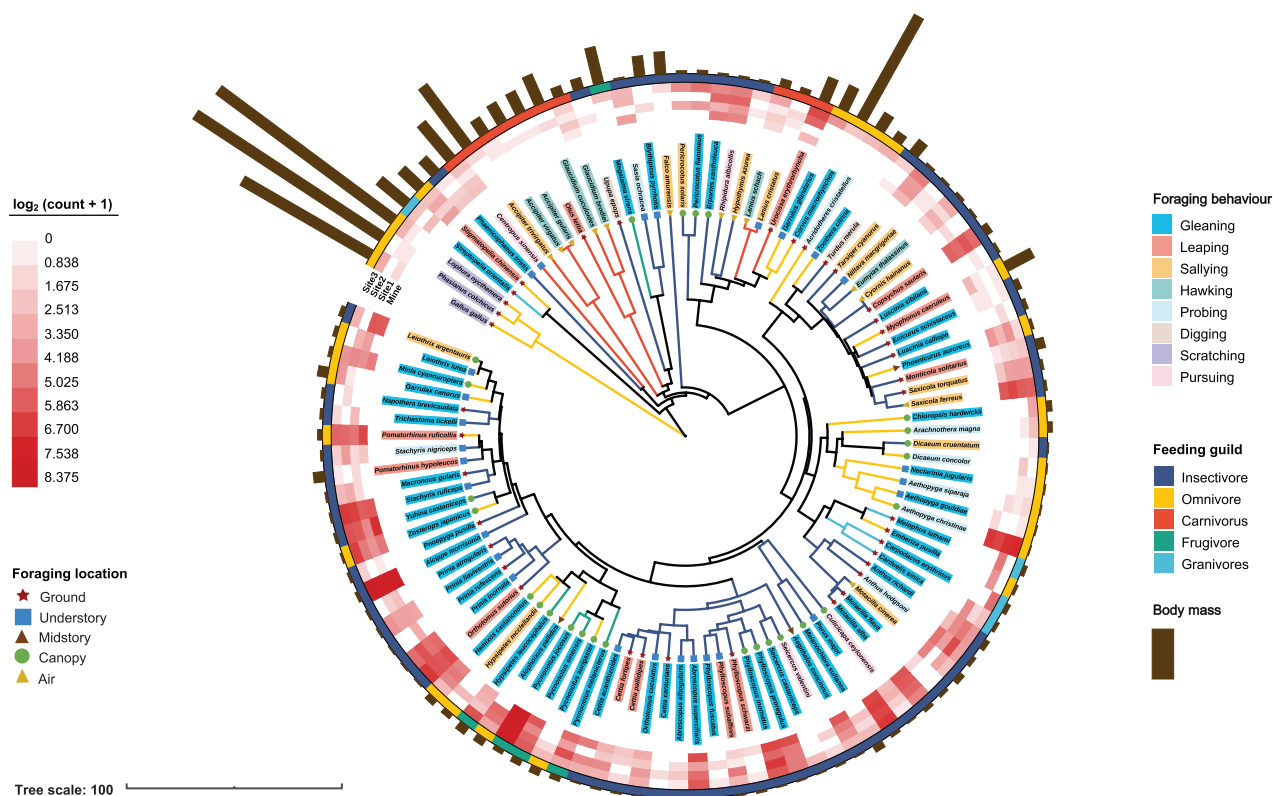


Figure 2. Phylogeny tree of the 107 bird species that were recorded in this study. Besides, the phylogenetic tree contained foraging locations, foraging behavior, feeding guild, and body mass of every bird species.

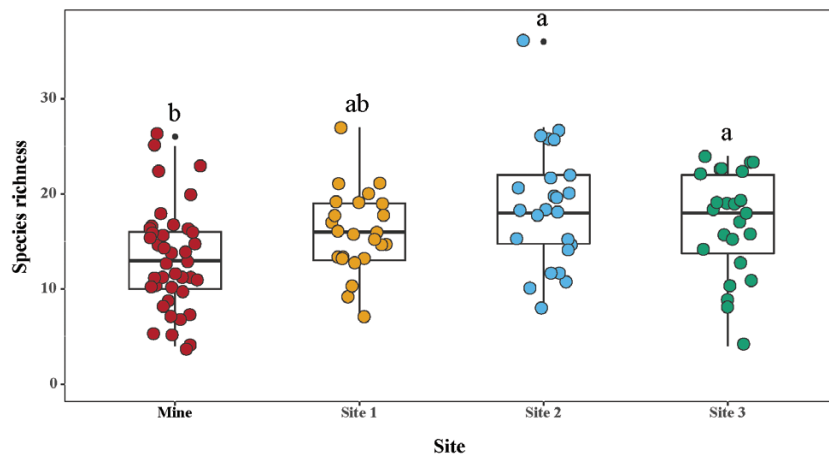


Figure 3. The difference analysis of species richness between the mine and reference sites. The difference (or same) letters indicate (no) significant difference at the $P < 0.05$ level using Tukey's post hoc test.

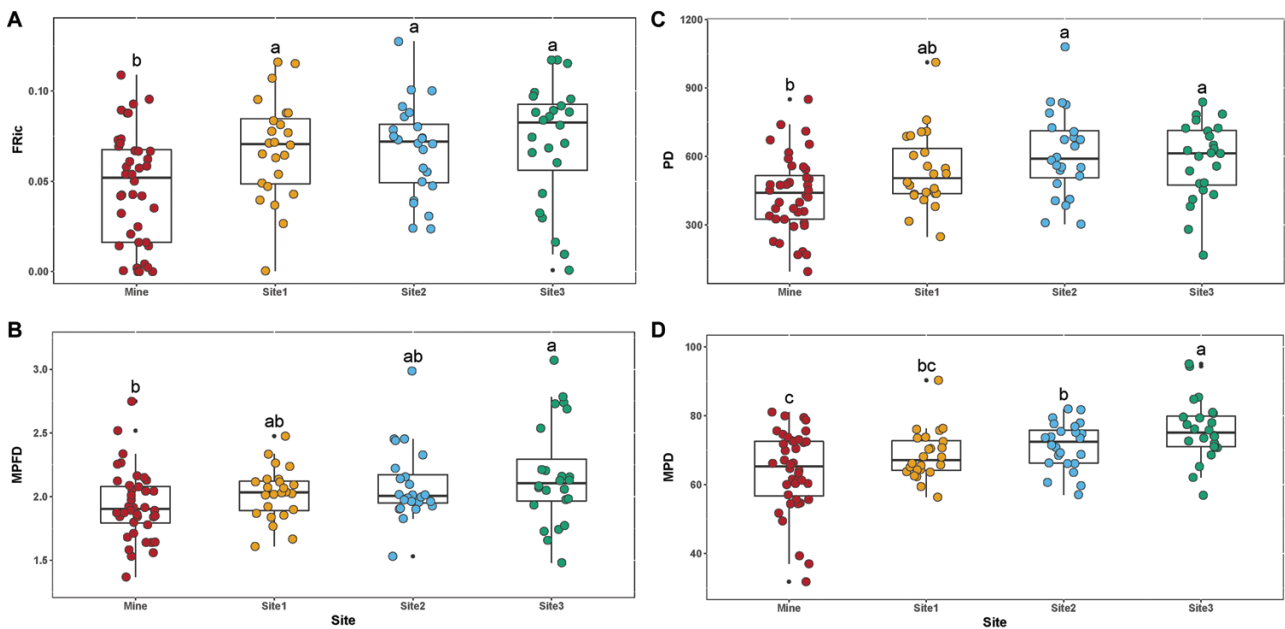


Figure 4. The difference in functional diversity and phylogenetic diversity between mine and 3 reference sites. (A) Functional richness (FRic). (B) Mean pairwise functional distance (MPFD). (C) Faith's phylogenetic diversity (Faith's PD) and (D) Mean pairwise distance (MPD) are the average distances among species pairs in the phylogeny and the functional trait space, respectively. The difference (or same) letters indicate (no) significant difference at the $P < 0.05$ level using Tukey's post hoc test.

The mean values of NRI for the mine area (+ 1.71), reference site 1 (+ 1.69), site 2 (+ 1.92), and site 3 (+ 1.46) were all less than +1.96. And, the mean values of NFRI for the mine area (+ 1.41), reference site 1 (+ 1.22), site 2 (+ 1.34), and site 3 (+ 1.10) were significantly lower than + 1.96 (Figure 5B). This indicated that the deterministic process was not significant in shaping the bird assemblages.

Stochastic processes of bird community assembly

The results of the community-level habitat niche breadths (*Bcom*) revealed that there was no difference in *Bcom* values among the 4 sites (Figure 6E). The goodness of fit was better for 3 reference sites (0.69, 0.81, and 0.74 of the variations explained at sites 1, 2, and 3, respectively) than the mine area (0.64 of the variations explained) (Figure 6A–D). The *Nm* values (12) at the mine area were lower than 3 reference sites

(site 1 = 19, site 2 = 18, site 3 = 13), indicating that mine bird taxa were more limited by dispersal. We further performed the normalized stochasticity ratio (NST) to quantify the role of deterministic and stochastic processes in bird community assembly (Figure 6F). The NST value was above the 0.50 boundary point for bird communities between the mine and reference sites, suggesting that the stochasticity process played a more important role than deterministic during the bird assembly. Moreover, the NST value of the bird community at the mine area was significantly lower ($P < 0.05$) than that at the 3 reference sites (Figure 6F).

Discussion

In this study, we first evaluated the difference of trace metal concentrations in the tail feathers of Grey-checked Fulvetta at the mine area and reference sites. The results revealed that

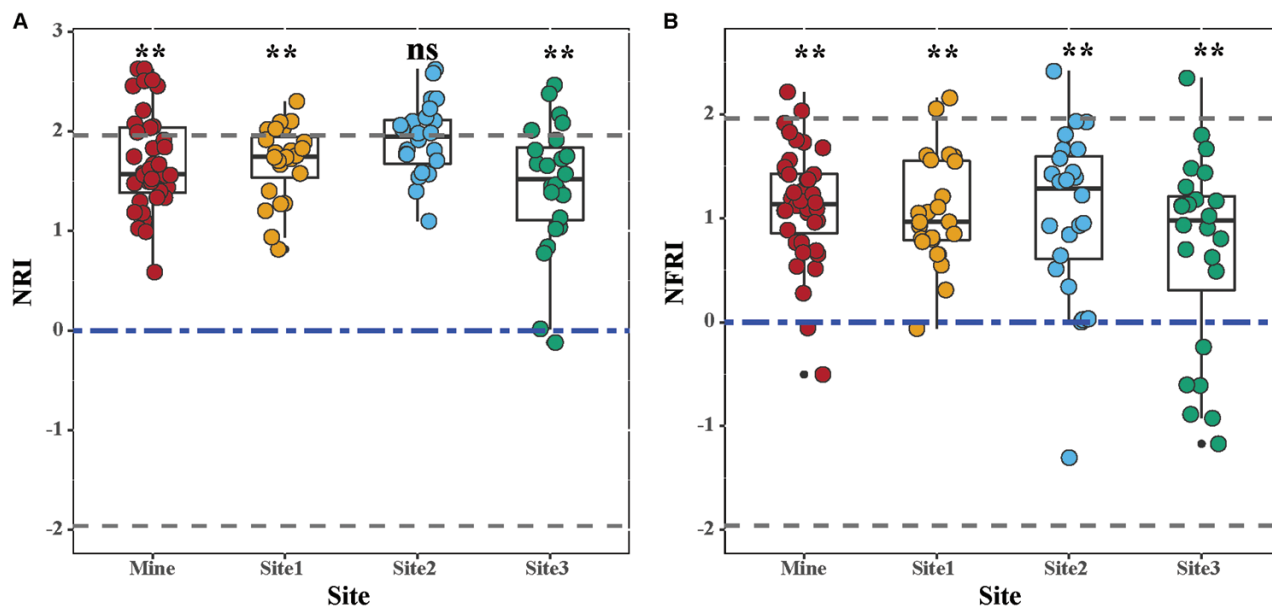


Figure 5. Functional and phylogenetic assemblage structure for birds between the mine and 3 reference sites. (A) NRI and (B) NFRI are standard effect sizes of observed values of mean pairwise phylogenetic distance and mean pairwise functional distance against 999 sets of simulated assemblages. Asterisks denoted that mean NRI/ NFRI values significantly lower than 1.96, i.e., the deterministic process was not significant during the shaping of bird community.

the concentrations of Cd and Pb at the mine area were significantly higher than the 3 reference sites. Burger and Gochfeld (2000b) put the threshold limit of potential threat to avian populations for Cd in bird's feathers at the levels of $2.00 \mu\text{g g}^{-1}$. In our study, the concentrations of Cd in about 80% of feathers would result in an ecotoxicological concern. Pb concentrations in feathers were above the threshold ($4.00 \mu\text{g g}^{-1}$), which can cause adverse effects in birds, reproductive problems and stunted growth (Burger and Gochfeld 2000a). There was no significant difference in Zn and Cu levels between the mine area and 3 reference sites. This might be because the two metals are essential elements for living organisms, having a biological role (Swaileh and Sansur 2006). At present, no threshold data would help interpret Zn and Cu concentrations in the feathers (Liu et al. 2022). Further, we explored species richness, functional and phylogenetic diversity, and community assembly mechanisms. The results showed that all types of alpha diversity were lowest at the mine area compared with the 3 reference sites. The assembly of bird communities at the mine area and reference sites were mainly driven by stochastic processes.

At the mine area, species richness was significantly lower than that at the reference sites (Figure 3). The changes in bird species richness at the mine area were similar to other areas subjected to environmental pollution (Eeva et al. 2012; Alaya-Ltifi and Selmi 2014; Belskii and Mikryukov 2018). However, these results did not permit us in identifying the way they led to the decrease in bird diversity. A study about copper pollution showed that the decrease in bird diversity was not associated with litter copper concentrations in a strictly dose-dependent manner (Eeva et al. 2012). Some reasons might explain our results. The main reason would be that trace metal pollution could decrease the food resources needed for reproduction and survival (Bel'skii and Lyakhov 2003; Eeva et al. 2010; Alaya-Ltifi and Selmi 2014), which could cause birds to spread outward. And this investigation was conducted in winter with relatively low food abundance,

birds could respond to the changes by moving from unsuitable to suitable sites (Baselga et al. 2015). Unfortunately, we did not sample the food resources to compare their availability for birds at the 4 sites. Such data are likely to provide information that would help to understand whether the observed decrease in the abundance of bird near the mine area was related to prey depletion. The second potential explanation would be that Reproductive dysfunctions caused by trace metals pollution, such as smaller clutches, hatching failure, and nestling mortality could affect indirectly the population levels (Burger 1995; Dauwe et al. 2005).

The decrease in species richness at the mine region also led to a shrink of PD, MPFD, and MPD (Figure 4C,D). Similar results were found in Russia (Belskii and Mikryukov 2018) and the Sierra de Guadalupe, Mexico (Ibarra-Meza et al. 2022). The shrink of PD, MPFD, and MPD reflected a loss of species with special trait combinations, suggesting that species that fulfil specialized functional roles disappear successively at the mine region. For instance, some species of larger bodies, such as ring-necked pheasant *Phasianus colchicus*, silver pheasant *Lophura nycthemera*, red junglefowl *Gallus gallus* et al., have disappeared from mining areas (Figure 2). Niche comparison (Figure 6E) showed that the reduction of some exclusive niche species caused differences within the community, indicating that most species were not sensitive to the effects of trace metals. For SES.FRic, we did not find the differences between the mine area and 3 reference sites (Supplementary Figure S3), revealing pure functional diversity at the mine area and 3 reference sites were nearly the same, that is, functional diversity may be mainly driven by the variations of species richness (Ding et al. 2021).

The results of NRI and NFRI in our study indicated that the assembly of bird community was not driven by deterministic process, that is, mining activities did not affect the main cause of bird community clustering. Thus, ecosystem disturbances did not always affect the structure of the bird communities. For example, the bird community structure in the Amazon

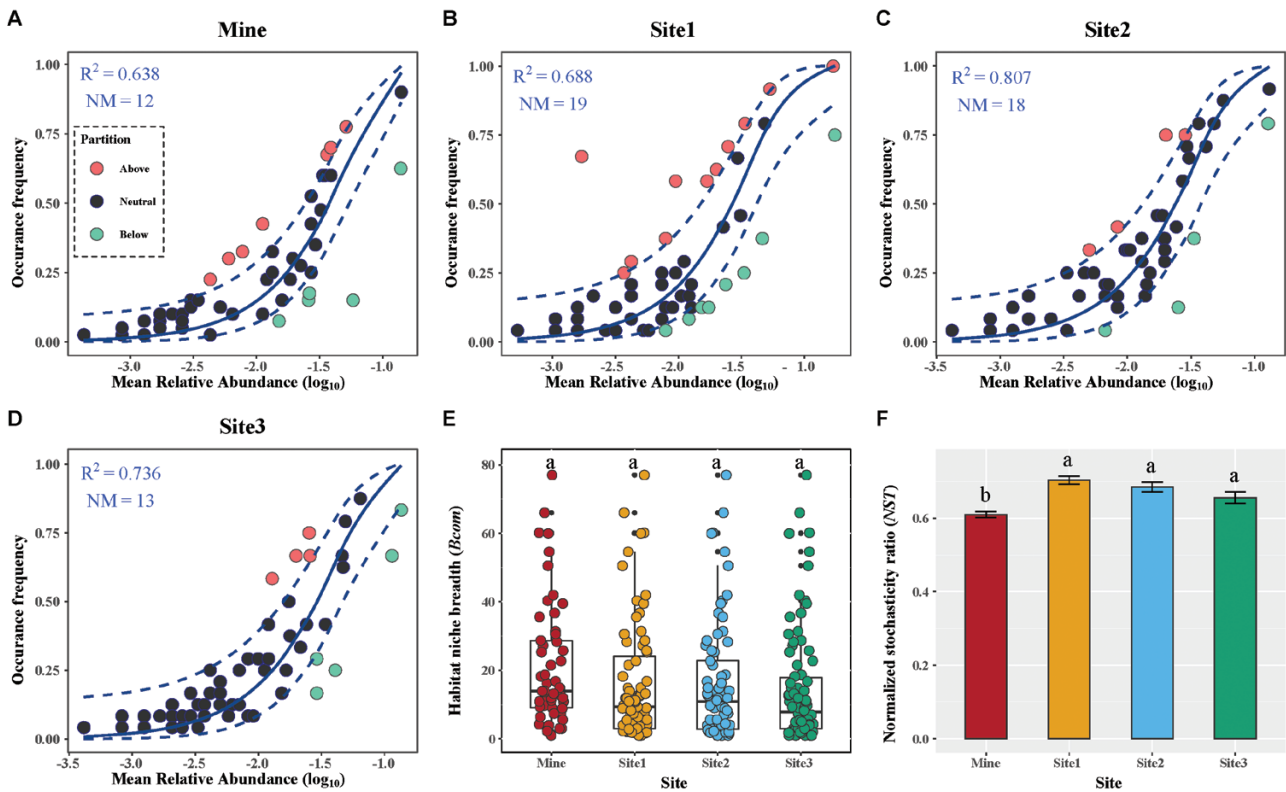


Figure 6. Ecological processes shaping the bird community assembly at the mine and reference sites. The fit of the neutral community model (A–D) showing the species predicted occurrence frequencies versus the relative abundance among 4 sites. The blue solid lines indicate the best fit for Sloan's neutral model. The blue dashed lines represent 95% confidence intervals around the model prediction. R^2 represents the goodness of fit to the model. Nm quantifies an estimate of dispersal between communities, determining the correlation between occurrence frequency and regional relative abundance. Species that occur more frequently than predicted by the model are shown in red, while those that occur less frequently than predicted are shown in green. (E) Comparison of mean habitat niche breadth (B_{com}) for all taxa among the mine and 3 reference sites (same letters indicate no significant difference at the $P < 0.05$ level using Tukey's post hoc test). (F) The comparison of normalized stochasticity ratio (NST) between the mine and reference sites for bird communities (difference letters show significant difference at the $P < 0.05$ level using Tukey's post hoc test).

forest undergoing wildfire did not differ from that expected by chance (Hidasi-Neto et al. 2012). In our study, the results of NCM and NST clearly support the dominant role of stochastic processes in shaping the bird community assembly (Figure 6A–D, F). This revealed that the mine environment seems to have a weak selection pressure on bird communities. It might be that birds at the mine area presented phenotypic adaptation and behavioral changes which allowed species to persist in situ (Charmantier et al. 2008; Schaefer et al. 2008). The result of the community-level habitat niche breadth (Figure 6E) also demonstrated the relative contribution of stochastic processes, because higher niche widths tend to be accompanied by a higher proportion of stochastic processes (Pandit et al. 2009). This indicates that the bird assemblages at the mine area and reference sites were not subjected to extreme environmental selection (same or different resource allocation) to form a highly specialized niche. In summary, we provide important new information about the effects of mining activities on understory birds, the processes such as dispersal and survival might be more important than biological traits to community assembly. The construction of bird communities dominated by stochastic process was also common. For example, Baselga et al. (2015) found that the bird community structure in their study was not dominated by deterministic process (land cover change), but by stochastic process. Stochastic processes might play a surprisingly large role in driving community composition of forest bird, and drive most

of the variation of local bird assemblages (Renner et al. 2014). Local random extinctions and dispersal events from occupied to non-occupied suitable habitats would produce neutral processes in species distributions that, at the assemblage level, would result in neutral variation in assemblage composition (Baselga et al. 2015). Although these studies used different methods, they all emphasized the importance of stochastic processes in community assembly. Therefore, assessing the impacts of global change on biological assemblages should consider the existence of non-deterministic processes in addition to deterministic ones.

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Conflict of Interest

The authors declare that they have no competing interests.

Ethical Approval

All samples of feathers of the Grey-cheeked Fulvetta were obtained for this research under the permission of Chongzuo Forestry Department (2018.1) and Animal Ethics Committee, Guangxi University (GXU2018-039), China. Grey-cheeked Fulvetta are not on the key protected species lists of Guangxi Zhuang Autonomous Region or China.

Author Contributions

S.L.: Study concept and design, Acquisition of data, Wrote the manuscript. T.Z. and X.T.: Acquisition of data. W.M.M.: Modification of manuscript. A.J.: Study concept and design, Acquisition of data, Wrote the manuscript. All authors read and approved the final manuscript.

Supplementary Material

Supplementary material can be found at <https://academic.oup.com/cz>.

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