
**PROGRAMA DE PÓS-GRADUAÇÃO EM ECOLOGIA,
EVOLUÇÃO E BIODIVERSIDADE**

**DIVERSIDADE FUNCIONAL DE PLANTAS DISPERSAS POR ANIMAIS EM UMA
CRONOSSEQUÊNCIA DE FLORESTAS SECUNDÁRIAS DA MATA ATLÂNTICA**

WILLIAN BARBOSA SIMIONI

**Rio Claro – SP
2024**

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WILLIAN BARBOSA SIMIONI

Dissertação apresentada ao Instituto de Biociências do Câmpus de Rio Claro, Universidade Estadual Paulista, como parte dos requisitos para obtenção do título de Mestre em Ecologia, Evolução e Biodiversidade.

Orientadora: Prof.^a. Dra. Marina Corrêa Côrtes

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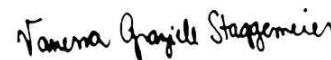
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*Dedico esta dissertação aos meus pais Dirce e Antonio,
às minhas irmãs Daniele e Juliana, e aos meus sobrinhos
Victor, Pedro, Isac, Matheus e Gabriel.*

Dedico especialmente à memória de minha querida Tia Neide.

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RESUMO

Frutos zoocóricos apresentam grande variedade de atributos funcionais que são importantes para as interações mutualísticas de dispersão de sementes, sobretudo para o processo de regeneração passiva de florestas secundárias. À medida que a composição de espécies vegetais varia em resposta ao processo de sucessão ecológica e às variáveis ambientais e bióticas, é esperado que os atributos funcionais também variem ao longo da (re-)organização das novas comunidades. Nesse estudo, nós caracterizamos o espaço funcional de atributos de frutos em comunidades de plantas dispersas por animais ao longo de uma cronosequência de florestas de regeneração natural da Mata Atlântica Semidecídua. Nós também investigamos a influência da idade, cobertura vegetal e distância geográfica entre manchas de florestas sobre a diversidade funcional alfa e beta. Nós utilizamos inventários florísticos de espécies zoocóricas em 55 parcelas de 20 x 45m localizadas em fragmentos de floresta secundária na região da Bacia Hidrográfica do Rio Corumbataí – SP, e os atributos das 130 espécies zoocóricas registradas foram obtidos a partir de uma extensa compilação de bases de dados, estudos científicos publicados e de amostras coletadas em campo. Os dados faltantes foram obtidos utilizando um algoritmo de imputação de dados com base na filogenia das espécies. Nossa análise de coordenadas principais foi capaz de capturar ao todo 71.35% da variação dos atributos para os primeiros cinco eixos, e 39.48% para os primeiros dois eixos. A primeira dimensão (PCoA1) representou 24.17% da variação dos atributos. Encontramos evidências de que a idade de restauração e a distância entre as comunidades contribuem para aumentar a diversidade funcional de características de frutos e sementes em comunidades de espécies zoocóricas, o que está alinhado com nossas hipóteses anteriores. Embora não tenhamos encontrado efeito significativo da idade e da distância nos índices de diversidade alfa FRic e na FEve, os índices FMPD e FDis mostraram uma tendência a aumentar à medida que as comunidades envelhecem e com distância entre elas. Da mesma forma, a diversidade funcional beta foi influenciada positivamente pela diferença de idade e distância geográfica entre as comunidades. A dissimilaridade de Jaccard e o turnover foram maiores entre comunidades maior diferença de idade e distância. Uma maior diversidade funcional na dispersão de sementes pode contribuir para a manutenção da biodiversidade e de processos ecossistêmicos essenciais em florestas secundárias em regeneração.

Palavras-chaves: Ecologia de comunidades, ecologia funcional, diversidade funcional alfa e beta, atributos funcionais, frugivoria, restauração.

ABSTRACT

Zoochorous fruits exhibit a wide range of functional attributes that are important for mutualistic seed dispersal interactions, especially for the passive regeneration process of secondary forests. As the composition of plant species varies in response to ecological succession and environmental and biotic variables, it is expected that functional attributes will also vary throughout the (re-)organization of new communities. In this study, we characterized the functional space of fruit traits in animal-dispersed plant communities along a natural regeneration chronosequence of Semideciduous Atlantic Forest. We also investigated the influence of forest age, forest cover, and geographic distance between forest patches on alpha and beta functional diversity. We used floristic inventories of zoochorous species in 55 plots of 20 x 45m located in secondary forest fragments in the Corumbataí River Watershed – SP region, and the attributes of the 130 recorded zoochorous species were obtained from an extensive compilation of databases, published scientific studies, and field-collected samples. Missing data were obtained using a data imputation algorithm based on species phylogeny. Our principal coordinate analysis was able to capture in total 71.35% of trait variation for the first five axes, and 39.48% for the first two axes. The first dimension (PCoA1) represented 24.17% of trait variation. We found evidence that restoration age and distance between communities contribute to increased functional diversity of fruit and seed characteristics in zoochorous species communities, aligning with our previous hypotheses. Although we did not find a significant effect of age and distance on the alpha diversity indices FRic and FEve, the indices FMPD and FDis showed a tendency to increase as the communities age and with greater distance between them. Similarly, beta functional diversity was positively influenced by the difference in age and geographical distance between communities. Jaccard dissimilarity and turnover were higher between communities with greater differences in age and distance. Greater functional diversity in seed dispersal may contribute to the maintenance of biodiversity and essential ecosystem processes in regenerating secondary forests.

Keywords: Community ecology, functional ecology, alpha and beta functional diversity, functional traits, frugivory, restoration.

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1 INTRODUCTION

Frugivory and seed dispersal represent key processes in terrestrial ecosystem ecology (Herrera, 1985). Through frugivory, plants have their seeds dispersed by animals, allowing them to be deposited in different locations as animals move through the landscape, contributing to seedling recruitment and consequently, to the colonization and establishment of both primary and secondary forests (Kitamura, 2011; Rozendaal et al., 2019). Several factors determine the mutualistic interactions of frugivory and seed dispersal (Jordano, 2000). The occurrence of interaction depends not only on the co-occurrence of interacting species in space and time but also on the correspondence between fruit and frugivore characteristics (Dehling et al., 2016; González-Castro et al., 2015).

On one hand, the optimal diet theory postulates that foraging, ingesting, and digesting food resources incur energetic costs for the consumer. On the other hand, the seed dispersal syndrome hypothesis suggests that fruit-bearing plants offset the energetic expenditure of frugivores by enhancing fruit attractiveness through investment in nutritive compounds (Debussche et al., 1987; Van der Pijl, 1982) in response to the dietary needs and sensory capacities of dispersers (Lei et al., 2021). However, plants dispersed by animals face an evolutionary dilemma between producing excessively attractive fruits (Cazetta et al., 2008), susceptible to herbivore and pathogen attacks, and investing in physical and chemical defenses against predation, which might hinder frugivory and seed dispersal (Cipollini et al., 2004; Cipollini & Levey, 1997; Schaefer et al., 2003). Secondary compounds, for instance, serve as chemical defenses against microorganisms and predators, making interaction with frugivores more challenging (Whitehead & Bowers, 2014).

Angiosperm fruits have evolved a wide array of attractive features that constitute the fruit-frugivore syndromes (Valenta et al., 2017; Van der Pijl, 1982), known as functional or phenotypic traits (Violle et al., 2007). Fleshy fruits or those with nutritious seeds generally exhibit detectable traits for dispersing frugivores, such as fruit color and size (Jordano et al., 2011; Valido et al., 2011). Fruit shape, the presence of secondary structures (Burns et al., 2009; Galetti et al., 2003; Valido et al., 2011), nutritional composition, and fruit energy content (Jordano, 2000; Nevo et al., 2019) are other important traits for frugivory. For example, fruits dispersed by birds must fit the opening of the bird's beak, and after ingestion, the bird must be able to digest it and discard viable seeds in favorable microsites (Jordano, 2000).

The functional diversity of plants dispersed by animals encompasses a spectrum of traits associated with fruit morphology, nutritional composition, and adaptation to frugivore preferences. These traits play a crucial role in determining the interactions between plants and their dispersers, influencing seed dispersal effectiveness, and ultimately shaping the structure and dynamics of regenerating communities (Knapp et al., 2016). Variations in fruit traits, such as size, color, pulp-to-seed ratio, and nutritional content, contribute to the establishment of diverse frugivore-plant networks, where specific traits attract different frugivore species (Ordano et al., 2017). This functional diversity not only enhances the chances of successful seed dispersal but also promotes the establishment of a wide range of plant species, fostering biodiversity in regenerating ecosystems (Hawes et al., 2020).

The environmental variables present in naturally regenerating communities exert significant influence on the functional diversity of plants dispersed by animals. Factors such as habitat structure, successional stage, and landscape connectivity impact the availability and diversity of resources for frugivores, consequently affecting the selection pressure on plant traits (Monteiro et al., 2022; Stevenson et al., 2023). For instance, in early successional stages characterized by open habitats, fruit traits favoring visibility and attraction may predominate to entice dispersers (Cote et al., 2017). Conversely, in more mature stages with denser vegetation, i.e. high connectivity, fruit traits may evolve towards adaptations, like large fruits with big seeds and attractive colors, that aid in long-distance dispersal or appeal to specific frugivore guilds (Valenta & Nevo, 2020). These environmental variables contribute to shaping the functional diversity of zoochorous plants by driving selective pressures on fruit traits, thereby influencing the composition and interactions within the frugivore-plant network during community regeneration (Poorter et al., 2019; Zuñe-da-Silva et al., 2022).

Neotropical forests naturally exhibit spatial variation in plant species composition (Myers et al., 2013) and functional diversity (Aslan et al., 2019). This variation can be further accentuated in ecological communities facing the impacts of deforestation, forest fragmentation (Haddad et al., 2015), and natural or assisted forest regeneration processes (Lohbeck et al., 2012). In this context, considering the use of functional diversity metrics in community studies is crucial to understand how these species establish themselves in communities and their role in providing ecosystem services (Lohbeck et al., 2013). Furthermore, evaluating functional diversity metrics can provide valuable insights into the effectiveness of the regeneration process and can guide future restoration strategies (Poorter et al., 2019).

Approximately half of the world's tropical forests are in a secondary stage of ecological succession (Wright & Muller-Landau, 2006). This implies an opportunity for the establishment of new taxonomic and functional configurations during the ecological succession process, where variables such as the land history prior to the restoration process, connectivity, and forest age are crucial in shaping these communities and their functional traits (Poorter et al., 2019; Zuñe-da-Silva et al., 2022).

The restoration process favors the spontaneous regeneration of forests, enabling ecological succession and consequently affecting the diversity and composition of the species present (Rozendaal et al., 2019). The presence and behavior of seed-dispersing animals play a crucial role in reintroducing seeds and re-establishing ecological interactions, directly influencing trait (dis)similarity of plants that colonize these restored environments. Variation in food preferences and movement patterns of dispersing animals results in different seed dispersal strategies, thus shaping the diversity and composition of plant communities (Almeida et al., 2022). Around 75% of tree species in the Atlantic Forest are animal-dispersed (Almeida-Neto et al., 2008), with birds and mammal groups standing out as crucial for seed dispersal due to their ability to move between fragments and use degraded areas and regenerating vegetation (Kitamura, 2011; Tiffney, 2004).

In this scenario, knowledge of how environmental factors shape the diversity of fruit traits and the associated frugivore-plant interactions informs restoration strategies aimed at enhancing seed dispersal and promoting species diversity. In this study, we characterized the functional space of fruit traits in animal-dispersed plant communities along a natural regeneration chronosequence of Semideciduous Atlantic Forest. We also investigated the influence of forest age, forest cover, and geographic distance between forest patches on alpha and beta functional diversity. We hypothesized that the oldest plant communities in terms of regeneration have higher functional diversity of traits and, therefore, greater heterogeneity of traits, and that the geographic distance between plant communities increases the functional dissimilarities between them due to seed dispersal distance limitation.

2 MATERIAL AND METHODS

2.1 STUDY AREA

Our study areas consisted of secondary forest remnants in the Atlantic Semideciduous Forest domain undergoing passive restoration (without human intervention) (see Figure 1,

Table S1), located in the Corumbataí River Watershed, Southeast region of the State of São Paulo (Brazil).

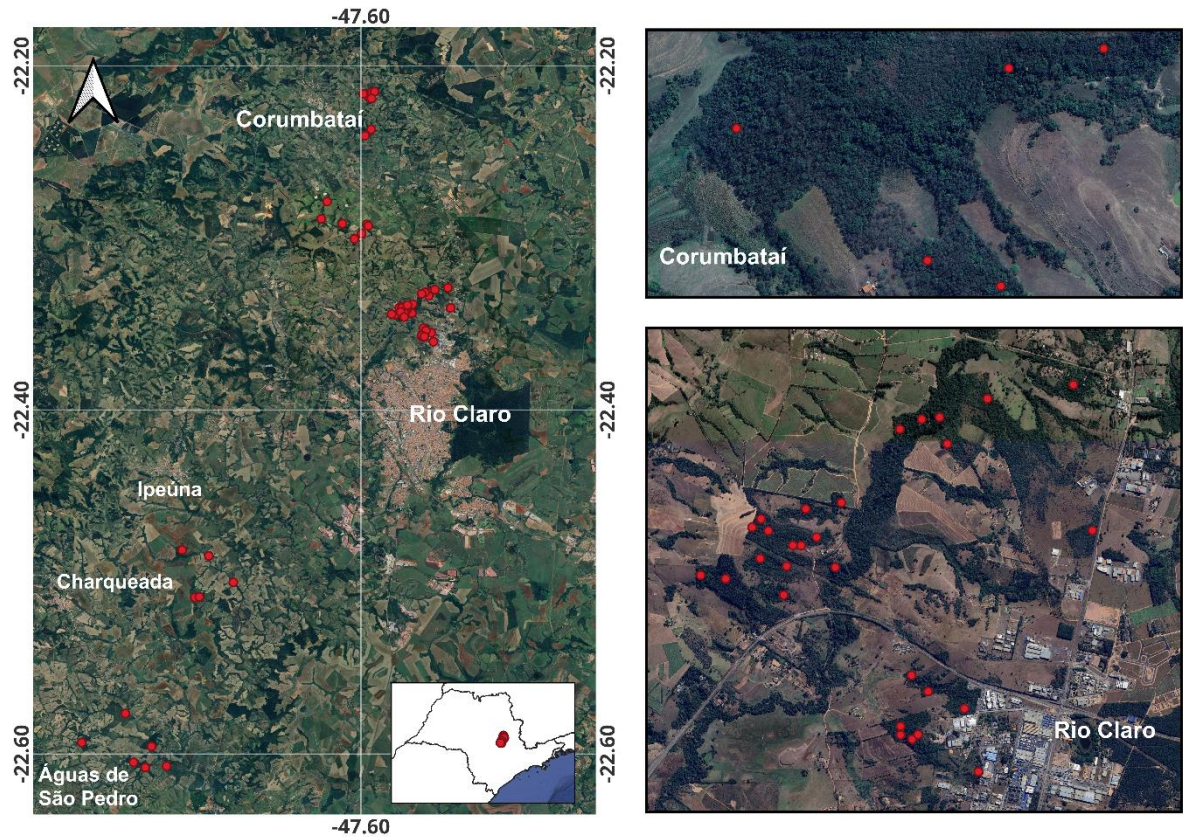


Figure 1 Localization map of 55 zoochoric plant communities (red dots) in fragments of semi-deciduous Atlantic Forest in the Corumbataí River Watershed - SP, Brazil.

These areas comprise a predominantly agricultural landscape with sugar cane, *Eucalyptus* spp. plantations and other monocultures, and also pasture areas for livestock. The Köppen climate classification for the region is Cwa, with dry winters and rainy summers (Alvares et al., 2013). The average annual precipitation is 1,367 mm, around 80% of which occurs in the rainy season from October to March, and the average monthly temperature is 20.5 °C (minimum monthly average of 15.6 °C and maximum of 29.5 °C).

From the 1970s onwards, several areas of the Corumbataí River Watershed, including some of our study areas, were abandoned due to rural-urban migration, initiating the process of passive restoration with the formation of an understory of native and invasive plant species (César et al., 2018). We worked on an extensive inventory of plant communities conducted previously by R. César under the supervision of P. Brancalion (César et al., 2021). The inventory was conducted in 55 plots of 20 x 45 m placed inside secondary forest remnants and included all individuals with arboreal and shrubby life forms with DBH $\geq$ 5 cm (diameter at

breast height). From now on, we refer to each plot as an ecological community because we assume each inventory is a representative sample of the plant community in that remnant, although some plots are within the same forest remnant and, therefore there is spatial dependence between them. Among the recorded plant species, we only selected the species that produce attractive fruits and whose seeds are dispersed by animals (see section 2.2).

2.2 ZOOCHORIC SPECIES AND TRAITS

We accounted for 130 animal-dispersed plant species at the 55 communities belonging to 42 taxonomic families (see Table S2). Species names, genera and families were retrieved and standardized from The Plant List (<http://www.theplantlist.org>) e Global Biodiversity Information Facility (<https://www.gbif.org/pt/>).

We selected a total of 20 quantitative and qualitative functional traits that included dispersal traits and vegetative traits (see Table 1). Dispersal traits consisted of those related to the attraction of seed-dispersing frugivores and vegetative traits related with plant size and form. First, we compiled information from existing databases. The two databases that represented the highest contribution to this study were TRY Plants (Kattge et al., 2011) and Neotropical Tree Communities (TreeCo, version 4.0), which can be made available upon request.

Secondly, for the plant species and traits not covered by these large databases, we extensively searched scientific literature for trait values using as key-words the following terms both in English and in Brazilian Portuguese: “Semi-deciduous Atlantic Forest”, “plant communities”, “frugivory and seed dispersal”, “functional traits”, “morphological traits of fruits and seeds”, and the species or genus name, when needed. We compiled data from around 38 studies published in scientific journals and nine books that met the research aims. The list of selected studies can be verified in Session 2 of the Supplementary Material. Compiled data were stored at the online ReSeeD database platform (<https://souzayuri.shinyapps.io/reseedproject/>). Fruits of some species were collected on field expeditions to supply possible missing data in the compilation, and all variables of interest were extracted.

Table 1 Quantitative and qualitative traits and its ranges selected to study the functional space and functional diversity of zoochoric species in regenerating secondary Atlantic forests in Corumbataí River Watershed - SP.

Traits	Numerical range/Categories
<i>Quantitative</i>	
Maximum plant height*	5 – 32 (m)
Woody density*	0.3257 – 1.1278 (g/cm ³)
Fruit length	3.2 – 130 (mm)
Fruit diameter*	2.3 – 80 (mm)
Fruit shape index*	0.73 – 9.6
Fruit mass*	0.011 – 88 (g)
Pulp mass	0.0069 – 50.5 (g)
Seed length	1.1 – 55 (mm)
Seed diameter*	0.5 – 45 (mm)
Seed total mass*	0.002 – 46.1 (g)
Seed number*	1 – 300
Pulp/seed ratio*	0.056 – 153.2
<i>Qualitative</i>	
Growth form*	Tree and shrub
Deciduousness*	Deciduous, semideciduous and evergreen
Shade tolerance*	Shade-tolerant and light-demanding
Dispersal group*	Birds, mammals and mixed ^a
Fruit type*	Berry, capsule, drupe, other ^b
Fruit secondary structure*	Presence and absence
Fruit color*	Black, brown, green, purple, red, yellow, other ^c
Aril*	Presence and absence

* Traits that were selected for data analysis after correlation tests (see section 2.5).

^a Dispersal group mixed: both birds and mammals as dispersers for a given plant species.

^b Fruit type other: few entries for other types of fruits reported in literature.

^c Fruit color other: few entries for other types of colors reported in literature.

The compiled data was verified for inconsistencies and revised for differences in the order of magnitude of the values. After the standardization process, the resulting data set was used to calculate the arithmetic average of numerical traits for each plant species in order to obtain a single value per trait per species, since the priority of our study is to preserve general information about traits of each species. In the case of categorical variables and their levels, the most frequently found level for a variable of a given species was selected and adopted as the only one.

To look for possible missing data, we structured a matrix with the 130 species in the rows and the 20 traits in the columns, resulting in 2470 value entries. We found 6.9% missing values in quantitative traits, and to avoid excluding species with missing data, we applied a data imputation method as described in section 2.4.

2.3 PHYLOGENETIC DISTANCE

Phylogenetic distance between pairs of all plant species considered in this study was calculated using the function *get_tree* from the package *RTREES* (Li, 2023), which downloads phylogenetic distances from the extended R implementation of the Open Tree of Life (Smith & Brown, 2018). Using these distances, we built a phylogenetic tree of our species set (see Figure S1).

2.4 DATA IMPUTATION

To prevent excluding species with missing trait data, we used a Multivariate Imputation with Chained Equations method implemented by the *MICE* package. Among the different possibilities of multiple imputation using *MICE*, we chose the classification and regression trees because it preserves non-linear relationships between traits (Buuren & Groothuis-Oudshoorn, 2011). For doing this imputation, we considered all quantitative traits and also accounted for the phylogenetic distance among species during the process by including the first ten eigenvectors from a principal component analysis (PCoA) of the phylogenetic distance (section 2.3), which can improve the performance of *MICE* (Penone et al., 2014). To extract the eigenvectors, we used the function *PVRdecomp* from the package *PVR* based on a previous conceptual framework that considers phylogenetic eigenvectors (Diniz-Filho et al., 2012).

2.5 MULTIDIMENSIONAL SPACE OF TRAITS

To analyze the functional multidimensional space, we first excluded a set of highly correlated traits. For this, we conducted Pearson's correlation tests between quantitative traits (see Figure S2, Table S3), setting a cutoff value equal to or higher than 0.75. Fruit length, seed length and pulp mass were excluded from the following steps because they were highly correlated to fruit diameter, seed diameter and fruit mass respectively (Pearson's correlation = 0.77, $p < 0.01$; 0.94, $p < 0.01$, and 0.79, $p < 0.01$). We decided to maintain both fruit and seed diameters since these traits represent the smallest dimensions that limit the diaspore ingestion by animals. We also decided to keep fruit shape index and seed number because they are traits whose relationships with the set of dispersal traits are not well known in the scientific literature. Our dataset ended up with eight qualitative traits and nine

quantitative. All quantitative traits were log transformed to reduce the influence of extreme values.

We estimated the multidimensional trait space from log transformed traits using a principal coordinates analysis (PCoA) implemented by the package *MFD* in R (Magneville et al., 2022). First, we obtained the Gower's distance (Gower, 1966) between species and their multivariate set of traits with the *funct.dist* function. In order to compute the multidimensional space of traits for plant species we used the function *quality.fspaces*. We assessed the quality of n-dimensional functional spaces resulting from the PCoA by looking for the lowest mean absolute deviation (MAD) which was used as a cutoff for retaining the PCoA axes as new trait variables (Magneville et al., 2022). The MAD index can ranges from 0 to 1, and the lowest value is indicative of a functional space of higher quality, which means that the distance between each pair of species is more congruent with the initial functional distance (Maire et al., 2015). The first five PCoA axes were retained for overall traits (MAD = 0.49), although the lowest MAD reached the first seven axes (MAD = 0.31) (see Figure S3, Table S4). We chose five axes to represent the n-dimensional space because the number of axes should be strictly less than the number of species within the community (Villéger et al., 2008) and it would compromise the beta diversity analyses. In the end, the five PCoA axes were able to retain the representation of most traits which explained 74.2% of the variation (see Figure S4, Table S5 for quantitative traits, and Figure S5, Table S6 for qualitative traits), that were used to calculate both functional alpha and beta diversity indices (see sections 2.7.2 and 2.7.3). Then, we kept the first two PCoA axes to provide a two-dimensional representation of trait functional space between species.

2.6 PHYLOGENETIC SIGNAL

Phylogenetic signal of the different quantitative traits for the 130 zoochoric species was calculated using the function *phylosig* implemented by the *PHYTOOLS* package (Revell, 2012) in R. We used Blomberg's K as a measurement of the phylogenetic signal. A Blomberg's K value closer or higher to 1 means the trait is evolving more conservatively than expected along the phylogenetic tree, and therefore is more strongly influenced by phylogenetic history than it would be if evolution were random; for a Blomberg's K value closer to 0, trait is evolving more divergently than expected under a random evolution model and is, therefore, less affected by phylogenetic history (Blomberg et al., 2003).

2.7 RELATIONSHIP BETWEEN FUNCTIONAL DIVERSITY AND ENVIRONMENTAL VARIABLES

We estimated both alpha and beta functional diversity and tested them in response to environmental variables as described in the following steps:

2.7.1 Environmental variables

In order to investigate the variation across plant community traits, we considered as predictor variables of functional diversity indices the age since the restoration started (in years), forest cover index, and the minimum and mean geographic distance between communities. The age of the forests were previously estimated from aerial and satellite images (César et al., 2021; Ferraz et al., 2014) and varied from 17 to 60 years. The forest coverage index was calculated based on land use and coverage data from MapBiomas website (<https://brasil.mapbiomas.org>) in the surrounding area through the construction of buffers with a radius of 1 km centered on the communities. Buffers were generated using GIS software and subsequently used to extract information about vegetation cover. To calculate geographic distance, we used the *distm* function from the GEOSPHERE package (Hijmans et al., 2022) implemented in R, which calculates a distance matrix between pairs of communities based on their geographic coordinates. We then estimated the minimum and average absolute distances of each focal plant community in relation to the other sampled communities. We also tested for Pearson's correlation between environmental variables and did not find any strong correlation (see Table S7).

2.7.2 Alpha functional diversity

The diversity metrics were calculated using the function *alpha.fd.multidim* of the MFD package (Magneville et al., 2022), that uses as input the five PCoA axes extracted previously (section 2.5). Species richness was calculated as the number of taxonomic species in each community. Functional richness (FRic) represents the minimum convex hull volume of all species belonging to a single community (Mouillot et al., 2013). Functional dispersion (FDis) represents the abundance weighted deviation of species trait values from the center of the functional space, in which communities with species more divergent from the functional space center will have a higher FDis (Mouillot et al., 2013). Functional Evenness (FEve) was calculated as the regularity of the distribution and relative abundance of species in functional space for a given community (Mouillot et al., 2013). Functional Mean Pairwise Distance

(FMPD) represents the functional (dis)similarity between all species pair in a community (Mouillot et al., 2013; Webb et al., 2002). We tested for Pearson's correlation between the observed alpha diversity indices (see Figure S6, Table S8), setting a cutoff value equal to or higher than 0.25. Only FMPD index was moderately correlated with species richness (Pearson's correlation = 0.27, $p < 0.01$), so we decided to keep it in the next analysis.

We tested the effect of the environmental predictor variables age, forest cover, minimum distance, and the mean distance on each alpha functional diversity index (FRic, FMPD, FEve, and FDis) for each community. Variables were centered and scaled to allow for linear models with multiple covariates. We used generalized linear models (GLM) implemented by the *glm* function in the R STATS package, following the general model:

$$\text{Model} = \text{Alpha Functional Index} \sim \text{Age} + \text{Forest cover} + \\ \text{Mean distance} + \text{Minimum distance}$$

After building the generalized linear regression models, we used the *dredge* function from the MUMIN package to rank candidate models. This approach explores different combinations of independent variables (environmental variables) to determine which provides the best fit to the data, using the AICc weight (w_i) that represents the probability that the model is the best between the set of candidate models (Wagenmakers & Farrell, 2004). Models were then selected for interpretation based on the ΔAICc , which represents the probability that a given model minimizes information loss (Burnham & Anderson, 2004; Wagenmakers & Farrell, 2004). Based on this criterion, we interpreted the best ranked model whenever the null model was not included among the models with $\Delta\text{AICc} < 2$. If the null model was included among the plausible models ($\Delta\text{AICc} < 2$) we considered that the response variable was not associated with any of the covariates included in this study.

2.7.3 Beta functional diversity

We estimated beta functional diversity using the function *beta.fd.multidim* of the MFD package (Magneville et al., 2022). Metrics were calculated based on species occurrence and the five PCoA axes extracted previously (section 2.5). We chose Jaccard's dissimilarity index which can be decomposed into functional turnover and functional nestedness-resultant components (Villéger et al., 2013).

To investigate the relationship between beta functional diversity indices and environmental variables between pairs of communities, we followed a model selection approach using maximum-likelihood population effects models (Clarke et al., 2002). Because the data is based on pairwise dissimilarity and pairs share communities, observations are not independent. To account for the lack of independence we used MLPE to include a correlation structure of the errors as random effect. Generalized least squares (GLS) models were fitted with a random effect that included the identification of the pair of communities, using the *gls* function from the NLME package, following the general model:

$$\begin{aligned} \text{Model} = \text{Beta Functional Diversity} \sim & \text{Age dissimilarity between communities} + \\ & \text{Forest cover dissimilarity between community buffers} + \\ & \text{Geographic distance} + \text{Correlation structure (Community 1 + Community 2)} \end{aligned}$$

Jaccard dissimilarity index and their turnover and nestedness components were considered as response variables and were modeled as a function of the three predictor variables: age dissimilarity between communities, forest cover dissimilarity between community buffers and geographic distance between communities. Age dissimilarity and forest cover dissimilarity were estimated by calculating the Euclidean distance of each variable between communities using the *dist* function of the *stats* package in R. Again, the *dredge* function was implemented after fitting the GLS models to explore different combinations of the predictor variables, to identify the most informative candidate model based on ΔAICc , and to select for interpretation (Burnham & Anderson, 2004; Wagenmakers & Farrell, 2004), similar to the approach used for modeling alpha diversity

3 RESULTS

3.1 PHYLOGENETIC SIGNAL AND MULTIDIMENSIONAL SPACE OF TRAITS

We found a strong phylogenetic signal ($p < 0.01$) for most quantitative traits (see Table S10). The traits that showed the highest phylogenetic signal were seed number with a Blomberg's K of 1.633 ($p < 0.01$), followed by fruit shape index ($K=0.822$), fruit mass ($K=0.558$), fruit length ($K=0.548$) and total seed mass ($K=0.538$). Traits that had a moderate phylogenetic signal were pulp mass ($K=0.419$) and fruit diameter ($K=0.444$). Finally, maximum plant height ($K=0.293$), seed diameter ($K=0.386$), seed length ($K=0.393$) had the

weakest phylogenetic signal between all traits, which indicates these traits can be under evolutionary pressure (Blomberg et al., 2003; Revell, 2012).

In the phenotypic profile of the communities, we found that the majority of our species have fruits with a diameter of up to 20mm and seeds of up to 10mm (Fig. 2A). Furthermore, most species produce fruits weighing up to 25g (Fig. 2B), and seeds weighing up to 10g (Fig. 2C). Regarding fruit type, most species have drupe-type fruits, and those of the capsule type are mostly bird-dispersed (Fig. 2D).

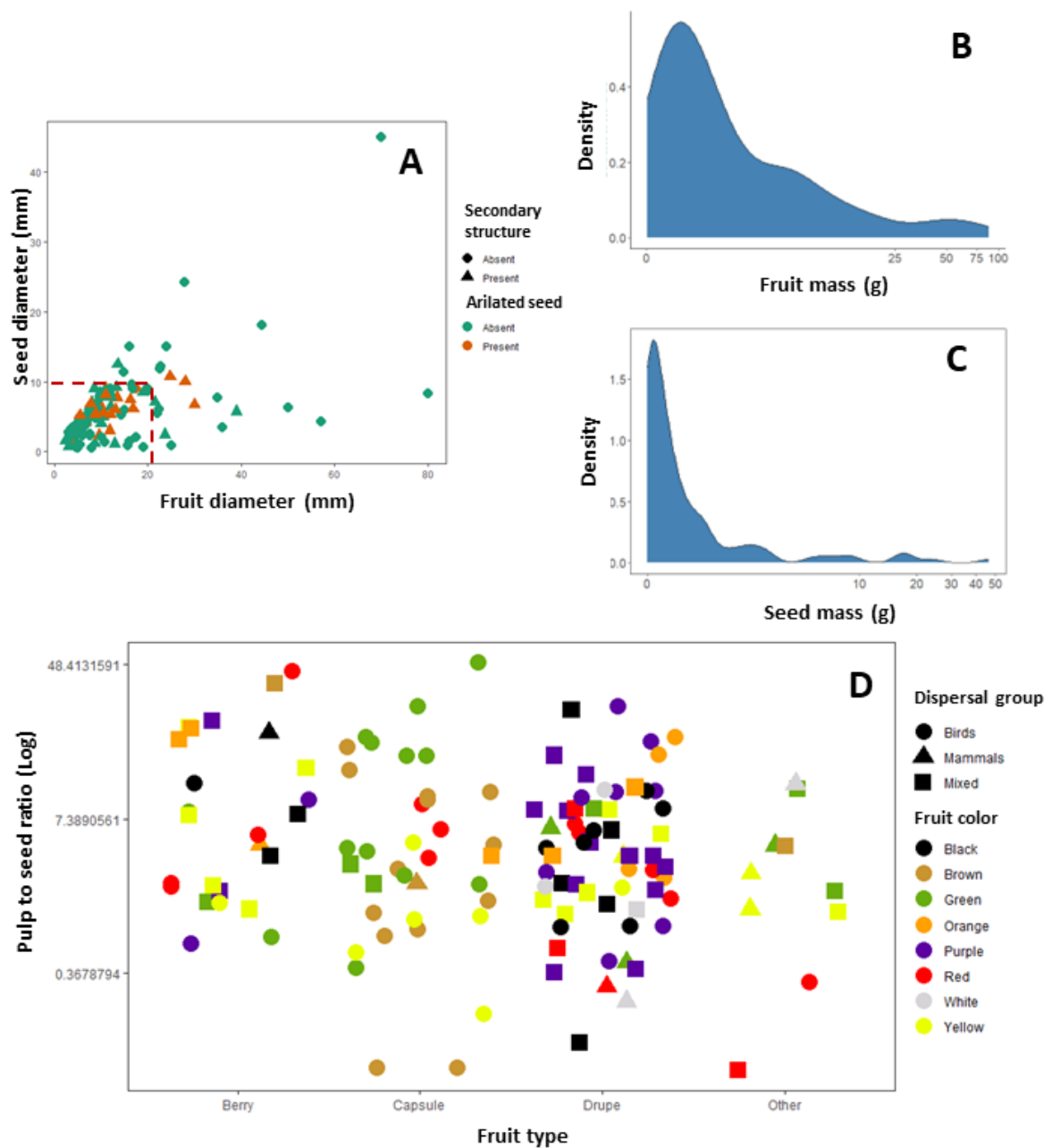


Figure 2 Fruit and seed traits characterization for 130 zoochoric species of 55 animal-dispersed plant communities in Corumbataí River Watershed remnants.

The multidimensional space of the attributes of the 130 zoochoric species resulted in a large, well-defined cluster of species concentrated closer to the center of the multidimensional space and two smaller clusters at the ends (Figure 3A).

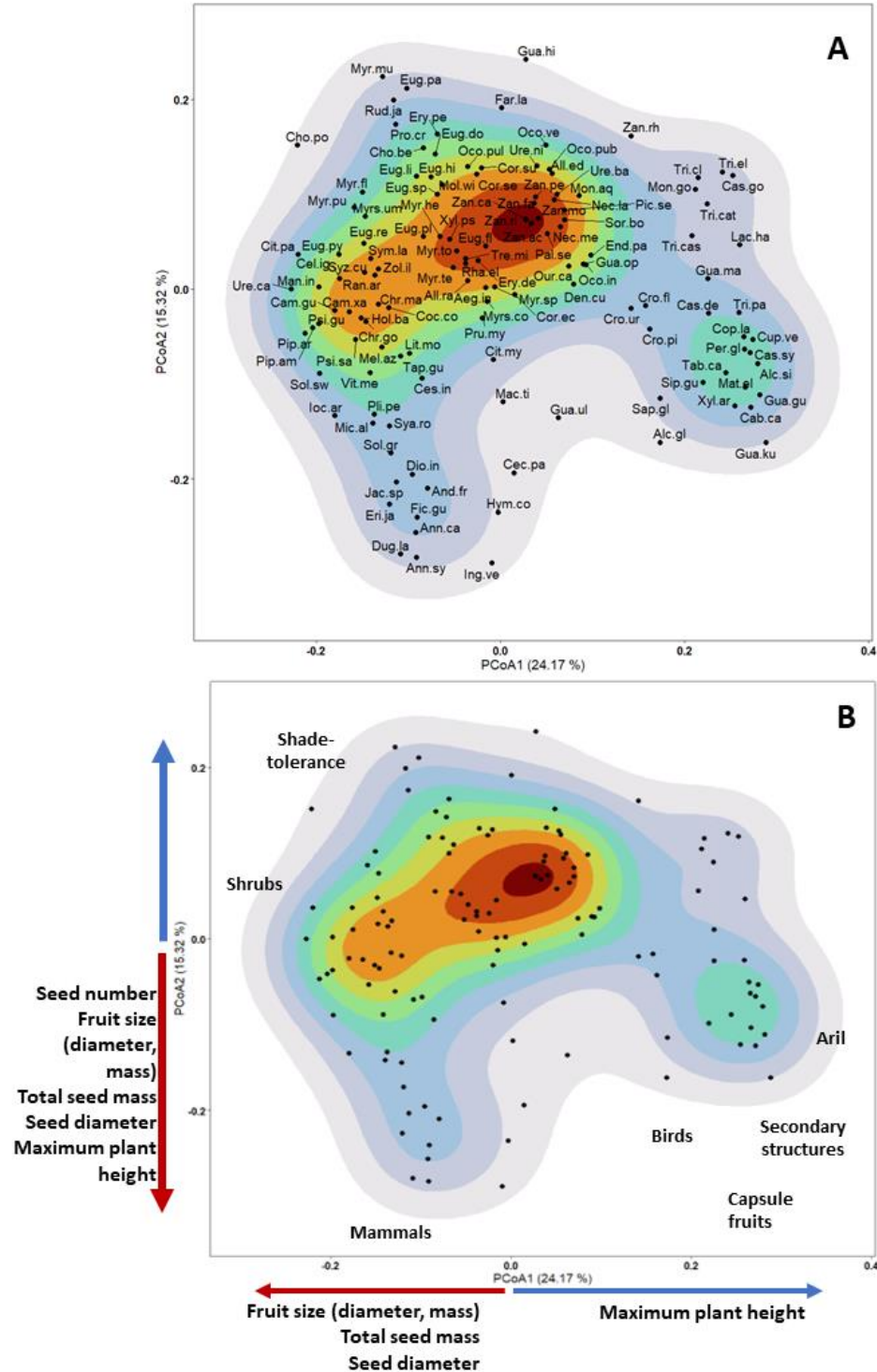


Figure 3 Multidimensional space of traits for 130 zoochoric species of Corumbataí River Watershed remnants, based on five PCoA axis that included quantitative and qualitative traits. Blue and red arrows indicate respectively, positive and negative correlation between traits and the two first PCoA axis.

Our principal coordinate analysis was able to capture in total 71.35% of trait variation for the first five axis, and 39.48% for the first two axis. The first dimension (PCoA1) represented 24.17% of trait variation. The main contributing traits to PCoA1 were maximum plant height, fruit diameter, fruit mass and pulp-to-seed ratio (Figure 3B, see Figure S4, Table S5). Lower values of the first axis represent species with larger fruits, higher seed production and shorter plants. Most of the qualitative traits contributed with the representation in PCoA1 but deciduousness (Figure S5). Capsule fruits, presence of secondary structure and aril are more correlated with higher values of PCoA1 (Figure 3B, Figure S5, Table S6).

The second dimension (PCoA2) represented 15.32% of trait variation and indicated a negative correlation between seed mass and seed number, fruit size (diameter and mass), and plant height (Figure 3B, see Figure S4, Table S5). Higher values of the second axis were associated with shrub life form, shade-tolerance, presence of secondary structure and absence of aril.

3.2 RELATIONSHIP BETWEEN FUNCTIONAL DIVERSITY AND ENVIRONMENTAL VARIABLES

3.2.1 Alpha functional diversity and models

Model selection for alpha functional diversity revealed that the most plausible and statistically significant models incorporate the regeneration age of communities and the average distance between communities, combining a positive effect of these two predictor variables on the FMPD index (Figure 4A and 4B, Table S11), suggesting that the functional divergence of traits between pairs of zoochoric species is influenced by the age of regeneration and the mean distance between communities. High values of FMPD indicate higher functional divergence between species in the community and higher variety of functional strategies.

The FDis index also showed a positive association with age and forest cover (Figure 4C and 4D, Table S11), indicating that communities with more advanced regeneration ages and more forested tend to have a greater variety of functional traits between species. Higher FDis values indicate a wider species distribution in the functional space, implying that the community may have a wider range of functional strategies. Even though the best ranked model (Table S11) includes minimum distance between focal and neighboring communities, its coefficient was not significant, therefore, we consider that distance to other communities is

less important for explaining FDis. Models for the other alpha functional diversity indices (Species richness, FRic, and FEve) included the null model among the plausible statistical hypotheses, therefore, we interpret that these functional metrics are not associated with any of the considered covariates in this study.

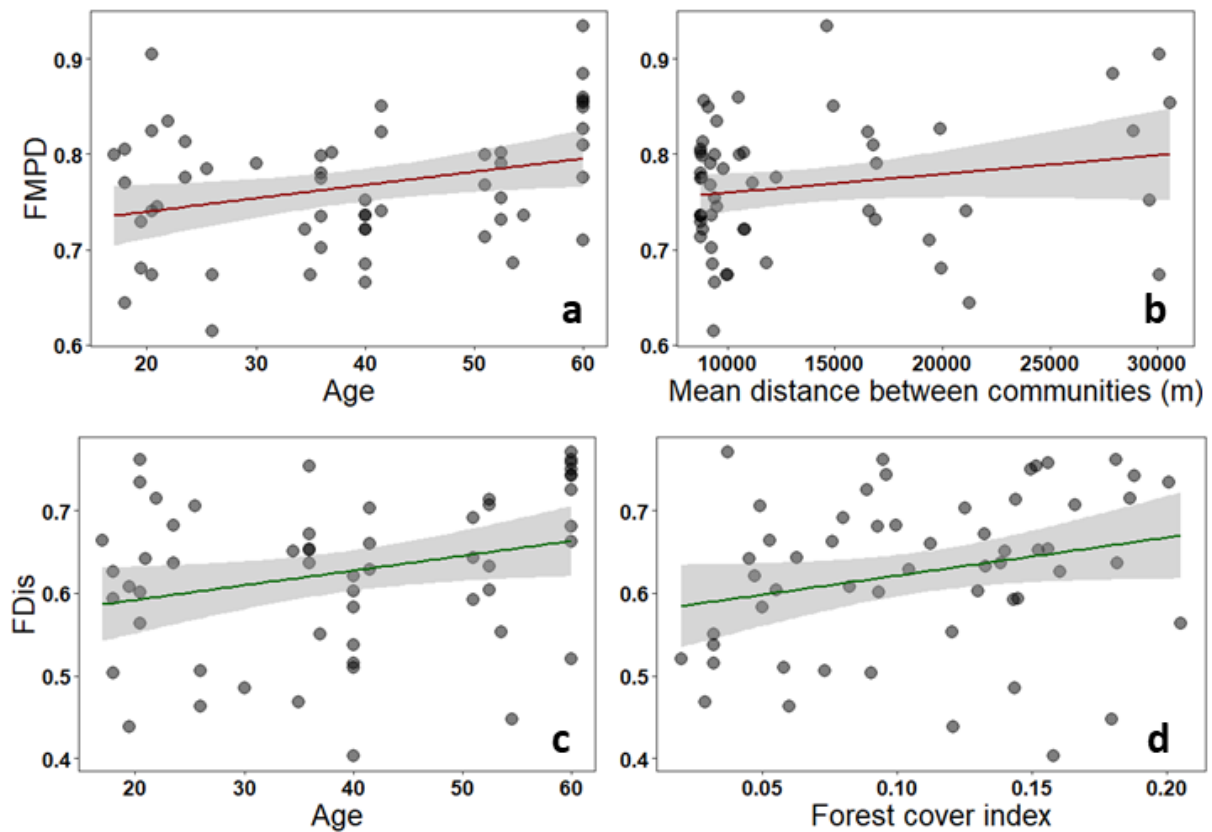


Figure 4 Relationship between alpha functional diversity indices and environmental variables in 55 zoochoric plant communities in the region of the Corumbataí River Watershed – SP, Brazil. FMPD, functional mean pairwise distance; FDis, functional dispersion. Graphics were based on models that fitted $\Delta AICc < 2$.

3.2.2 Beta functional diversity and models

Beta functional diversity was predominantly explained by the effect of trait turnover between observed communities (Pearson's correlation between overall Jaccard dissimilarity and turnover = 0.45, $p = 0.043$, Table S9) compared to the nesting process (Pearson's correlation between overall Jaccard dissimilarity and nestedness = 0.02, $p = 0.215$, Table S9). In a similar way to alpha diversity, total functional dissimilarity and turnover dissimilarity were explained by the dissimilarity in regeneration age and geographic distance between communities (Figure 5, Table S12). The nestedness component was not associated with any of the covariates (Table S12)

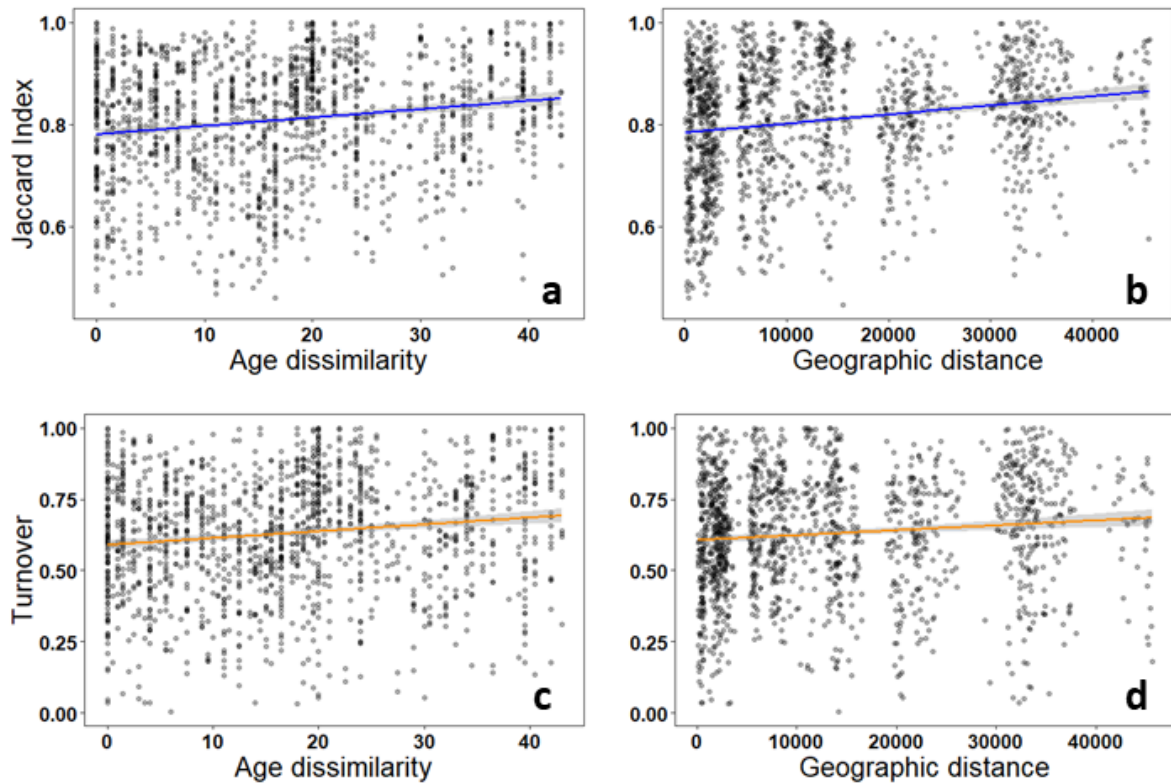


Figure 5 Relationship between beta functional diversity indices and environmental variables in 55 zoochoric plant communities in the region of the Corumbataí River Watershed – SP, Brazil. Graphics were based on models that fitted $\Delta AICc < 2$.

4 DISCUSSION

The composition and trajectory of assembling plant communities may be influenced by environmental factors. This influence is important, especially for functional traits of plants that play crucial roles in attracting their seed-dispersing frugivores that can maintain this cycle by bringing more plant species and a variety of traits to the community. Here, we found evidence that forest age and connectivity (measured as forest cover and distance between communities) contribute to increasing functional diversity of fruit and seed traits in communities of zoochoric species, which is aligned with our previous hypotheses. Although there was no significant effect of age, forest cover and distance on functional richness and evenness, both functional mean pairwise distance (FMPD) and functional dispersion (FDis) indices revealed a tendency to increase as communities became older, immersed in more forested landscapes, but more isolated to other plant communities. Beta diversity was mainly explained by turnover processes indicating that functional dissimilarity is affected by shifts in traits instead of loss of traits across communities. Beta functional diversity was also

influenced positively by the age difference and the geographic distance between communities. Jaccard dissimilarity and its component turnover were higher between communities of different ages and more distant from each other.

High FMPD values found in this study indicate that, in average, pairs of species in a given community have different functional traits, which can be positive in terms of increasing the diversity of functions performed by plants in the community. Furthermore, species with discrepant functional traits can explore different ecological niches (Ordano et al., 2017), in this case, serving as a food resource for a different set of dispersing animals in interaction networks (Moran & Catterall, 2010). Although the FMPD values found were higher in older communities, it is suggestive that these communities are still relatively young (17-60 years), since the FMPD tends to decrease as ecological succession progresses (Botta-Dukát, 2005; Chiu & Chao, 2014). This process is due to the community's occupation by species that are more abundant, competitively superior, or more adapted to the regeneration process (Chazdon et al., 2020). FMPD was also positively related to mean distance between communities. This indicates that the more isolated is the community, the higher the chance of presenting a discrepant trait, increasing pairwise dissimilarity between pairs of species within a community and, therefore, increasing diversity. More isolated forests (distant from others) share fewer species, however, unique species and, therefore, must present greater functional dissimilarity of traits in relation to other communities (Myers et al., 2013). Therefore, FMPD may represent a dynamic and diverse phase during forest regeneration, which can become more multifunctional ecosystems with time and according to spatial configuration (Lohbeck et al., 2013).

The FDis index is a measure that describes the overall amplitude of functional traits between species in a community (Mouillot et al., 2013). It quantifies the extent or diversity of functional traits present in a community in relation to the set of functional traits (Aslan et al., 2019). Higher FDis values in older plant communities located in more forested landscapes may indicate that the species have a wider range of ecological and seed dispersal traits compared to younger forests, which can result in different survival strategies (for example, shade tolerance modes), resource use (signals or rewards for attracting animal dispersers), and interactions with other organisms and the environment (Almeida et al., 2022). Secondary forests in more advanced regeneration stages, i.e. older age, are more susceptible to the arrival of different species via seed dispersal by different guilds of frugivores and, consequently, to the increase in greater functional diversity of traits in plant communities (Chazdon & Guariguata, 2016).

Over time, these older communities receive via seed dispersal a greater variety of traits and functional strategies among species that may include morphological adaptations and different ways of attracting different dispersing animals (Hawes et al., 2020; Tiffney, 2004). Similarly, communities immersed in more forested landscapes are better connected to other sites that may function as propagule and trait sources (Camargo et al., 2020; Han et al., 2019).

By investigating the beta functional diversity index, especially using the Jaccard index and functional turnover, in response to regeneration age and geographic distance between regenerating plant communities, we can reveal patterns of change in the functional composition of communities (Chazdon & Guariguata, 2016; Villéger et al., 2013). The Jaccard index expresses the functional dissimilarity between communities, while the functional turnover quantifies changes in functional composition over time or between different locations (Villéger et al., 2008). Jaccard and functional turnover values were positively associated with age difference and geographic distance between communities indicating that communities of similar age and closer to each other are more functionally similar. The effect of age suggests that trait composition in assembling communities may follow a predictable trajectory and reinforces the significant results found for the alpha functional diversity metrics (Marcilio-Silva et al., 2016).

The effect of geographic distance was expected under the assumption that seed dispersal is distance limited (Camargo et al., 2020), therefore, closely located communities are more functionally connected and share species and traits more easily (Matos et al., 2019), especially because most of the zoochoric species in the region are dispersed by highly mobile animals, such birds. Having a network of local communities in the region may be crucial to advance regeneration in contexts like the Corumbataí River Watershed, which is highly degraded and dynamic. Multiple local, sparsely distributed communities, can increase the efficiency of forest regeneration, as different dispersal strategies can facilitate the colonization of different species and promote functional diversity in the community undergoing regeneration (Camargo et al., 2020). The presence of multiple functional seed dispersal strategies between communities can promote ecosystem resilience in response to environmental changes, as different species can respond differently to variability in the environment (Cote et al., 2017). Greater functional diversity in seed dispersal can contribute to biodiversity maintenance and essential ecosystem processes in secondary forests under regeneration (César et al., 2021; Rozendaal et al., 2019).

Functional turnover, which represents the replacement of species in the community by others with different functional traits may be important for seed dispersal (García et al., 2018).

Higher functional turnover values between communities may indicate a greater diversity of seed dispersal strategies when looking at the regional level, contributing to a greater variety of species arriving in these communities (Marcilio-Silva et al., 2016). High species replacement over time potentially implies a change in the dynamics of plant-disperser interactions, promoting the coexistence of different species with different preferences for resources, and enabling the maintenance of biodiversity in regenerating forest environments (Wandrag et al., 2017). This functional variability plays a crucial role in the adaptation and survival of plant and animal communities in the face of environmental changes, ensuring the continuity of ecological processes that maintain the stability of these ecosystems (Lanuza et al., 2023).

It is imperative to consider that the impact of passive restoration on the (dis)similarity of animal-dispersed plant traits is sensitive to a range of contextual factors (García et al., 2018). The availability of habitat for dispersing animals, the presence of competitors, and human intervention can substantially influence the effectiveness of this restoration process (Bello et al., 2021). In some restored areas, the limited attraction of dispersing animals can restrict plant diversity and distribution, thus impacting the number of traits in the community (Estrada-Villegas et al., 2023). Passive restoration plays an essential role in influencing the diversity of traits in plants dispersed by animals during the regeneration process of degraded ecosystems (Ferraz et al., 2014). This approach facilitates the recovery of ecological connectivity in degraded areas, enabling recolonization by a variety of plant species (Monteiro et al., 2022). The interaction between passive restoration and seed-dispersing animals has a direct impact on the configuration of plant traits by triggering unique patterns of spatial distribution and genetic diversity among colonizing plants (Estrada-Villegas et al., 2023).

Understanding the functional diversity of frugivory and dispersal traits in regenerating forests is fundamental for the conservation and management of these ecosystems (Knapp et al., 2016). The promotion of conservation strategies that recognize and foster functional diversity in these communities, considering the importance of plant-animal interactions, is essential to preserve not only biodiversity but, also the functionality and stability of these internal ecosystems for environmental balance and life quality (Carlucci et al., 2020). Thus, studies and practices that aim to understand and preserve functional diversity are significantly important for nature conservation and the sustainability of natural resources.

5 CONCLUSION

Our study sheds light on the intricate relationships between zoochorous fruit traits and the dynamics of seed dispersal in regenerating Semideciduous Atlantic Forests. The investigation unveiled how these functional attributes vary across communities undergoing ecological succession, showing congruent responses to factors like restoration age and geographic distance between forest fragments. Our findings highlight the significance of considering fruit and seed traits as key elements shaping the assembly and persistence of plant communities reliant on animal-mediated seed dispersal. We found that alpha and beta functional diversity indices demonstrated noticeable trends towards increased variation with the aging of communities and greater geographic isolation between them. These outcomes underscore the importance of preserving a diverse array of functional traits in seed dispersal mechanisms for long-term resilience and biodiversity conservation within secondary forest ecosystems. Ultimately, recognizing and preserving the multifaceted functional diversity of seed dispersal mechanisms can prove crucial for fostering the resilience and vitality of regenerating secondary forests, thereby ensuring the sustainability of essential ecosystem processes and the conservation of biodiversity in these ecosystems.

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SUPPLEMENTARY MATERIAL – SESSION 1

Table S1 List of zoochoric plant communities (plots) inventoried in Semideciduous Atlantic Forest remnants undergoing passive restoration located in the Corumbataí River Watershed region, São Paulo State, Brazil.

Plot ID	Age	Forest cover index	Richness	Abundance
E108	19.5	0.082349	24	52
E134	20.5	0.205144	11	17
E144	34.5	0.139882	19	86
E150	26	0.073178	21	124
E154	25.5	0.049226	18	60
E156	51	0.080211	17	41
E163	18	0.090487	12	29
E201	40	0.047117	12	52
E202	20.5	0.093391	12	63
E203	20.5	0.181198	18	78
E208	20.5	0.200868	12	61
E29	18	0.144847	10	16
E32	40	0.032238	10	19
E33	40	0.032208	11	70
E46	40	0.130124	11	41
E52	40	0.157993	10	49
E58	23.5	0.099597	10	38
E70	54.5	0.179535	12	65
E73	36	0.181621	18	152
E78	23.5	0.138347	12	46
E83	51	0.063043	18	46
E89	52.5	0.05528	18	60
P12	41.5	0.112384	11	28
P18	41.5	0.104315	12	28
P19	52.5	0.132694	20	53
P20	30	0.143696	9	89
P205	35	0.029102	20	72
P206	22	0.186493	7	45
P207	53.5	0.120236	17	51
P22	41.5	0.125271	11	82
P31	37	0.032168	13	35
P48	19.5	0.120855	12	44
P49	52.5	0.144139	15	49
P53	18	0.160348	12	80
P54	36	0.155852	24	100
P56	51	0.143078	18	71
P62	36	0.152268	19	63
P63	36	0.132385	17	43
P64	36	0.151412	18	64
P71	52.5	0.165942	18	69

P84	21	0.045115	14	48
P85	40	0.049969	22	57
P87	40	0.058038	24	68
P88	26	0.060118	17	56
P90	17	0.052779	14	49
SF1	60	0.092966	11	39
SF2	60	0.088737	9	59
SF3	60	0.076134	18	69
SF4	60	0.095916	17	31
SF5	60	0.094691	14	33
SF6	60	0.155804	17	39
SF7	60	0.188042	26	53
SF8	60	0.020205	16	55
SF9	60	0.037279	12	19
SF10	60	0.149518	13	13

Information about plot age, richness and abundance of zoochoric species was obtained from a previous estimation study (César et al., 2021).

Table S2 List of animal-dispersed plant species inventoried in Semideciduous Atlantic Forest remnants undergoing passive restoration located in the Corumbataí River Watershed region, São Paulo State, Brazil. Species names were organized in alphabetical family order (130 spp, 47 taxonomic families).

Family	Species name	Abbreviation
Lamiaceae	<i>Aegiphila integrifolia</i> (Jacq.) Moldenke	Aeg.in
Euphorbiaceae	<i>Alchornea glandulosa</i> Poepp. & Endl.	Alc.gl
Euphorbiaceae	<i>Alchornea sidifolia</i> Müll.Arg.	Alc.si
Sapindaceae	<i>Allophylus edulis</i> (A.St.-Hil. et al.) Hieron. ex Niederl.	All.ed
Sapindaceae	<i>Allophylus racemosus</i> Sw.	All.ra
Fabaceae	<i>Andira fraxinifolia</i> Benth.	And.fr
Annonaceae	<i>Annona cacans</i> Warm.	Ann.ca
Annonaceae	<i>Annona sylvatica</i> A.St.-Hil.	Ann.sy
Meliaceae	<i>Cabralea canjerana</i> (Vell.) Mart.	Cab.ca
Myrtaceae	<i>Campomanesia guazumifolia</i> (Cambess.) O.Berg	Cam.gu
Myrtaceae	<i>Campomanesia xanthocarpa</i> (Mart.) O.Berg	Cam.xa
Salicaceae	<i>Casearia decandra</i> Jacq.	Cas.de
Salicaceae	<i>Casearia gossypiosperma</i> Briq.	Cas.go
Salicaceae	<i>Casearia sylvestris</i> Sw.	Cas.sy
Urticaceae	<i>Cecropia pachystachya</i> Trécul	Cec.pa
Cannabaceae	<i>Celtis iguanaea</i> (Jacq.) Sarg.	Cel.ig
Solanaceae	<i>Cestrum intermedium</i> Sendtn.	Ces.in
Rubiaceae	<i>Chomelia bella</i> (Standl.) Steyerf.	Cho.be
Rubiaceae	<i>Chomelia pohliana</i> Müll.Arg.	Cho.po
Sapotaceae	<i>Chrysophyllum gonocarpum</i> (Mart. & Eichler ex Miq.)	Chr.go
Sapotaceae	<i>Chrysophyllum marginatum</i> (Hook. & Arn.) Radlk.	Chr.ma
Verbenaceae	<i>Citharexylum myrianthum</i> Cham.	Cit.my
Cardiopteridaceae	<i>Citronella paniculata</i> (Mart.) R.A.Howard	Cit.pa
Polygonaceae	<i>Coccoloba coronata</i> Jacq.	Coc.co
Fabaceae	<i>Copaifera langsdorffii</i> Desf.	Cop.la
Boraginaceae	<i>Cordia ecalyculata</i> Vell.	Cor.ec
Boraginaceae	<i>Cordia sellowiana</i> Cham.	Cor.se
Boraginaceae	<i>Cordia superba</i> Cham.	Cor.su
Euphorbiaceae	<i>Croton floribundus</i> Spreng.	Cro.fl
Euphorbiaceae	<i>Croton piptocalyx</i> Müll.Arg.	Cro.pi
Euphorbiaceae	<i>Croton urucurana</i> Baill.	Cro.ur
Sapindaceae	<i>Cupania vernalis</i> Cambess.	Cup.ve
Araliaceae	<i>Dendropanax cuneatus</i> (DC.) Decne. & Planch.	Den.cu
Ebenaceae	<i>Diospyros inconstans</i> Jacq.	Dio.in
Annonaceae	<i>Duguetia lanceolata</i> A.St.-Hil.	Dug.la
Lauraceae	<i>Endlicheria paniculata</i> (Spreng.) J.F.Macbr.	End.pa
Rosaceae	<i>Eriobotrya japonica</i> (Thunb.) Lindl.	Eri.ja
Erythroxylaceae	<i>Erythroxylum deciduum</i> A.St.-Hil.	Ery.de
Erythroxylaceae	<i>Erythroxylum pelleterianum</i> A.St.-Hil.	Ery.pe
Myrtaceae	<i>Eugenia dodonaeifolia</i> Cambess.	Eug.do
Myrtaceae	<i>Eugenia florida</i> DC.	Eug.fl
Myrtaceae	<i>Eugenia hiemalis</i> Cambess.	Eug.hi

Myrtaceae	<i>Eugenia ligustrina</i> (Sw.) Willd.	Eug.li
Myrtaceae	<i>Eugenia paracatuana</i> O.Berg	Eug.pa
Myrtaceae	<i>Eugenia pluriflora</i> DC.	Eug.pl
Myrtaceae	<i>Eugenia pyriformis</i> Cambess.	Eug.py
Myrtaceae	<i>Eugenia repanda</i> O.Berg	Eug.re
Myrtaceae	<i>Eugenia speciosa</i> Cambess.	Eug.sp
Rubiaceae	<i>Faramea latifolia</i> (Cham. & Schltdl.) DC.	Far.la
Moraceae	<i>Ficus guaranitica</i> Chodat	Fic.gu
Nyctaginaceae	<i>Guapira hirsuta</i> (Choisy) Lundell	Gua.hi
Nyctaginaceae	<i>Guapira opposita</i> (Vell.) Reitz	Gua.op
Meliaceae	<i>Guarea guidonia</i> (L.) Sleumer	Gua.gu
Meliaceae	<i>Guarea kunthiana</i> A.Juss.	Gua.ku
Meliaceae	<i>Guarea macrophylla</i> Vahl	Gua.ma
Malvaceae	<i>Guazuma ulmifolia</i> Lam.	Gua.ul
Fabaceae	<i>Holocalyx balansae</i> Micheli	Hol.ba
Fabaceae	<i>Hymenaea courbaril</i> L.	Hym.co
Fabaceae	<i>Inga vera</i> Willd.	Ing.ve
Solanaceae	<i>Iochroma arborescens</i> (L.) J.M.H. Shaw	Ioc.ar
Caricaceae	<i>Jacaratia spinosa</i> (Aubl.) A.DC.	Jac.sp
Lacistemataceae	<i>Lacistema hasslerianum</i> Chodat	Lac.ha
Anacardiaceae	<i>Lithraea molleoides</i> (Vell.) Engl.	Lit.mo
Moraceae	<i>Maclura tinctoria</i> (L.) D.Don ex Steud.	Mac.ti
Anacardiaceae	<i>Mangifera indica</i> L.	Man.in
Sapindaceae	<i>Matayba elaeagnoides</i> Radlk.	Mat.el
Meliaceae	<i>Melia azedarach</i> L.	Mel.az
Melastomataceae	<i>Miconia albicans</i> (Sw.) Steud.	Mic.al
Monimiaceae	<i>Mollinedia widgrenii</i> A.DC.	Mol.wi
Celastraceae	<i>Monteverdia aquifolium</i> (Mart.) Biral	Mon.aq
Celastraceae	<i>Monteverdia gonoclada</i> (Mart.) Biral	Mon.go
Myrtaceae	<i>Myrcia hebeptala</i> DC.	Myr.he
Myrtaceae	<i>Myrcia multiflora</i> (Lam.) DC.	Myr.mu
Myrtaceae	<i>Myrcia splendens</i> (Sw.) DC.	Myr.sp
Myrtaceae	<i>Myrcia tomentosa</i> (Aubl.) DC.	Myr.to
Myrtaceae	<i>Myrcianthes pungens</i> (O.Berg) D.Legrand	Myr.pu
Myrtaceae	<i>Myrciaria floribunda</i> (H.West ex Willd.) O.Berg	Myr.fl
Myrtaceae	<i>Myrciaria tenella</i> (DC.) O.Berg	Myr.te
Primulaceae	<i>Myrsine coriacea</i> (Sw.) R.Br. ex Roem. & Schult.	Myrs.co
Primulaceae	<i>Myrsine umbellata</i> Mart.	Myrs.um
Lauraceae	<i>Nectandra lanceolata</i> Nees	Nec.la
Lauraceae	<i>Nectandra megapotamica</i> (Spreng.) Mez	Nec.me
Lauraceae	<i>Ocotea indecora</i> (Schott) Mez	Oco.in
Lauraceae	<i>Ocotea puberula</i> (Rich.) Nees	Oco.pub
Lauraceae	<i>Ocotea pulchella</i> (Nees & Mart.) Mez	Oco.pul
Lauraceae	<i>Ocotea velutina</i> (Nees) Rohwer	Oco.ve
Ochnaceae	<i>Ouratea castaneifolia</i> (DC.) Engl.	Our.ca
Rubiaceae	<i>Palicourea sessilis</i> (Vell.) C.M.Taylor	Pal.se
Peraceae	<i>Pera glabrata</i> (Schott) Baill.	Per.gl
Picramniaceae	<i>Picramnia sellowii</i> Planch.	Pic.se

Piperaceae	<i>Piper amalago</i> L.	Pip.am
Piperaceae	<i>Piper arboreum</i> Aubl.	Pip.ar
Myrtaceae	<i>Plinia peruviana</i> (Poir.) Govaerts	Pli.pe
Salicaceae	<i>Prockia crucis</i> P.Browne ex L.	Pro.cr
Rosaceae	<i>Prunus myrtifolia</i> (L.) Urb.	Pru.my
Myrtaceae	<i>Psidium guajava</i> L.	Psi.gu
Myrtaceae	<i>Psidium sartorianum</i> (O.Berg) Nied.	Psi.sa
Rubiaceae	<i>Randia armata</i> (Sw.) DC.	Ran.ar
Rhamnaceae	<i>Rhamnidium elaeocarpum</i> Reissek	Rha.el
Rubiaceae	<i>Rudgea jasminoides</i> (Cham.) Müll.Arg.	Rud.ja
Euphorbiaceae	<i>Sapium glandulosum</i> (L.) Morong	Sap.gl
Siparunaceae	<i>Siparuna guianensis</i> Aubl.	Sip.gu
Solanaceae	<i>Solanum granuloseprosum</i> Dunal	Sol.gr
Solanaceae	<i>Solanum swartzianum</i> Roem. & Schult.	Sol.sw
Moraceae	<i>Sorocea bonplandii</i> (Baill.) W.C.Burger et al.	Sor.bo
Arecaceae	<i>Syagrus romanzoffiana</i> (Cham.) Glassman	Sya.ro
Symplocaceae	<i>Symplocos laxiflora</i> Benth.	Sym.la
Myrtaceae	<i>Syzygium cumini</i> (L.) Skeels	Syz.cu
Apocynaceae	<i>Tabernaemontana catharinensis</i> A.DC.	Tab.ca
Anacardiaceae	<i>Tapirira guianensis</i> Aubl.	Tap.gu
Cannabaceae	<i>Trema micrantha</i> (L.) Blume	Tre.mi
Meliaceae	<i>Trichilia casaretti</i> C.DC.	Tri.cas
Meliaceae	<i>Trichilia catigua</i> A.Juss.	Tri.cat
Meliaceae	<i>Trichilia clausenii</i> C.DC.	Tri.cl
Meliaceae	<i>Trichilia elegans</i> A.Juss.	Tri.el
Meliaceae	<i>Trichilia pallida</i> Sw.	Tri.pa
Urticaceae	<i>Urera baccifera</i> (L.) Gaudich. ex Wedd.	Ure.ba
Urticaceae	<i>Urera caracasana</i> (Jacq.) Griseb.	Ure.ca
Urticaceae	<i>Urera nitida</i> (Vell.) P.Brack	Ure.ni
Lamiaceae	<i>Vitex megapotamica</i> (Spreng.) Moldenke	Vit.me
Annonaceae	<i>Xylopia aromatica</i> (Lam.) Mart.	Xyl.ar
Salicaceae	<i>Xylosma pseudosalzmannii</i> Sleumer	Xyl.ps
Rutaceae	<i>Zanthoxylum acuminatum</i> (Sw.) Sw.	Zan.ac
Rutaceae	<i>Zanthoxylum caribaeum</i> Lam.	Zan.ca
Rutaceae	<i>Zanthoxylum fagara</i> (L.) Sarg.	Zan.fa
Rutaceae	<i>Zanthoxylum monogynum</i> A.St.-Hil.	Zan.mo
Rutaceae	<i>Zanthoxylum petiolare</i> A.St.-Hil. & Tul.	Zan.pe
Rutaceae	<i>Zanthoxylum rhoifolium</i> Lam.	Zan.rh
Rutaceae	<i>Zanthoxylum riedelianum</i> Engl.	Zan.ri
Fabaceae	<i>Zollernia ilicifolia</i> (Brongn.) Vogel	Zol.il

Figure S1 Phylogenetic tree reconstructed for 130 animal-dispersed plant species considered in this study.

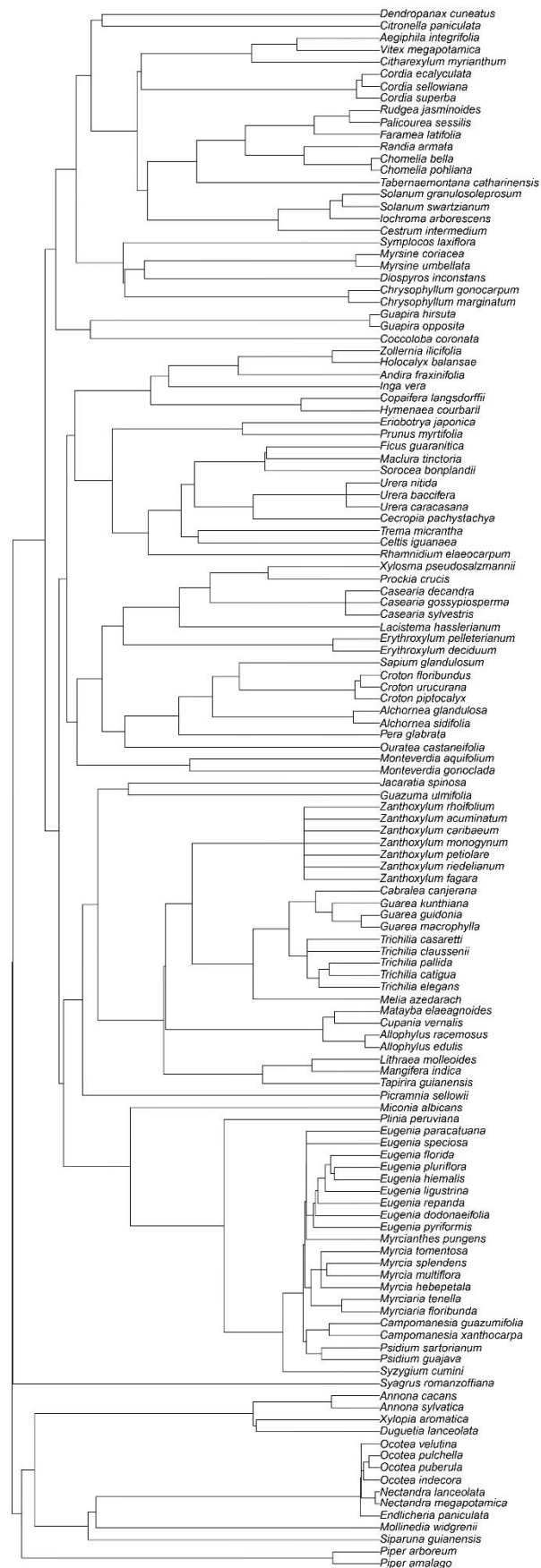


Figure S2 Pearson's correlation plot for all qualitative traits of 130 zoochoric species in the region of the Corumbataí River Watershed – SP, Brazil. Only correlated traits with p-value < 0.05 are showed.

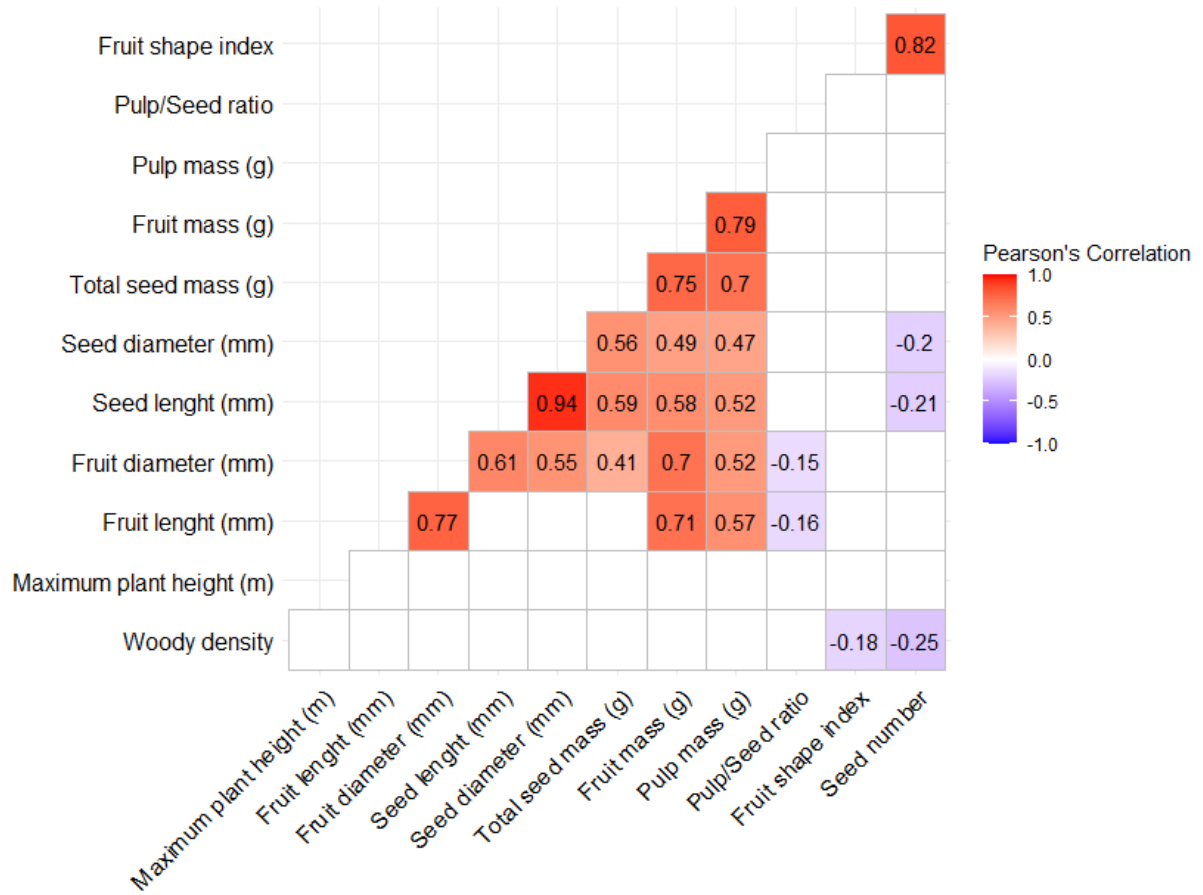


Table S4 Quality index of functional spaces 130 zoochoric species in the region of the Corumbataí River Watershed – SP, Brazil (assessed using the mean absolute deviation, MAD) from one to ten dimensions. For each n-dimensional functional space resulting from a principal coordinates analysis, correlation between pairwise distances computed on species traits (Gower distance) and standardized (Euclidean) distance.

PCoA Axis	MAD	RMSD
PCoA1	0.209	0.236
PCoA2	0.141	0.166
PCoA3	0.099	0.124
PCoA4	0.070	0.090
PCoA5	0.049	0.064
PCoA6	0.037	0.048
PCoA7	0.031	0.039
PCoA8	0.031	0.039
PCoA9	0.034	0.042
PCoA10	0.038	0.046
Tree_average	0.061	0.076

Figure S3. Quality representation of the functional spaces of 130 zoochoric species in the region of the Corumbataí River Watershed – SP, Brazil (assessed using the mean absolute deviation, MAD) from one to ten dimensions. For each n-dimensional functional space resulting from a principal coordinates analysis, correlation between pairwise distances computed on species traits (Gower distance) and standardized (Euclidean) distance.

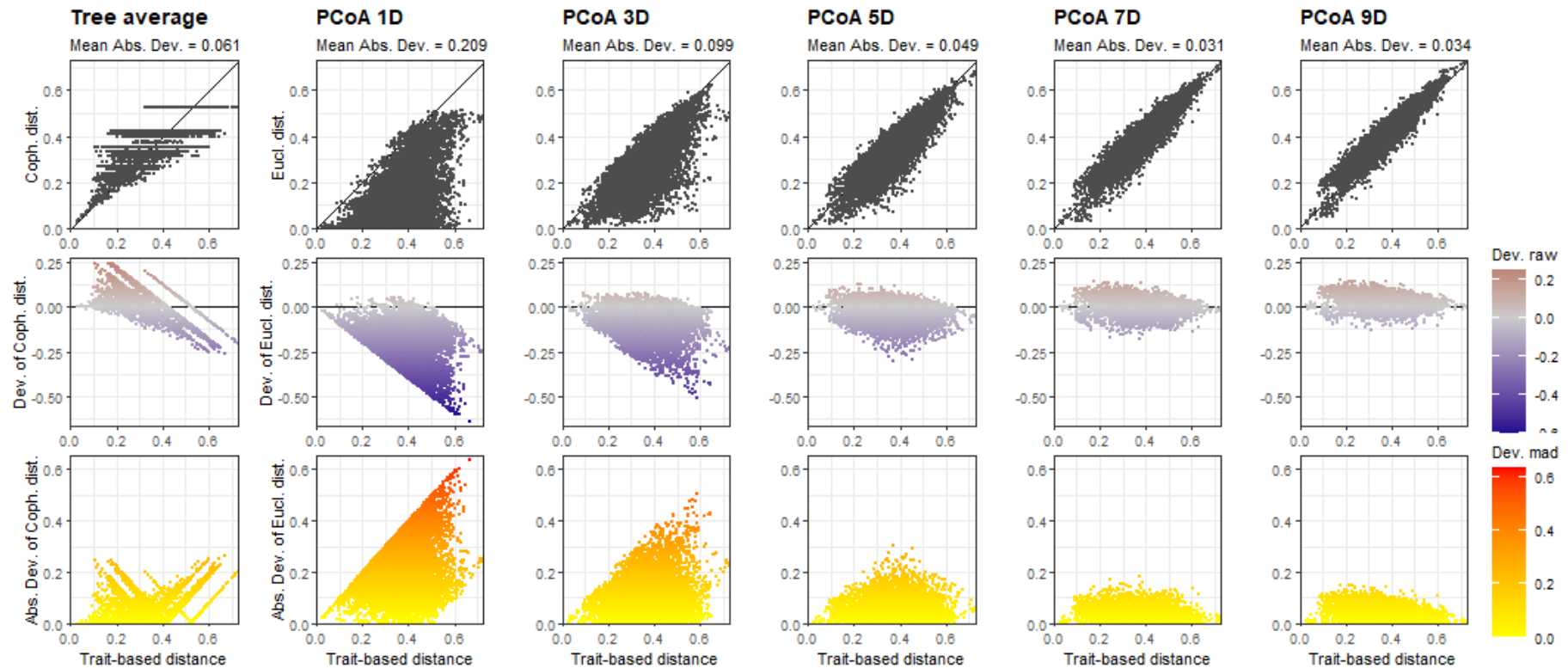
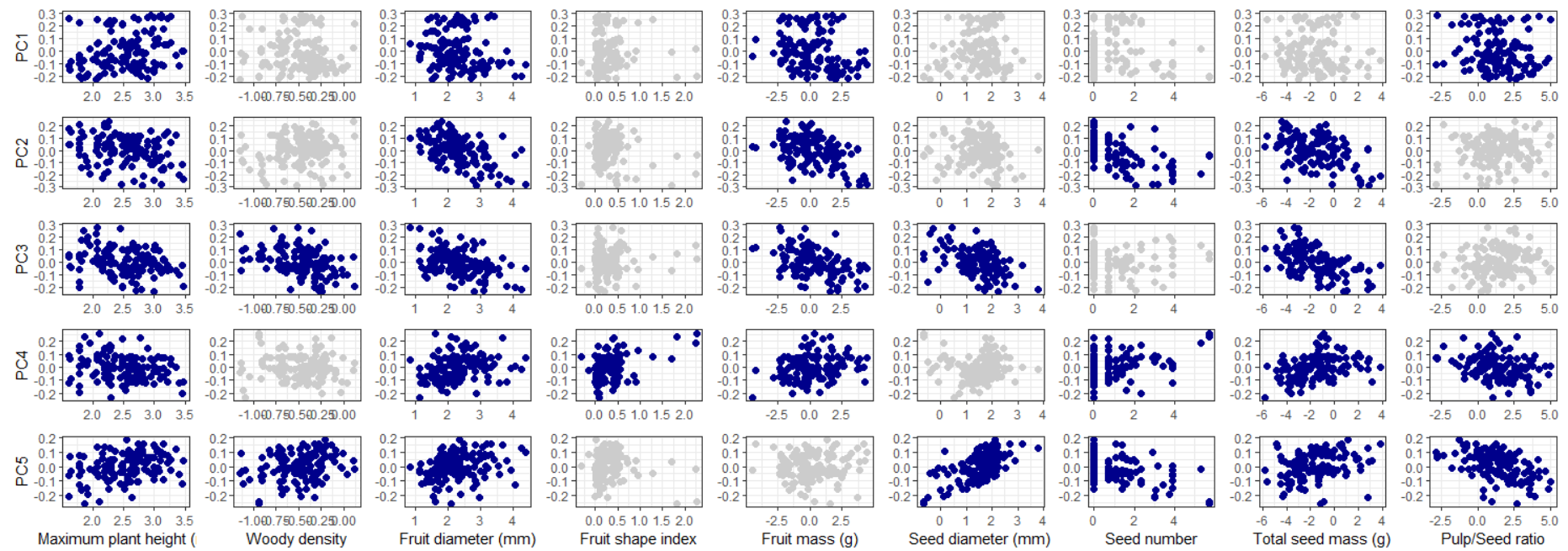


Table S5 Correlations between the first five axes of the principal coordinate analysis (PCoA) and quantitative species traits of zoochoric plant communities in the region of the Corumbataí River Watershed – SP, Brazil. For each relationship, a linear model was fitted, providing R^2 as a goodness-of-fit measure and associated p-values < 0.05 in bold.

Trait	Axis	Test	R^2	p-value
Maximum plant height (m)	PC1	Linear Model	0.055	0.0071
	PC2	Linear Model	0.079	0.0012
	PC3	Linear Model	0.075	0.0017
	PC4	Linear Model	0.035	0.0327
	PC5	Linear Model	0.114	0.0001
Woody density	PC1	Linear Model	0.006	0.3928
	PC2	Linear Model	0.029	0.0525
	PC3	Linear Model	0.137	0
	PC4	Linear Model	0.005	0.4398
	PC5	Linear Model	0.055	0.0072
Fruit diameter (mm)	PC1	Linear Model	0.034	0.0369
	PC2	Linear Model	0.295	0
	PC3	Linear Model	0.18	0
	PC4	Linear Model	0.06	0.0051
	PC5	Linear Model	0.078	0.0013
Fruit shape index	PC1	Linear Model	0.002	0.6556
	PC2	Linear Model	0.021	0.1008
	PC3	Linear Model	0.007	0.3356
	PC4	Linear Model	0.173	0
	PC5	Linear Model	0.016	0.1567
Fruit mass (g)	PC1	Linear Model	0.062	0.0043
	PC2	Linear Model	0.2	0
	PC3	Linear Model	0.204	0
	PC4	Linear Model	0.056	0.0068
	PC5	Linear Model	0.002	0.5811
Seed diameter (mm)	PC1	Linear Model	0.009	0.2823
	PC2	Linear Model	0.002	0.5762
	PC3	Linear Model	0.197	0
	PC4	Linear Model	0.001	0.7204
	PC5	Linear Model	0.387	0
Seed number	PC1	Linear Model	0.013	0.1979
	PC2	Linear Model	0.336	0
	PC3	Linear Model	0	0.8772
	PC4	Linear Model	0.122	0
	PC5	Linear Model	0.276	0
Total seed mass (g)	PC1	Linear Model	0.011	0.2418
	PC2	Linear Model	0.166	0
	PC3	Linear Model	0.254	0
	PC4	Linear Model	0.133	0
	PC5	Linear Model	0.098	0.0003
Pulp/Seed ratio	PC1	Linear Model	0.032	0.041
	PC2	Linear Model	0.012	0.22
	PC3	Linear Model	0.029	0.0515
	PC4	Linear Model	0.09	0.0005
	PC5	Linear Model	0.23	0

Figure S4 Correlations plots between the first five axes of the principal coordinate analysis (PCoA) and quantitative species traits of zoochoric plant communities in the region of the Corumbataí River Watershed – SP, Brazil. Traits with high correlation (p-values < 0.05) in blue.

Relation between traits and PCoA axes



Made with mFD package

Table S6 Correlations between the first five axes of the principal coordinate analysis (PCoA) and qualitative species traits of zoochoric plant communities in the region of the Corumbataí River Watershed – SP, Brazil. For each relationship, a Kruskal-Wallis test was fitted, providing f statistic as a goodness-of-fit measure and associated p-values < 0.05 in bold.

Trait	Axis	Test	f	p-value
Growth form	PC1	Kruskal-Wallis	0.076	0.0011
	PC2	Kruskal-Wallis	0.051	0.0061
	PC3	Kruskal-Wallis	0.186	0
	PC4	Kruskal-Wallis	0.095	0.0003
	PC5	Kruskal-Wallis	0.063	0.0027
Deciduousness	PC1	Kruskal-Wallis	-0.003	0.441
	PC2	Kruskal-Wallis	0.096	0.0008
	PC3	Kruskal-Wallis	0.129	0.0001
	PC4	Kruskal-Wallis	0.327	0
	PC5	Kruskal-Wallis	0	0.3591
Shade tolerance	PC1	Kruskal-Wallis	0.041	0.0123
	PC2	Kruskal-Wallis	0.443	0
	PC3	Kruskal-Wallis	0.343	0
	PC4	Kruskal-Wallis	0.082	0.0007
	PC5	Kruskal-Wallis	0.015	0.0857
Dispersal group	PC1	Kruskal-Wallis	0.527	0
	PC2	Kruskal-Wallis	0.077	0.0027
	PC3	Kruskal-Wallis	0	0.3591
	PC4	Kruskal-Wallis	0.061	0.0075
	PC5	Kruskal-Wallis	0.071	0.0041
Fruit type	PC1	Kruskal-Wallis	0.495	0
	PC2	Kruskal-Wallis	0.259	0
	PC3	Kruskal-Wallis	0.095	0.0019
	PC4	Kruskal-Wallis	0.08	0.0044
	PC5	Kruskal-Wallis	0.431	0
Fruit secondary structure	PC1	Kruskal-Wallis	0.539	0
	PC2	Kruskal-Wallis	0.068	0.0018
	PC3	Kruskal-Wallis	0.01	0.1267
	PC4	Kruskal-Wallis	0.122	0
	PC5	Kruskal-Wallis	0.023	0.0461
Fruit color	PC1	Kruskal-Wallis	0.24	0
	PC2	Kruskal-Wallis	0.163	0.0004
	PC3	Kruskal-Wallis	0.168	0.0003
	PC4	Kruskal-Wallis	0.043	0.093
	PC5	Kruskal-Wallis	0.084	0.0157
Aril	PC1	Kruskal-Wallis	0.447	0
	PC2	Kruskal-Wallis	0.026	0.0377
	PC3	Kruskal-Wallis	0.003	0.2397
	PC4	Kruskal-Wallis	0.031	0.025
	PC5	Kruskal-Wallis	0.003	0.242

Figure S5 Correlations plots between the first five axes of the principal coordinate analysis (PCoA) and qualitative species traits of zoochoric plant communities in the region of the Corumbataí River Watershed – SP, Brazil. Traits with high correlation (p-values < 0.05) in blue.

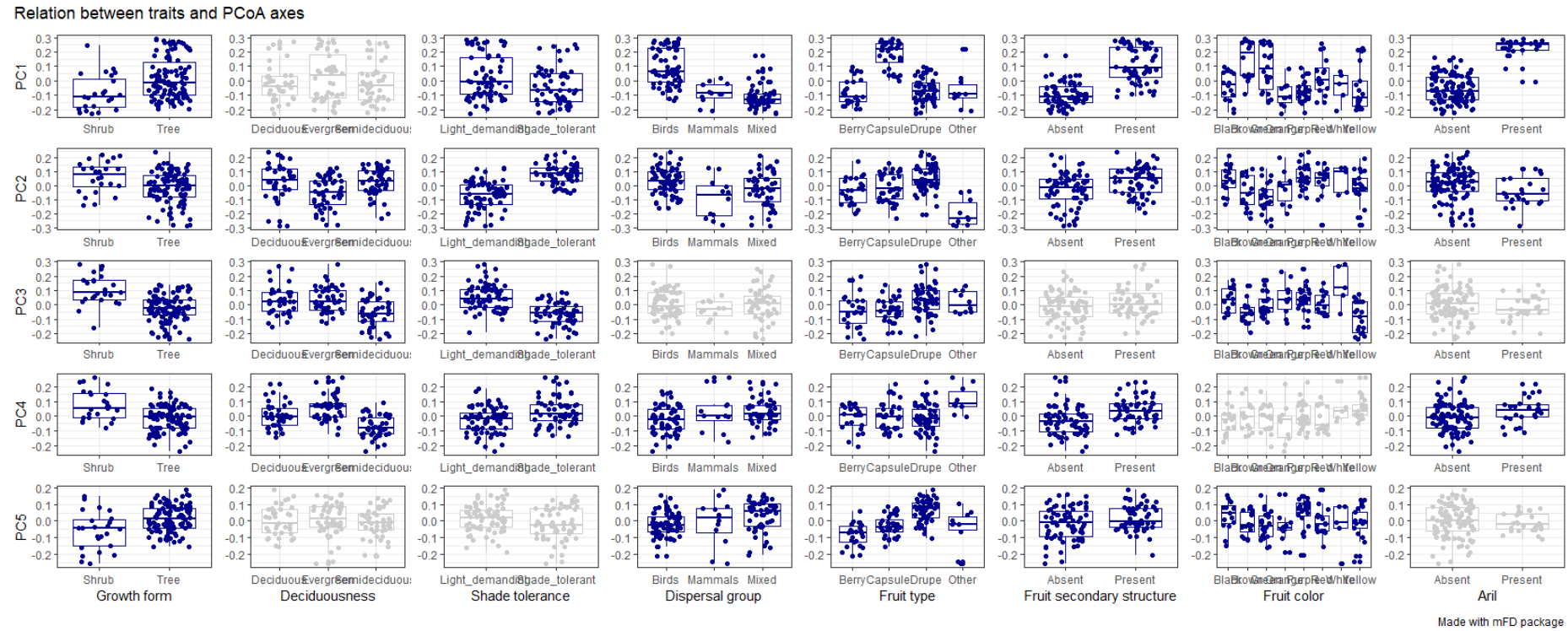


Table S7 Pearson's correlation test for environmental variables of the 55 zoochoric plant communities in the region of the Corumbataí River Watershed – SP, Brazil. No correlation was found between variables.

	Age	Forest_cover	meandist	mindist
Age	1	-0.102	-0.019	0.191
p-value		0.457	0.892	0.162
Forest_cover		1	0.118	-0.044
p-value			0.39	0.748
meandist			1	0.653
p-value				0.1
mindist				1

Table S8 Pearson's correlation test between alpha functional diversity indices of traits for 130 zoochoric species. Alpha diversity is measured based on species richness (Spp_rich), functional richness (FRic), functional mean pairwise distance (FMPD), functional evenness (FEve) and functional dispersion (FDis).

	sp_richn	fdis	fmpd	feve	fric
sp_richn	1	0.028	-0.324	0.149	0.757
p-value		0.839	0.016	0.277	0
fdis		1	0.761	0.369	0.354
p-value			0	0.006	0.008
fmpd			1	0.138	0.151
p-value				0.315	0.27
feve				1	0.261
p-value					0.054
fric					1

Figure S6 Pearson's correlation plots between alpha functional diversity indices of traits for 130 zoochoric species. Alpha diversity is measured based on species richness (Spp_rich), functional richness (FRic), functional mean pairwise distance (FMPD), functional evenness (FEve) and functional dispersion (FDis).

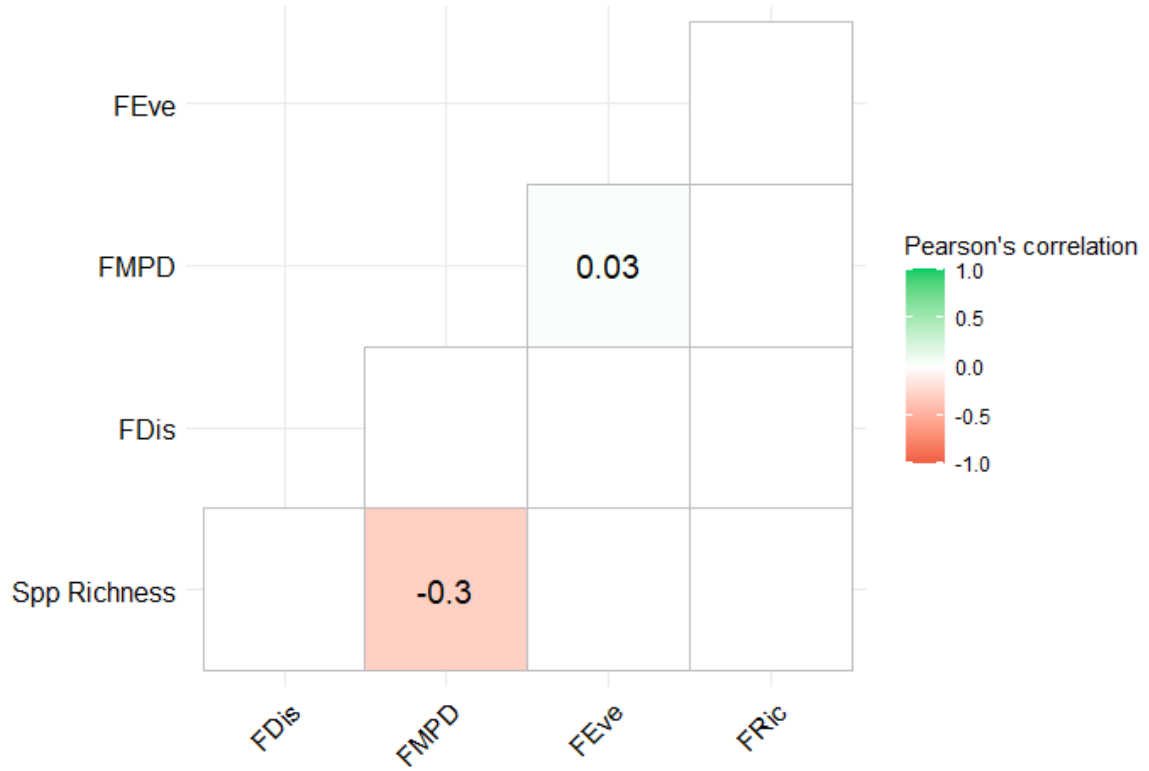


Table S9 Pearson's correlation test between beta functional diversity indices of traits for 130 zoochoric species in the 55 zoochoric plant communities in the region of the Corumbataí River Watershed – SP, Brazil. Functional beta diversity is measured based on Jaccard Dissimilarity Index (Jacc_diss), functional turnover (Turn) and functional nestedness (Nest). Statistically significant results (p-value<0.05) are denoted with *.

	Jacc_diss	Turn	Nest
Jacc_diss	1	0.45	0.02
p-value		0.043*	0.215
Turn		1	-0.88
p-value			0.002*
Nest			1

Table S10. Phylogenetic signal for all quantitative traits of 130 in zoochoric plant species in the region of the Corumbataí River Watershed – SP, Brazil measured with Blomberg's K index. Significant value of K ($p < 0.05$) in bold.

Functional traits	Blomberg's K	p-value
Seed number	1.633	0.0001
Fruit shape index	0.822	0.001
Fruit mass (g)	0.558	0.0015
Fruit length (mm)	0.548	0.0001
Total seed mass (g)	0.538	0.0149
Fruit diameter (mm)	0.444	0.0015
Pulp mass (g)	0.419	0.0086
Seed diameter (mm)	0.393	0.0139
Seed length (mm)	0.386	0.004
Maximum plant height (m)	0.293	0.0019
Pulp/Seed ratio	0.247	0.2448
Woody density (g/cm ³)	0.222	0.1025

Table S11 Generalized linear models selected for relationships between the alpha functional diversity indices and environmental variables in zoochoric plant communities in the region of the Corumbataí River Watershed – SP, Brazil. Alpha diversity is measured based on species richness (Spp_rich), functional richness (FRic), functional mean pairwise distance (FMPD), functional evenness (FEve) and functional dispersion (FDis). Fixed effects included age, forest cover index (For_cov), mean geographic distance between communities (Mean_dist), and minimum geographic distance between communities (Min_dist). df, degrees of freedom; logLik, log Likelihood; Δ AICc, difference between the AICc of each model and the AICc of the best model; weight, AICc weight. Only models with Δ AICc < 2 (highlighted in gray) were selected for interpretation. Null model is marked with X.

Response variable	Null Model	Intercept	Predictor variables				Model descriptors				
			Age	For_cov	Mean_dist	Min_dist	df	logLik	AICc	Δ AICc	weight
<i>Spp_rich</i>	X	15.15			-1.801	1.639	4	-156.589	322	0	0.244
		15.15					2	-159.634	323.5	1.52	0.114
		15.15	0.4543		-1.687	1.478	5	-156.291	323.8	1.83	0.098
		15.15	0.7686				3	-158.801	324.1	2.09	0.086
		15.15			-0.73		3	-158.883	324.2	2.26	0.079
		15.15		0.000491	-1.801	1.639	5	-156.589	324.4	2.42	0.073
		15.15	0.7551		-0.7158		4	-158.057	324.9	2.94	0.056
		15.15				0.4635	3	-159.334	325.1	3.16	0.05
		15.15		-0.2852			3	-159.521	325.5	3.53	0.042
		15.15	0.7058			0.3286	4	-158.651	326.1	4.12	0.031
		15.15	0.7472	-0.2087			4	-158.739	326.3	4.3	0.028
		15.15	0.456	0.02755	-1.693	1.483	6	-156.29	326.3	4.35	0.028
		15.15		-0.2016	-0.7062		4	-158.826	326.5	4.47	0.026
		15.15		-0.2652		0.4517	4	-159.235	327.3	5.29	0.017
		15.15	0.7425	-0.1262	-0.7011		5	-158.034	327.3	5.31	0.017
		15.15	0.6862	-0.2006		0.3234	5	-158.594	328.4	6.43	0.01
<i>FRic</i>	X	0.04855	0.01059				3	100.49	-194.5	0	0.211
		0.04855	0.009351			0.006487	4	101.222	-193.6	0.87	0.137
		0.04855				0.008274	3	99.722	-193	1.54	0.098
		0.04855					2	98.561	-192.9	1.62	0.094
		0.04855	0.01086	0.002599			4	100.609	-192.4	2.09	0.074

		0.04855	0.01062		0.001395	4	100.524	-192.2	2.26	0.068	
		0.04855	0.008578		-0.00519	0.01002	5	101.495	-191.8	2.74	0.054
		0.04855			-0.00734	0.01307	4	100.262	-191.7	2.78	0.052
		0.04855	0.00962	0.002763		0.006557	5	101.36	-191.5	3.01	0.047
		0.04855		0.001858		0.008356	4	99.782	-190.8	3.75	0.032
		0.04855		0.001488			3	98.597	-190.7	3.78	0.032
		0.04855			0.001195		3	98.584	-190.7	3.81	0.031
		0.04855	0.01086	0.002469	0.001107		5	100.631	-190	4.47	0.023
		0.04855	0.008798	0.003578	-0.00605	0.0107	6	101.722	-189.7	4.81	0.019
		0.04855		0.003056	-0.00812	0.01371	5	100.421	-189.6	4.89	0.018
		0.04855		0.001366	0.001034		4	98.615	-188.4	6.08	0.01
FMPD		0.6781	0.01442		0.01324		4	90.481	-172.2	0	0.188
		0.6781	0.0154	0.009752	0.01211		5	91.655	-172.1	0.08	0.181
		0.6781	0.01532	0.01118			4	89.848	-170.9	1.27	0.1
		0.6781	0.01417				3	88.392	-170.3	1.85	0.075
		0.6781	0.01367	0.01139		0.008729	5	90.75	-170.3	1.89	0.073
		0.6781	0.01464		0.01395	-0.00107	5	90.489	-169.8	2.41	0.056
		0.6781	0.01256			0.008437	4	89.19	-169.6	2.58	0.052
		0.6781			0.01297		3	88.02	-169.6	2.59	0.052
		0.6781	0.01524	0.009836	0.01157	0.000803	6	91.66	-169.6	2.59	0.052
		0.6781		0.00819	0.012		4	88.779	-168.8	3.4	0.034
		0.6781				0.01084	3	87.451	-168.4	3.73	0.029
		0.6781		0.01011		0.01128	4	88.606	-168.4	3.75	0.029
	X	0.6781					2	86.178	-168.1	4.04	0.025
		0.6781		0.00961			3	87.174	-167.9	4.29	0.022
		0.6781			0.01028	0.004124	4	88.131	-167.5	4.7	0.018
		0.6781		0.008931	0.007987	0.006017	5	89.016	-166.8	5.36	0.013
FEve		0.6893	0.01984				3	61.546	-116.6	0	0.156
		0.6893	0.0168			0.01591	4	62.622	-116.4	0.18	0.143
		0.6893				0.01912	3	61.426	-116.4	0.24	0.138

	X	0.6893				2	59.895	-115.6	1.06	0.092	
		0.6893			-0.01414	0.02835	4	61.924	-115	1.57	0.071
		0.6893	0.02042	0.005635			4	61.682	-114.6	2.06	0.056
		0.6893	0.01526		-0.01032	0.02294	5	62.887	-114.5	2.07	0.055
		0.6893	0.01993		0.004755		4	61.644	-114.5	2.13	0.054
		0.6893	0.01739	0.006036		0.01607	5	62.784	-114.3	2.28	0.05
		0.6893		0.004402		0.01932	4	61.509	-114.2	2.4	0.047
		0.6893			0.00438		3	59.974	-113.5	3.15	0.032
		0.6893		0.003547			3	59.947	-113.4	3.2	0.032
		0.6893		0.006742	-0.01587	0.02978	5	62.116	-113	3.61	0.026
		0.6893	0.01573	0.007676	-0.01217	0.0244	6	63.144	-112.5	4.08	0.02
		0.6893	0.02044	0.005146	0.004156		5	61.757	-112.3	4.33	0.018
		0.6893		0.003071	0.004017		4	60.012	-111.2	5.4	0.01
	FDis		0.6167	0.01945	0.01883		0.01873	5	62.713	-114.2	0
0.6167			0.02147		0.01914		4	61.369	-113.9	0.26	0.102
0.6167			0.0231	0.01634	0.01724		5	62.512	-113.8	0.4	0.095
0.6167			0.02298	0.01837			4	61.23	-113.7	0.54	0.089
0.6167			0.01762			0.01825	4	61.174	-113.5	0.65	0.084
0.6167				0.01701		0.02237	4	61.13	-113.5	0.74	0.081
0.6167						0.02161	3	59.927	-113.4	0.82	0.078
0.6167			0.02111				3	59.839	-113.2	0.99	0.071
0.6167					0.01874		3	59.459	-112.4	1.75	0.049
X		0.6167	0.02063	0.01766	0.008694	0.01277	6	62.895	-112	2.16	0.04
		0.6167					2	58.086	-111.9	2.26	0.038
		0.6167	0.01955		0.01296	0.009416	5	61.572	-111.9	2.28	0.037
		0.6167		0.01602			3	59.082	-111.7	2.51	0.033
		0.6167		0.01399	0.01708		4	60.243	-111.7	2.51	0.033
	0.6167			0.008062	0.01635	4	60.08	-111.4	2.84	0.028	
	0.6167		0.01644	0.003842	0.01983	5	61.164	-111.1	3.1	0.025	

Table S12 Generalized least squares models selected for relationships between the beta functional diversity indices and environmental variables in zoochoric plant communities in the Region of the Corumbataí River Watershed - SP, Brazil. Functional beta diversity is measured based on Jaccard Dissimilarity Index (Jacc_diss), functional turnover (Turn) and functional nestedness (Nest). Fixed effects included age, forest cover index (For_cov) and geographic distance between communities (Geo_dist. df, degrees of freedom; logLik, log Likelihood; Δ AICc, difference between the AICc of each model and the AICc of the best model; weight, AICc weight. Only models with Δ AICc < 2 (highlighted in gray) were selected for interpretation. Null model is marked with X.

Response variable	Predictor variable					Model descriptors				
	Null Model	Intercept	Age	For_cov	Geo_dist	df	logLik	AICc	Δ AICc	weight
Jacc_diss		0.8806	0.006742		0.009442	5	2168.259	-4326.5	0	0.957
		0.8806			0.009905	4	2163.483	-4318.9	7.54	0.022
		0.8806	0.007063			4	2163.324	-4318.6	7.86	0.019
		0.8806	0.006768	0.001576	0.009373	6	2163.225	-4314.4	12.08	0.002
	X	0.8806				3	2157.649	-4309.3	17.19	0
		0.8806	0.007091	0.001799		5	2158.447	-4306.9	19.62	0
		0.8806		0.001455	0.009843	5	2158.373	-4306.7	19.77	0
		0.8806		0.001683		4	2152.688	-4297.3	29.13	0
Turn		0.7344	0.01442		0.01807	5	899.338	-1788.6	0	0.748
		0.7344	0.01506			4	896.979	-1785.9	2.7	0.193
		0.7344			0.01907	4	895.59	-1783.2	5.48	0.048
	X	0.7344				3	892.519	-1779	9.61	0.006
		0.7344	0.01446	0.002556	0.01795	6	894.887	-1777.7	10.92	0.003
		0.7344	0.0151	0.003011		5	892.625	-1775.2	13.43	0.001
		0.7344		0.002296	0.01897	5	891.095	-1772.1	16.49	0
		0.7344		0.002766		4	888.115	-1768.2	20.43	0
Nest	X	0.1462				3	906.728	-1807.4	0	0.932
		0.1462	-0.00804			4	904.618	-1801.2	6.23	0.041
		0.1462			-0.00894	4	904.006	-1800	7.45	0.022
		0.1462		-0.00098		4	902.071	-1796.1	11.32	0.003
		0.1462	-0.00772		-0.00838	5	901.692	-1793.3	14.1	0.001
		0.1462	-0.00806	-0.00111		5	899.971	-1789.9	17.54	0

0.1462		-0.00074	-0.00891	5	899.334	-1788.6	18.81	0
0.1462	-0.00774	-0.00088	-0.00834	6	897.027	-1782	25.44	0

SUPPLEMENTARY MATERIAL – SESSION 2

List of published studies and books used in compiling the attributes of fruits, seeds, and general traits of plants dispersed by animals

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