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ORIGINAL ARTICLE

Avian-Mediated Microalgal Dispersal in Neotropical Wetlands: The Case of the Southern Screamer (*Chauna torquata*)

Filipe Cambeiro Fatturi[1,2] | Cínthia Negrine Fernandez[1,3] | Pablo Santos Guimarães[1] | Cristina Stenert[1,2] | Leandro Bugoni[1,3] | Leonardo Maltchik[1,2,4]

[1]Graduate Program in Biology of Continental Aquatic Environments, Federal University of Rio Grande (FURG), Rio Grande, Brazil | [2]National Institute for Science and Technology in Wetscapes (INCT-Wetscapes), Manaus, Brazil | [3]Waterbirds and Sea Turtles Lab, Institute of Biological Sciences, Federal University of Rio Grande (FURG), Rio Grande, Brazil | [4]Graduate Program in Agroecology, Federal University of Santa Catarina (UFSC), Florianópolis, Brazil

Correspondence: Leonardo Maltchik (maltchikleo@gmail.com)

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ABSTRACT

1. Dispersal is the process of movement of organisms among habitats across the landscape, and passive dispersal occurs when the transport of organisms or their propagules is mediated by vectors. Research on the role of waterbirds in the dispersal of microalgae through epizoochory and endozoochory remains scarce. We evaluated the ability of a large-bodied, resident Neotropical waterbird species, the southern screamer (*Chauna torquata*), to disperse microalgae through both epi- and endozoochory in Neotropical wetlands.
2. The study was conducted in a Ramsar Site located in the southernmost region of Brazil. Microalgal samples were collected from a natural wetland for reference, from two body regions (toes and feathers) of five adult birds, and from 15 fresh faecal samples of the species. All samples were collected in the same locality and during the cold season.
3. A total of 92 microalgal taxa were recorded in the wetland, while 61 taxa and 154 individuals were found on the toes, 44 taxa and 93 individuals on the feathers, and 18 taxa and 194 individuals in faeces. Microalgal richness differed among the wetland, toes, feathers, and faeces, with the highest richness observed in the wetland. Richness observed on the toes and feathers was higher than that in faeces, whereas richness did not differ between toes and feathers. Pairwise comparisons revealed that the composition of microalgae found in faeces differed significantly from that found in the wetland, toes, and feathers.
4. Our findings demonstrate that southern screamer has a strong potential to disperse microalgae through both epizoochory and endozoochory, although each pathway operates under distinct selective filters.
5. This study highlights the importance of waterbirds in maintaining microalgal connectivity across wetland ecosystems.

1 | Introduction

Dispersal is the process of movement of organisms among habitats across the landscape (Soomers et al. 2013). Passive dispersal occurs when the transport of organisms and/or their propagules is mediated by vectors, which may be physical or biological, such as wind (anemochory), water (hydrochory), and animals (zoochory) (Soomers et al. 2013; Green et al. 2022). Animal-mediated dispersal may occur via epizoochory (when transport takes place through the integument, fur, feathers, or beaks) or endozoochory (when transport occurs through the digestive tract). In South American wetlands, the passive dispersal of seeds and

aquatic invertebrates has been studied in waterbirds, capybaras, coypus, and otters (Silva et al. 2018; Green et al. 2023; Hoffmann et al. 2024, 2025).

In waterbirds, the importance of seed and invertebrate dispersal via epizoochory and endozoochory may vary among species and according to the nature of the propagules (Wehr et al. 2015; Mogles et al. 2018; Carbonell et al. 2021; Fernandez et al. 2021; Martín-Vélez et al. 2022; Almeida et al. 2025). However, studies comparing the efficiency of higher plant and invertebrate dispersal via epi- and endozoochory have been conducted mainly in passerines (Costa et al. 2014), waterbirds (Brochet et al. 2010), and wild mammals (Albert et al. 2015; Chuong et al. 2016; Martin et al. 2022; Tomowski et al. 2025). For the dispersal of seeds by waterbirds, transport is more frequent by endozoochory (Green et al. 2023). Nevertheless, information on the role of waterbirds in the dispersal of algae through epizoochory and endozoochory remains scarce (Proctor 1959; Schlichting 1960; Atkinson 1971; Green et al. 2023).

Microalgae are an extremely diverse group of organisms that play an important role in primary production in continental wetlands (Reynolds 2006; Wehr et al. 2015). Despite their wide geographical distribution (van Gremberghe et al. 2011), the active mobility of microalgae is limited and depends on vectors for the colonisation of new habitats and for gene flow among isolated populations (Kristiansen 1996; Sassenhagen et al. 2015; Tesson et al. 2016, 2018).

The morpho-functional traits of microalgae can act as ecological filters to identify which algal species are more likely to be dispersed by animal vectors. The analysis of *Diplosphaera chodatii* conducted by Medwed et al. (2021) revealed morpho-functional traits associated with adhesion and retention on biological substrates, as well as high desiccation resistance. The production of mucilage and capsules (e.g., *Nitzschia*, *Trachelomonas*), colony formation (e.g., *Scenedesmus*, *Pediastrum*), and resistance forms (cysts/spores) increase the likelihood of external retention and gut passage, and can be used to infer susceptibility to dispersal by epizoochory and endozoochory (Reynolds 2006; Litchman and Klausmeier 2008; Kruk et al. 2010; Wehr et al. 2015). Adhesion to feathers and legs/ft may be enhanced by extracellular proteoglycans present in diatoms (Lind et al. 1997), while mucilage increases adherence and buffers against desiccation (Lewis and Flechtner 2004; Wehr et al. 2015).

Here, we evaluated the ability of a Neotropical aquatic bird species, the southern screamer (*Chauna torquata*), to disperse microalgae through both epi- and endozoochory in Neotropical wetlands. The southern screamer (as well as all three species within the Anhimidae) is an endemic South American species, abundant in the subtropical grasslands of southern Brazil (Fontana et al. 1994; Fernandez et al. 2021). Despite part of the Anseriformes order, screamers lack interdigital membranes but can swim when under threat. Nests are built as floating platforms over water, within dense macrophyte stands, where nidifugous chicks develop (Brady 2020). The southern screamer (hereafter screamer) exhibits a predominantly herbivorous diet, based on aquatic macrophytes such as *Eichhornia crassipes*, *Egeria densa*, *Hydrocotyle ranunculoides*, and *Myriophyllum aquaticum*, as well as associated periphytic material (Pereyra 1942; Valle 1991). Foraging occurs by grazing on macrophyte stands and along wetland margins, maximizing contact of feet and plumage with biofilms and periphyton (Valle 1991; Fernandez et al. 2021). It also relies heavily on terrestrial habitats, usually with waterlogged soil, where it grazes within cattle and sheep (Fernandez et al. 2021). In addition, the species performs daily movements between roosting and foraging areas (Valle 1991).

The lifestyle of screamers predicts a strong potential for microalgal dispersal through both epi- and endozoochory. Direct contact of its feet and feathers with surface biofilms and with submerged and floating macrophytes may facilitate the external transport of colonial, filamentous, and diatomaceous forms that adhere and withstand short periods of desiccation (Lind et al. 1997; Lewis and Flechtner 2004; Wehr et al. 2015). The ingestion of macrophytes hosting dense epiphytic communities (epiphyton) may promote the indirect intake of microalgae and cysts into the digestive tract, which can subsequently be transported to other water bodies via excreta (Reynolds 2006; Brochet et al. 2010; Wehr et al. 2015). In this context, we tested the following hypotheses: 1. screamers disperse microalgae through both endozoochory and epizoochory; 2. the richness of microalgae dispersed by screamers is greater via epizoochory than endozoochory; and 3. the taxonomic and functional composition of microalgae dispersed by screamers differs between epi- and endozoochory.

2 | Methods

2.1 | Study Area

The study was conducted at the Taim Ecological Station (ESEC Taim), a Ramsar Site located in the southernmost region of Brazil. The ESEC Taim lies within the Pampa biome, approximately 500 km from Uruguay, and covers an area of 32,797 ha. The Pampa biome is a vast grassland formation occurring in southern Brazil, Uruguay, and Argentina, historically explored for cattle grazing, and more recently for agriculture, making it a biome under severe threat. The ESEC Taim encompasses a mosaic of isolated wetlands of varying sizes and hydrological regimes (permanent and intermittent). These habitats hold high ecological and hydrological importance, functioning as water retention zones, regulators of hydrological flows, providers of aquatic biodiversity support, and maintainers of regional ecological connectivity (Convention on Wetlands 2025). The climate is humid subtropical, with a mean annual temperature of 18°C and annual precipitation ranging from 1000 to 1500 mm, evenly distributed throughout the year (Tomazelli et al. 2000). The vegetation is dominated by natural grasslands of the Pampas biome, associated with aquatic macrophyte communities.

2.2 | Sampling Design

Qualitative samples of microalgae were collected at three equidistant sampling points (300 m apart) within a permanent

wetland inside ESEC Taim during the cold season (between May and August 2025). At each sampling point, microalgae were collected using a 20 μm plankton net, manually towed at the subsurface layer of the water column for 15 m. In addition, macrophytes were washed and the detached sediments were collected to include periphytic and benthic algae. All concentrated material was transferred into 50 mL tubes.

Quantitative samples of microalgae adhered to the body surface and contained in the faeces of screamers were collected from different individuals and during the cold season (between May and August 2025). A total of five screamer individuals were captured in the field during the same period in which environmental and faecal samples were collected. Captures were carried out at night (between 19:00 and 22:00 h) using headlamps and a hand net with a 0.5 m radius. After capture, a mask was placed over the individual's head to reduce stress. Algae attached to the feet and plumage were then collected, after which the individuals were released. Algae adhered to the birds' bodies were collected from two body regions of five different adult individuals, totalling ten samples ($n = 5$ toes and $n = 5$ ventral plumage): (i) the toes, which remain in direct contact with water and sediment during locomotion, and (ii) the ventral plumage (feathers), which frequently contacts the water surface and aquatic vegetation during resting and foraging activities. Microalgae were collected by gentle directed washing with distilled water jets applied using a wash bottle directly over the selected regions. The washing water was collected using adapted funnels made from 2 L PET bottles cut and moulded into semicircular shapes to fit the anatomical contour of each sampled region. All microalgal samples collected from the environment and from the birds' bodies (feathers and feet) were fixed in 4% (v/v) formaldehyde and stored at room temperature. A 50 mL centrifuge tube was attached to the lower end of each funnel to collect the detached material. After each washing, all equipment was carefully rinsed with distilled water to avoid cross-contamination between individuals. Control samples (open 50 mL centrifuge tubes with distilled water) collected near each bird showed no microalgae, confirming that windborne contamination did not occur during sampling.

A total of 15 fresh faecal samples were collected along the wetland margin (within 30 m from the shore), at least 4 m apart from each other, to reduce the likelihood of sampling faeces from the same individual, in places used as foraging or roosting sites by screamers. Fresh faecal samples were stored in a refrigerator (±4°C) and processed within 6 weeks. From each faecal sample, a subsample of approximately 1 g was taken from which 0.1 g was diluted in 10 mL of water. From the initial 10 mL, a 1 mL aliquot was removed, leaving 9 mL of sample. To this, 1 mL of neutral red solution (400 μg/L) was added, totaling 10 mL for viable cell staining.

Microalgal viability was assessed based on the integrity of the main structural components. Microalgae displaying an intact cell wall, well-preserved organelles, particularly the chloroplast, and cytoplasm were considered viable. Additionally, the cellular viability of microalgae in faeces was assessed using the neutral red staining technique, which allows discrimination between live and dead cells based on cytoplasmic coloration (da Luz et al. 2016). This approach enabled the detection of potentially viable structures with colonisation capacity after passage through the avian digestive tract. The samples stained with neutral red were fixed two hours after exposure.

Microalgal richness was assessed in the wetland samples, and two slides (for qualitative and quantitative analysis) were prepared from the zoochorous samples (epi- and endozoochory) under an optical microscope (Olympus CX21). Taxonomic identification was carried out to the lowest possible level, based on specialised literature and the AlgaeBase database (Guiry and Guiry 2025).

2.3 | Data Analysis

Microalgal taxa were grouped into five morpho-functional groups: (1) pennate diatoms (PD); (2) unicellular mixotrophic flagellates (UMF); (3) unicellular green algae (UG); (4) filamentous algae (FA); and (5) colonial and mucilaginous colonial algae (CMA), adapted from Salmaso and Padisák (2007) and Kruk et al. (2010).

We used a generalised linear model (GLM) to evaluate the effect of treatment (wetland, toes, feathers, and faeces) on total microalgal richness. Because algae from toes and feathers were sampled from the same individual, sample ID was included as a random effect in an additional generalised linear mixed-effects model (GLMM). As richness is a discrete variable, models were fitted using a negative binomial distribution with a log link function, after diagnostic tests indicated no overdispersion under this distribution. The full model (GLMM) was compared with the reduced model (GLM without the random effect) using a likelihood ratio test (LRT). When the test indicated a significant improvement in model fit ($p < 0.05$), the model including the random effect was retained; otherwise, the simpler GLM was preferred. Significant differences among treatment groups were examined using Tukey's post hoc test. In addition, a chi-square test of association (contingency table) was performed to assess whether the frequency of microalgal taxa within each functional group differed among the wetland, toes, feathers, and faeces.

To assess variation in microalgal composition among wetland, toes, feathers and faeces of screamers, we used principal coordinate analysis (PCoA) and permutational multivariate analysis of variance (PERMANOVA) using the Jaccard distance matrix (presence-absence) and 999 permutations to validate the model significance. Permutations were constrained within individuals to account for the non-independence of paired samples (toes and feathers from the same bird), whereas independent samples (wetland and faeces) were permuted freely within a common stratum. Homogeneity of multivariate dispersion among treatments was evaluated with betadisper method from vegan package (Oksanen et al. 2024). Additionally, a multi-level pattern analysis (De Cáceres and Legendre 2009) was performed to identify associations between taxa occurrence and specific combinations of study groups. The statistical significance of each association was tested with 999 permutations, and taxa with $p < 0.05$ were considered significant indicators of a particular group or combinations of groups (wetland, toes, feathers and

faeces). All statistical analyses were conducted in R v 4.4.0 (R Core Team 2024).

3 | Results

3.1 | Community Structure and Function

A total of 139 microalgal taxa were found in the study, of which 103 were identified to the species level and 36 to the genus level. The genera with the highest number of species were *Nitzschia* (17 species) and *Cosmarium* (11 species), followed by *Closterium*, *Navicula*, *Scenedesmus*, *Staurastrum*, *Staurodesmus*, and *Trachelomonas*, each represented by four species (Table S1). Regarding morpho-functional groups, 38 taxa were classified as pennate diatoms (PD), 31 taxa as filamentous algae (FA), 30 taxa as colonial and mucilaginous colonial algae (CMA), 29 taxa as unicellular green algae (UG), and 11 taxa as unicellular mixotrophic flagellates (UMF) (Table S1).

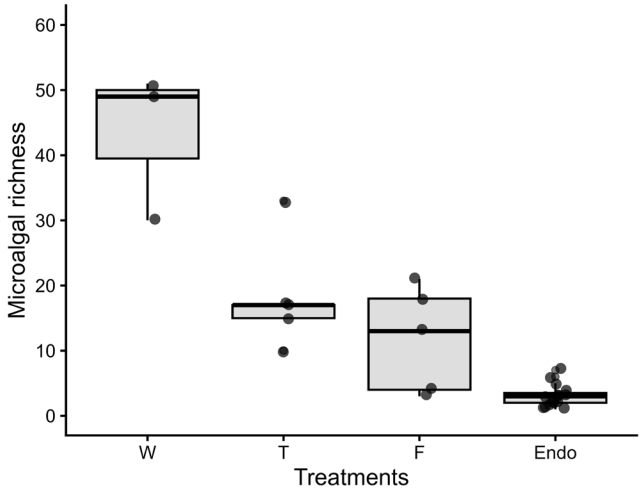

FIGURE 1 | Microalgal richness variation among wetland (W), feathers (F), and toes (T) ($n = 5$ birds sampled) and faeces (Endo) ($n = 15$) of southern screamers (*Chauna torquata*) in a southern Brazilian wetland.

3.2 | Wetland, Epizoochory and Endozoochory

From the total of 139 microalgal taxa recorded in this study, 92 were found in the wetland, 61 taxa and 154 individuals on the toes, 44 taxa and 93 individuals on the feathers, and 18 taxa and 194 individuals in the faeces of screamers, totaling 441 viable individuals overall. Among these, 44 taxa were exclusive to the wetland, 22 occurred only on the toes, 11 only on the feathers, and five were shared between toes and feathers. Of the 92 taxa recorded in the wetland, 16 taxa (17.4%) were also found on the toes, nine taxa (9.8%) on the feathers, and 14 taxa (15.2%) on both toes and feathers. Regarding endozoochory, six taxa were found exclusively in faeces (*Coleochaete* sp., *Synechocystis* sp., *Gomphosphaeria* sp., *Microspora* sp., *Leptolyngbya* sp., and *Trachelomonas volvocina*), and three taxa were shared between faeces and feathers (*Eutetramorus* sp., *Scenedesmus bijugatus*, and *Cosmarium laeve*). Among the taxa recorded in the wetland, five taxa (5.4%) were detected in faeces, and four taxa (4.3%) occurred in both faeces and feathers and/or toes. Two taxa accounted for 75.8% of all microalgae found in faeces (*Pleurocapsa fuliginosa* and *Oedogonium* sp.). Three algal cysts were recorded, one of which belonged to *Oedogonium* sp.

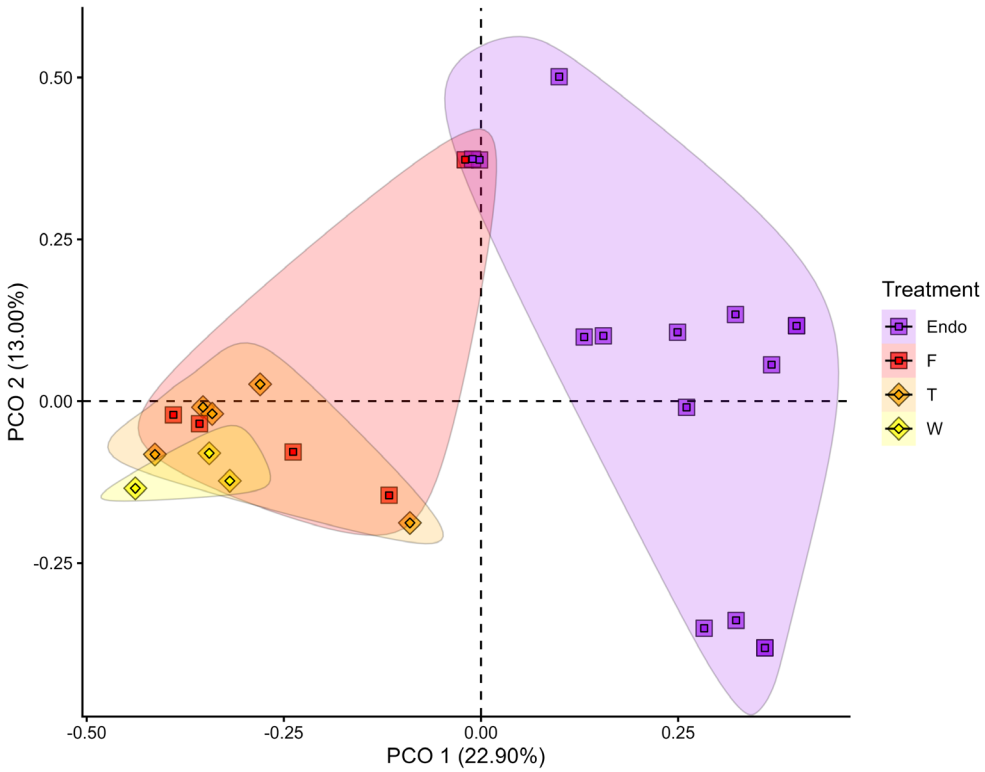

FIGURE 2 | PCoA plot showing variation in microalgal composition among wetland (W), feathers (F), and toes (T) ($n = 5$ birds sampled) and faeces (Endo) ($n = 15$) of southern screamers (*Chauna torquata*) at Taim Ecological Station, in southern Brazil.

TABLE 1 | Summary of the multilevel pattern analysis showing the associations between microalgal taxa occurrence and specific combinations of study groups (wetland, feathers, toes and faeces) of southern screamers (*Chauna torquata*) sampled in southern Brazil in 2025.

Group	Microalgal taxa	IndVal statistic (stat)	*p*
Wetland	*Staurastrum manfeldtii*	0.866	0.003**
	Merismopedia glauca	0.816	0.010**
	Zygnema sp.	0.816	0.008**
	Melosira sp.	0.816	0.010**
	Oscillatoria princeps	0.816	0.010**
	Nitzscha filiformis	0.816	0.017*
	Nitzschia gracilis	0.816	0.010**
	Euastrum sp.	0.816	0.010**
	Desmodesmus comunnis	0.667	0.028*
	Pediastrum duplex	0.667	0.033*
	Scenedesmus linearis	0.667	0.028*
	Geitlerinema sp.	0.667	0.038*
	Closterium parvulum	0.667	0.033*
	Cosmarium subtumidum	0.667	0.035*
	Cosmarium venustum	0.667	0.033*
	Euglena ehrenbergii	0.667	0.028*
Faeces	*Pleurocapsa* sp.	0.800	0.039*
Toes	*Eunotia sigmoidea*	0.894	0.001***
Wetland + Feathers	*Navicula* sp.	0.791	0.004**
	Gonatozygon monotaenium	0.632	0.039*
Wetland + Toes	*Aulacoseira granulata*	0.722	0.013*
	Gyrossigma acuminatum	0.722	0.014*
	Pandorina morum	0.707	0.008**
	Pinnularia gibba	0.707	0.013*
	Nitzschia reversa	0.707	0.010**
	Hyalotheca sp.	0.632	0.030*
	Spirogyra sp.	0.632	0.044*
	Hantzschia amphioxys	0.612	0.046*
Feathers + Toes	*Nitzschia filiformis*	0.707	0.009**
Wetland + Feathers + Toes	*Nitzschia palea*	0.832	0.001***
	Oscilatoria sp.	0.784	0.003**
	Pinnularia sudetica	0.734	0.005**
	Anabaena sp.	0.679	0.032*
	Diadesmis confervaceae	0.679	0.021*

*$p < 0.05$.
**$p < 0.01$.
***$p < 0.001$.

3.3 | Microalgal Richness, and Taxonomic and Functional Composition Among Wetland and Waterbirds

Since the random effect did not significantly improve model fit ($\chi^2_1 = 1.125$, $p = 0.288$), the simpler GLM was selected. Microalgal richness differed among the wetland, toes, feathers, and faeces, with the highest richness observed in the wetland (GLM, $\chi^2_3 = 120.59$, $p < 0.001$). Richness on the toes and feathers was significantly higher than in the faeces ($p < 0.05$), whereas no significant difference was found between toes and feathers of screamers ($p > 0.05$; Figure 1).

The taxonomic composition of microalgae differed significantly among wetlands, toes, feathers, and faeces ($R^2 = 0.358$, $F_{3,24} = 4.469$, $p < 0.001$), indicating partial separation among treatments (Figure 2). This variation was not influenced by differences in within-group dispersion of beta diversity, as indicated by the Betadisper analysis ($F_{3,24} = 1.175$, $p = 0.334$). Pairwise comparisons revealed that the composition of microalgae found in faeces differed significantly from that found in the wetland, toes, and feathers ($p < 0.05$). In contrast, the composition of microalgae observed on the toes and feathers was similar to each other and did not differ from that of the wetland ($p > 0.05$; Figure 2). Although 18 microalgal taxa were associated with a single group (wetland, toes, or faeces), 11 taxa were linked to two groups (wetland + feathers, wetland + toes, or feathers + toes), and five taxa were associated with three groups (wetland + feathers + toes), as identified by the multilevel pattern analysis (Table 1).

The proportion of microalgal taxa across the five morpho-functional groups differed among wetlands, toes, feathers, and faeces of screamers ($\chi^2_{12} = 26.488$, $p = 0.009$). Examination of standardised residuals indicated that the strongest associations were observed for colonial and mucilaginous colonial algae in faeces, and for pennate diatoms on the toes. In contrast, unicellular mixotrophic flagellates and unicellular green algae were more strongly associated with the wetland (Figure 3).

4 | Discussion

Our study demonstrated that southern screamer has a strong potential to disperse microalgae via both epizoochory and endozoochory, although each pathway involves distinct selective filters. Moreover, this study showed that waterbirds disperse diverse morpho-functional groups of microalgae, such as pennate diatoms, filamentous algae, colonial and mucilaginous colonial algae, unicellular green algae, and mixotrophic flagellates. Green et al. (2023) emphasised the limited number of studies investigating microalgal dispersal by waterbirds, referencing early contributions by Proctor (1959), Schlichting (1960) and Atkinson (1971). Our results contribute to expanding the list of viable microorganisms known to be dispersed by these organisms. This study provides important evidence of microalgal dispersal by aquatic birds through two distinct mechanisms: epi- and endo-zoochory. Moreover, the study demonstrated an intense and regular mechanism for a vast range of microalgal species, mediated for a bird living in the aquatic and terrestrial ecotone, rather than an occasional event. However, there are still no data from other studies corroborating the potential of waterbirds to disperse microalgae, including whether the genera *Nitzschia* and *Cosmarium* indeed have the highest dispersal potential among them. These findings may serve as hypotheses to be tested in future research.

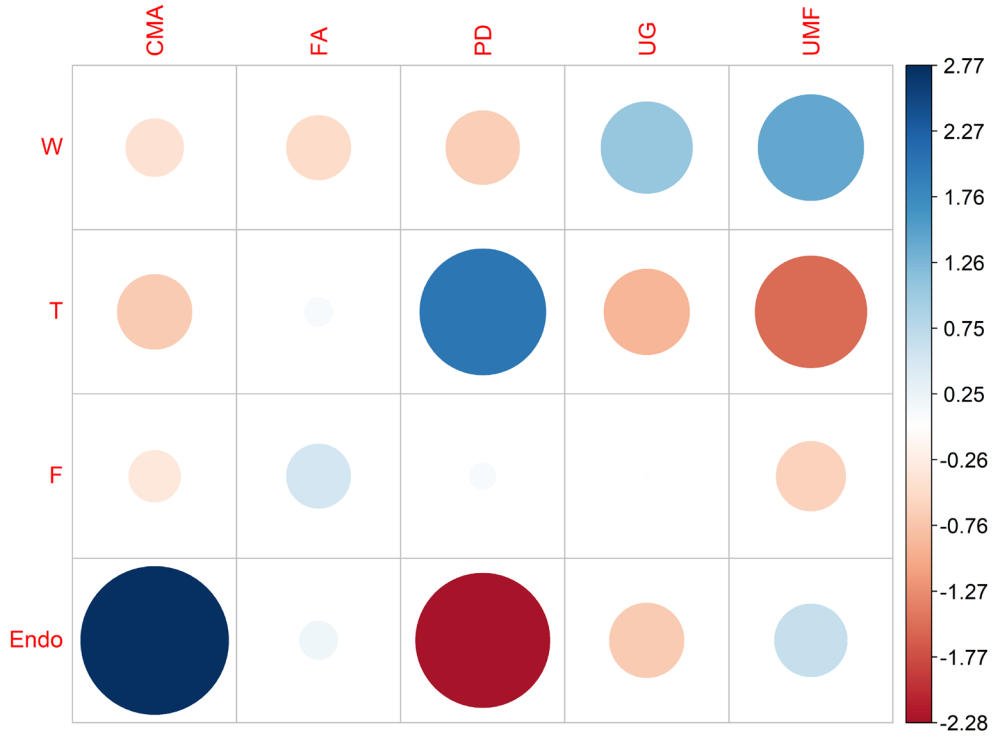

FIGURE 3 | Proportion of microalgal taxa of five morpho-functional groups among wetland (W), feathers (F) and toes (T) ($n = 5$ birds sampled) and faeces (Endo) ($n = 15$) of southern screamers (*Chauna torquata*) in a southern Brazilian wetland. Bubble size is proportional to the absolute value of the standardised residuals (see scale on the right), representing the magnitude of the relationship. Positive residuals (blue) indicate a positive association, whereas negative residuals (red) indicate a negative association.

This high dispersal ability reinforces the non-classical dispersal syndrome, suggesting that zoochory is an important vector for aquatic organisms in wetlands (Green et al. 2023). Studies on aquatic bird-mediated dispersal mark an important step in ecological research, as they go beyond the classical concept of frugivorous birds dispersing fleshy and colourful fruits (Green et al. 2023; Messeder et al. 2025). Thus, aquatic birds could disperse seeds of angiosperms with fleshy and colourful fruits (Orłowski et al. 2016), but also microalgae (Ellegaard and Ribeiro 2018), seeds of plants without colourful fruits (Silva et al. 2021; Lovas-Kiss et al. 2023), whole plants (Lovas-Kiss et al. 2018; Silva et al. 2018), invertebrates (Robertson et al. 2021), and fish eggs (Silva et al. 2019; Lovas-Kiss et al. 2020).

Our results showed that the richness of microalgae dispersed by screamers was higher via epizoochory than via endozoochory, and that the dispersed assemblages differed between these two mechanisms. This bird remains closely associated with surface water in wetlands, and the likelihood of algae adhering to its toes and ventral feathers is high. Pennate diatoms predominated on the toes, reflecting their epiphytic habit and the adhesive capacity conferred by their siliceous frustules and mucilage secretion (Letáková et al. 2018). The similarity between microalgae dispersed through epizoochory and those present in the wetland environment indicates that adhered taxa mainly originate from direct contact with the water surface and macrophyte biofilms. In contrast, the differences in composition between microalgae dispersed via the digestive tract and those dispersed externally suggest that the endozoochorous taxa largely correspond to epiphytic species ingested along with the macrophytes used as food. These findings reveal two complementary filters in microalgal dispersal by aquatic birds: while epizoochory favours taxa with adhesive traits and desiccation resistance (Tesson et al. 2018), endozoochory selects for protected forms and resistant stages capable of enduring adverse conditions derived from internal gut transit and digestive processes of birds.

The lower richness and distinct composition of microalgae dispersed through the digestive tract compared to external transport may result from the low resistance of many species to gut passage (Atkinson 1972; Tesson et al. 2016). Colonial/mucilaginous (CMA) and filamentous (FA) algae, as well as cyst forming microalgae (e.g., *Oedogonium* sp.), possess capsules, sheaths, or segmented thalli that provide mechanical and physiological protection during intestinal transit and temporary exposure to outside water (Atkinson 1972; Souffreau et al. 2013; Tesson et al. 2016). Cyst formation is considered an adaptation to adverse conditions (Anderson and Wall 1978), and microalgae with thick, mechanically resistant cell walls (Kokinos et al. 1998) have greater chances of surviving gut passage than vegetative cells (Kremp et al. 2003; Tesson et al. 2018).

Information on population size and flight distances of screamers is scarce in the literature; however, field observations and unpublished tracking data in southern Brazil indicate that this species is abundant and performs short flights restricted to foraging areas, found year-round at the same places, with fixed

territories during breeding, but performing regional movements. Our results show that screamers act as an important vector for short-distance dispersal of microalgae, potentially promoting progressive transport of propagules among isolated wetlands. This mechanism, known as step-by-step dispersal (Coughlan et al. 2015, 2017), may enhance connectivity among microalgal populations and sustain gene flow and colonisation processes at a local scale (Rengefors et al. 2012; Sassenhagen et al. 2015). Despite their limited movement range, the high abundance of screamers in the study area suggests that microalgal dispersal mediated by this waterbird species, and potentially many others, may occur frequently and in multiple directions, forming a regional dispersal network.

Author Contributions

Conceptualisation: F.C.F., L.M. Developing methods: F.C.F., C.N.F., P.S.G. Data analysis: F.C.F., C.S. Preparation of figures and tables: F.C.F., C.S. Conducting the research, data interpretation, writing: F.C.F., C.N.F., P.S.G., C.S., L.B., L.M.

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Ethics Statement

The procedures employed were ethically reviewed and approved by the Ethics Committee CEUA/FURG (No. Pq031/2024).

Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

Data are available from the authors upon reasonable request.

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Supporting Information

Additional supporting information can be found online in the Supporting Information section. **Table S1:** Microalgae taxa classified by Functional Group, Division, and Family. The table indicates each taxon's occurrence in the wetland (1 = present, 0 = absent) and its abundance (number of viable individuals) found on the toes, feathers, and faeces of *Chauna torquata*.