



Assessing the taxonomic sufficiency of macroinvertebrate communities and their potential to distinguish the impacts of land use on lowland streams in Uruguay

Avaliando a suficiência taxonômica das comunidades de macroinvertebrados e seu potencial para distinguir os impactos do uso da terra em riachos de terras baixas no Uruguai

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Abstract: Aim: Macroinvertebrates are extensively employed as bioindicators for evaluating how stream ecosystems respond to alterations in physical and chemical habitats caused by human activity. Although family-taxonomic level is usually used to identify macroinvertebrates in biomonitoring programs, coarser taxonomic resolution may provide similar information. We aim to evaluate taxonomic sufficiency by comparing macroinvertebrate communities at the order and family levels to differentiate the effects of different land uses. **Methods:** We conducted colonization experiments using artificial substrates in streams representing three land use types: urban (U, n=3), intensive agriculture - dairy production (AD, n=4), and extensive cattle ranching (CR, n=4). **Results:** We obtained similar results using both taxonomic levels, which effectively distinguished the impacts of different land uses. In the sites examined, the majority of indicator groups exhibited only one family per order, with the exception of Ephemeroptera (Leptophlebiidae, Baetidae, and Caenidae). Notably, Baetidae and Caenidae were more prevalent in streams associated with extensive cattle ranching (CR). **Conclusions:** Although this study provides a clear precedent, further investigation of these systems and other land uses (e.g., afforestation) is needed to validate this pattern. Coarser taxonomic assessment holds potential as a cost-effective method for stream monitoring and assessment in Uruguay.

Keywords: order; family; Amphipoda; Littorinimorpha; Ephemeroptera.

Resumo: Objetivo: Os macroinvertebrados são amplamente utilizados como bioindicadores para avaliar a forma como os ecossistemas de riachos respondem às alterações dos habitats físicos e químicos causadas pela atividade humana. Embora o nível taxonômico de família seja normalmente utilizado para identificar macroinvertebrados em programas de biomonitoramento, uma resolução taxonômica mais grosseira pode fornecer informações semelhantes. O objetivo é avaliar a suficiência taxonômica, comparando as comunidades de macroinvertebrados ao nível da ordem e da família, para diferenciar os efeitos de diferentes usos do solo. **Métodos:** Realizamos experimentos de colonização utilizando substratos artificiais em cursos de água representativos de três tipos de uso do solo: urbano (U, n=3), agricultura intensiva - produção de leite (AD, n=4), e pecuária extensiva (CR, n=4). **Resultados:** Obtivemos resultados semelhantes utilizando ambos os níveis taxonômicos, o que permitiu distinguir eficazmente



os impactos dos diferentes usos do solo. Nos locais examinados, a maioria dos grupos indicadores apresentava apenas uma família por ordem, com exceção dos Ephemeroptera (Leptophlebiidae, Baetidae e Caenidae). Notavelmente, Baetidae e Caenidae foram mais predominantes em riachos associados à criação extensiva de gado (CR). **Conclusões:** Embora este estudo forneça um precedente claro, é necessária uma investigação mais aprofundada destes sistemas e de outras utilizações do solo (por exemplo, reflorestamento) para validar este padrão. A avaliação taxonômica mais grosseira tem potencial para ser um método econômico de monitoramento e avaliação de cursos de água no Uruguai.

Palavras-chave: ordem; família; Amphipoda; Littorinimorpha; Ephemeroptera.

1. Introduction

Human land use changes usually promote the deterioration of stream and river ecosystems, affecting the aquatic communities and ecosystem functioning (Alonso Duré, 2018; Akamagwuna & Odume, 2020). In the assessment of the ecological status of fluvial ecosystems in response to human impacts, macroinvertebrate communities are widely recognized and extensively validated as effective bioindicators (Roldán Pérez, 2003; Springer, 2010; Chicas et al., 2010; Alonso Duré, 2018; Akamagwuna & Odume, 2020). This recognition of macroinvertebrate effectiveness has been mainly attributed primarily to their long lifespan, allowing them to reflect the effects of contaminants, even at low concentrations that may accumulate over time (Segnini, 2003; Springer, 2010). Moreover, their relatively immobile nature and ease of collection or sampling, combined with their tendency to form distinct communities associated with the physical and chemical conditions of stream waters, make them valuable for assessing varying levels of contamination (Plafkin et al., 1989; DeShon, 1995; Karr & Chu, 1999; Morley & Karr, 2002; Roldán Pérez, 2003; Segnini, 2003; Chicas et al., 2010; Springer, 2010; Akamagwuna & Odume, 2020; Burwood et al., 2021).

Typically, the family taxonomic level is the most widely employed in biomonitoring activities that use macroinvertebrates. This allows for the differentiation of impacted sites from less impacted ones or reference conditions (Cortelezzi & Paz, 2023). However, in some instances, a coarser taxonomic resolution may be sufficient to provide the same information as families (Suárez et al., 2022; Cortelezzi & Paz, 2023). Contrarily, more diverse ecosystems or specific circumstances may require a finer taxonomic resolution (Restello et al., 2020). Therefore, determining the taxonomic level to be used will depend on the circumstances of the environment, and as such, prior comparisons should be made to establish a methodology with a specific taxonomic level. On the other hand, the lack of taxonomic knowledge regarding macroinvertebrate

species, especially in tropical areas, represents a significant challenge for environmental policies and monitoring in freshwater ecosystems (Jones, 2008; Buss et al., 2015). Additionally, macroinvertebrates constitute highly diverse groups that vary according to the geographic region in which they are found. They also face multiple pressures from human activities; thus, assessing how they respond to such impacts is essential. This allows for identifying the most indicative groups and determining the taxonomic level at which they respond (Ricciardi & Rasmussen, 1999; Abell, 2002; Allan, 2004; Strayer, 2006; Lento et al., 2022; Milner et al., 2023).

Using higher taxa (such as genera and families) as surrogates for species richness has been the predominant approach in biodiversity assessment. However, research on assemblage structure patterns with higher resolution has received limited attention despite their crucial role in conservation planning as indicators of species composition among sites (Ferrier, 2002; Legendre et al., 2005; Nosad et al., 2021).

Typically, biotic patterns examined at the species level encompass both environmental variability and the geographic location of sampling units (Forero et al., 2014). However, our understanding of regional patterns in the taxonomic resolution at genus and family levels remains limited (Jones, 2008). Nonetheless, a recent regional study on invertebrate families demonstrated a significant association between assemblage variability, spatial location, and stream habitat characteristics (Murphy & Davy-Bowker, 2005). This finding was unexpected, considering that families generally exhibit broader distributions than species at regional scales, and family-level data were expected to display less spatial structure (Jones, 2008). Furthermore, spatial variability in higher taxonomic resolution has been observed on much larger scales, ranging from continental to global, based on extensive sampling grids (Gaston et al., 1995; Balmford et al., 1996; Williams et al., 1997). Therefore, it is crucial to test the applicability of higher taxon surrogates at the regional scale, leveraging local and site-specific

knowledge (Balmford et al., 2000; Chen et al., 2022).

The optimal level of taxonomic resolution required in bioindication has been extensively debated among authors, leading to varying perspectives. Some suggest employing bioindicators at the species level (e.g., Guerold, 2000; Lenat & Resh, 2001; Waite et al., 2004), while others advocate for their use at the family level (Warwick, 1988; Bailey et al., 2001; Pitacco et al., 2019). Several studies have indicated that macroinvertebrate assemblage variation exhibits minimal change when shifting from genus to order level regarding taxonomic resolution (Furse et al., 1984; Wright et al., 1995; Bowman & Bailey, 1997). Some authors have even proposed that higher taxonomic levels are more suitable than the species level due to the latter's heightened response to natural environmental variation, which can introduce noise and mask human impacts (Warwick, 1993; Bailey et al., 2001).

Many countries have adopted macroinvertebrates as bioindicators of water quality, using the family level (Queiroz et al., 2018; Cortelezzi et al., 2019; Castro et al., 2020). However, Germany stands out as the only country that requires the use of species-level identification in its saprobic method (Jones, 2008). In Latin America, the incomplete knowledge of the aquatic macroinvertebrate fauna presents a significant challenge, making it difficult to work at the genus level, and even more so at the species level (Jones, 2008; Buss & Vitorino, 2010; Cortelezzi & Paz, 2023). For instance, studies on bioindication assessing pollution caused by oil industry spills have consistently recommended using taxonomic diagnostic levels, specifically at the family level (but if it is possible, at the genus level), to interpret the environmental impact of the spill accurately (Bailey et al., 2001).

The level of taxonomic resolution necessary to meet the research objectives is called sufficient taxonomic resolution (Ellis, 1985). According to a previous study the order level could significantly distinguish between different land uses in lowland Uruguayan streams (Suárez et al., 2022). In this sense, we aimed to evaluate the taxonomic sufficiency by contrasting the macroinvertebrate community at the family and order taxonomic levels to assess its potential to differentiate the effects of different land use types in lowland subtropical streams.

2. Materials and Methods

2.1. Study area

The study was conducted in 11 streams with three land uses: extensive cattle ranching (CR; n=4) located in the Santa Lucía and Río Negro watersheds; intensive agriculture with dairy production (AD; n=4) located in the Santa Lucía River watershed; and urbanization (U; n=3) located in the Río de la Plata and Arroyo Maldonado watersheds (Table 1). When selecting the study sites, we initially focused on systems with a high predominance of land uses to be analyzed within their respective watersheds.

The CR sites selected for this study had extensive cattle use occupying $87.2 \pm 13.9\%$ of the watershed. In Uruguay, this extensive activity is characterized by an average of 0.7 cattle per hectare (DIEA, 2020). Uruguayan pristine ecosystems are practically nonexistent after European colonization (Torremorell et al., 2021), and lowland streams associated with extensive livestock production. Represent the least impacted streams and generally have better water quality conditions in our country (Arocena, 1996; Benejam et al., 2016; Barrios et al.,

Table 1. Study area.

Basin	Stream order	Stream	Land use	Localization
Santa Lucía	3	Chal Chal	CR-1	33°54'13.39"S, 56°0'22.43"W
	3	Talita	CR-2	33°47'45.94"S, 55°50'4.29"W
Río Negro	3	Ombú	CR-3	33°44'10.33"S, 55°39'48.86"W
	3	Pedreira	CR-4	33°40'35.09"S, 55°39'8.37"W
Santa Lucía	3	Las Piedras	AD-1	34°16'15.13"S, 56°20'8.01"W
	3	Sauce	AD-2	34°12'54.63"S, 56°20'52.00"W
	3	Sauce de Berdías	AD-3	34°9'45.06"S, 56°20'5.69"W
	3	Pedreira	AD-4	34°7'38.63"S, 56°19'59.96" W
Río de la Plata	2	Aguada	U-1	34°55'16.64"S, 54°58'11.59"W
Arroyo Maldonado	2	Cañada del Molino	U-2	34°54'48.56"S, 54°59'8.04" W
	2	Salada	U-3	34°54'52.37"S, 54°56'29.00"W

CR: extensive cattle ranching sites (n=4), AD: intensive agriculture and dairy production sites (n=4), and U: urbanization sites (n=3).

2024). For this reason, many of these streams can currently be considered reference streams in low-gradient areas in Uruguay (Barrios et al., 2024), and in this region, the small streams representative of the lowlands generally do not have riparian forests (Mary-Lauyé et al., 2023).

The AD sites represent two combined uses consisting of intensive agriculture and dairy production, with 100% of their watershed cultivated to generate fodder for dairy cattle, which is also present in the same area, this type of soil promotes increases in nutrient concentrations in the water. In Uruguay, 65% of the farms dedicated to dairy cattle production, have an area between 50 and 500 hectares, and more than 60% of their pastures are improved (DIEA, 2020). The U sites selected for this study represent sites with high urban coverage in their drainage basin ($70 \pm 17.3\%$). These streams are among the most urbanized systems in the city of Maldonado and are included in the monitoring system of the “Núcleo Interdisciplinario: Aguas Urbanas: Proyecto y Gestión”.

The aquatic habitat of the selected sites was characterized by medium-fine substrates, including sand, gravel, and stones (Suárez et al., 2022). The depths of these habitats did not exceed 30 cm, and their wet widths measured around 3 m. In terms of physicochemical water parameters, the temperature varied across the sites, with the livestock sites exhibiting the highest average values ($25.8 \pm 2.5^\circ\text{C}$), followed by agriculture and dairy sites ($24.2 \pm 1.9^\circ\text{C}$), and urban sites ($20.9 \pm 1.6^\circ\text{C}$). Another parameter considered was the specific conductivity (corrected conductivity at 25°C , $\mu\text{S. cm}^{-1}$), where agriculture with dairy sites recorded the highest value ($629.0 \pm 153.3 \mu\text{S. cm}^{-1}$), followed by livestock and urban sites ($395.3 \pm 35.8 \mu\text{S. cm}^{-1}$; $357.5 \pm 101.0 \mu\text{S. cm}^{-1}$, respectively). The highest values of the concentration of total phosphorus were reported in agriculture with dairy sites ($320.9 \pm 153.9 \mu\text{g. L}^{-1}$) and urban sites ($246.8 \pm 194.9 \mu\text{g. L}^{-1}$), while livestock sites had the lowest value ($42.7 \pm 27.7 \mu\text{g. L}^{-1}$). In terms of total nitrogen concentrations ($\mu\text{g. L}^{-1}$), the urban sites exhibited the highest values ($1437.5 \pm 325.7 \mu\text{g. L}^{-1}$), followed by the agricultural ($925.0 \pm 228.3 \mu\text{g. L}^{-1}$), and livestock sites ($421.8 \pm 134.5 \mu\text{g. L}^{-1}$) (Suárez et al., 2022). We also considered other relevant variables for the macroinvertebrate community in these systems, such as watershed area and channel depth (Death & Winterbourn, 1995).

2.2. Macroinvertebrate community sampling

An additional important small-scale component of the macroinvertebrate ecosystem is a certain kind

of sediment (Brooks & Boulton, 1991). To neutralize the impact of various sediment types that can occur in different streams, we utilized artificial substrates. This allowed us to consistently study a subsample of the macroinvertebrate community linked to a specific substrate type across all streams (Quesada-Alvarado & Solano-Ulate, 2020). We inserted 15 artificial substrates for the purpose of sampling macroinvertebrates in each stream. These substrates were 160 cm^3 of stones that had been sieved to a size of 1.3 to 1.5 cm. They were made of plastic mesh bags with 1.2 cm apertures. Each bag measured 11.2 cm in length and 7.3 cm in width. There were $73.3 \pm 5.8 \text{ cm}^3$ of interstitial water in this volume of stones. Every bag was positioned evenly throughout the watercourse's width. In order to facilitate macroinvertebrate colonization, we kept the devices in the streams for 15 days during the summer (February 2018). For every stream, we examined 10 replicates (110 replicates) of artificial substrates. Using a $500 \mu\text{m}$ filter, we removed the macroinvertebrates from the substrates and preserved them in 70% alcohol. In the laboratory, we identified the macroinvertebrates at the order and family level using the taxonomic keys of Domínguez & Fernández (2009) and Hamada et al. (2018).

2.3. Statistical analysis

To comprehend geographic heterogeneity in macroinvertebrate composition at the order and family levels, two nonmetric multidimensional scaling ordinations (NMDS) were utilized. To check for differences in macroinvertebrate structure among various land uses at the order and family levels, two permutational multivariate analyses of variance (PERMANOVA) were conducted. Both NMDS and PERMANOVA are appropriate for similarity or distance data, and they concentrate on displaying and evaluating variations in data structure. They are used to evaluate group similarities and differences (Anderson, 2014). Using 999 permutations and the Bray-Curtis dissimilarity measure, the abundance matrix was converted into a dissimilarity matrix for both the PERMANOVA and NMDS analyses (Quinn & Keough, 2002; Anderson, 2011). Indicator species analysis was performed at the order and family level to detect the macroinvertebrate groups responsible for the separation of each group. The aim of this analysis is to find species that are significantly associated with each group. This method focuses on identifying species that are highly prevalent in one group compared to others. It also evaluates the statistical significance of the

association between a species and a group (Bakker, 2008). The R packages “vegan” (Oksanen et al., 2013) and “indicpecies” (De Cáceres, 2020) were used for NMDS- PERMANOVA and indicator species analyses respectively.

3. Results

In total, 8105 macroinvertebrates were collected from the 110 artificial substrates analyzed. They were distributed across 22 order taxa, with Ephemeroptera, Littorinimorpha, and Amphipoda being the most abundant groups. A total of 50 families belonging to the phylum Arthropoda were identified, with 33 families representing 55.4% of the total abundance. Mollusca were represented by 10 families (30.3% of the total abundance) and Annelida by six families (14.3%). The families with the highest frequency of occurrence in the total samples were Cochliopidae (24.8% of the total abundance), Hyalellidae (11.3%), and Chironomidae (6.2%) (Table 2).

A total of 1892, 4842, and 1371 macroinvertebrates were captured at the CR, AD, and U sites, respectively. Regarding the abundance and richness of families in each order, Littorinimorpha, which Cochliopidae fully represents, predominated the AD sites (Figure 1). Caenidae comprised most of the Ephemeroptera group, followed by the Leptophlebiidae, while Baetidae and Leptohiphidae were less common (Figure 1). In contrast, the Hydropsychidae made up the majority of the Trichoptera. The CR sites showed a higher relative abundance of Ephemeroptera, with a higher proportion of Leprophlebiidae, followed by Canidae and Baetidae; this last family had a lower proportion. Leptoceridae was the main family

among the Trichoptera, with minor amounts of Hydroptilidae, Hydrobiosidae, Hydropsychidae, and Polycentropodidae (Figure 1). The U sites revealed that Amphipoda was only composed by Hyalellidae, and the same occurred with Rhynchobdellida, composed by Glossiphoniidae (Figure 1).

The ordination analysis (NMDS) of stream sites based on the relative abundance of macroinvertebrates at the order level revealed a separation between CR and AD from U sites (Figure 2A), and these group differences were statistically significant (PERMANOVA, $F = 8.26$, $p < 0.002$). Similarly, when considering the relative abundance at the family level, the same pattern was observed in the ordination (Figure 2B), and the differences between groups were also statistically significant (PERMANOVA, $F = 5.63$, $p < 0.001$).

The Indicator Species Analysis performed at the order level (Table 3) revealed that Amphipoda was the most abundant in U sites (Relative abundance: $U = 26.4 \pm 17.5$ vs. $AD = 4.5 \pm 2.4$ and $CR = 1.0 \pm 0.5$). At the same time, Littorinimorpha dominated in intensive AD sites (relative abundance: $AD = 47.0 \pm 52.2$ vs. $U = 0.3 \pm 0.5$ and $CR = 0.4 \pm 5.6$). Ephemeroptera was mostly represented in AD and CR streams (relative abundance: $AD = 14.9 \pm 14.2$ and $CR = 12.6 \pm 17.1$ vs. $U = 0$) (Table 3).

At the family level, the Indicator Species Analysis showed that Hyalellidae ($U = 26.4 \pm 17.5$ vs. $AD = 4.5 \pm 2.4$, and $CR = 1.0 \pm 0.5$) and Glossiphoniidae ($U = 19.2 \pm 16.8$ vs. $AD = 9.1 \pm 4.1$, and $CR = 1.3 \pm 0.4$) were the most abundant in U streams, while Cochliopidae ($AD = 50.1 \pm 36.2$ vs. $U = 1.0 \pm 0.5$, and $CR = 5.8 \pm 2.8$) dominated in intensive AD sites. Leptophlebiidae showed the

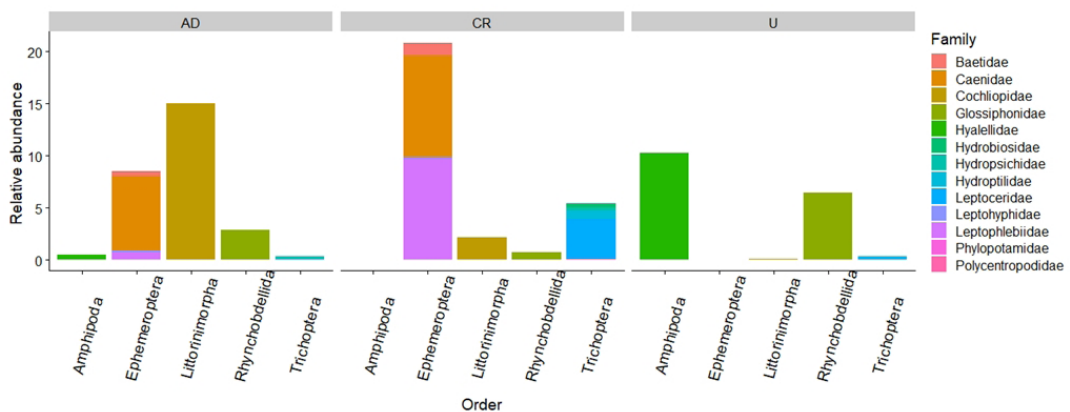


Figure 1. Distribution of the main total and relative family abundance for each order and land use type. Sampling sites: CR: extensive cattle ranching sites, AD: intensive agriculture and dairy production sites, and U: urbanization sites.

Table 2. Mean and standard deviation for the total abundance of aquatic macroinvertebrates for each land use: extensive cattle ranching (CR), intensive agriculture and dairy production (AD) and urban (U).

Order	Family	CR	AD	U
Alluroidea	Alluroidea	0	40.0±28.0	0
Haplotaenida	Haplotaenidae	20.0±10.0	90.0±64.0	30.0±17.0
Tubificida	Naididae	0	40.0±28.0	0
Narapida	Narapidae	43.0±33.0	169.0±149.0	105.0±69.0
Rhynchobdellida	Glossiphoniidae	30.0±44.0	91.1±41.0	19.2±16.8
Unionoida	Hyriidae	0	20.0±1.4	0
Imparientia	Corbiculidae	10.0±5.5	29.0±17.0	0
	Sphaeriidae	0	75.5±42.0	0
Mytiloidea	Mytilidae	0	0	77.0±56.0
Architaenioglossa	Ampullariidae	11.1±1.0	40.0±27.0	0
	Lymnaeidae	0	10.0±5.0	10.0±5.0
	Physidae	0	1.0±0.5	0
	Planorbidae	19.0±7.0	52.0±54.0	21.0±12.0
Littorinimorpha	Cochliopidae	58.0±28.0	501.0±362.0	10.0±5.0
Decapoda	Aegidae	10.0±5.0	20.0±9.0	0
Isopoda	Cymothoidae	0	0	20.0±12.0
Amphipoda	Hyalellidae	10.0±5.0	45.0±24.0	265.0±175.0
Entomobryomorpha	Entomobryidae	0	10.0±5.0	20.0±12.0
Trombidiformes	Hydrachnidae	10.0±0.5	0	0
Ephemeroptera	Baetidae	24.0±8.0	3.2±1.8	0
	Caenidae	206.0±151.1	217.0±99.0	0
	Leptohyphidae	20.0±10.0	45.0±59.0	0
	Leptophlebiidae	135.0±108.0	53.0±36.0	0
Odonata	Calopterygidae	20.0±10.0	10.0±5.0	10.0±5.0
	Coenagrionidae	14.0±3.0	18.0±6.0	0
	Lestidae	20.0±10.0	0	0
	Libellulidae	10.0±5.0	10.0±5.0	0
Plecoptera	Gripopterygidae	10.0±5.0	0	0
Megaloptera	Corydalidae	10.0±5.0	0	0
Heteroptera	Naucoridae	10.0±5.0	0	0
Trichoptera	Hydrobiosidae	26.0±26.0	0	0
	Hydropsychidae	19.0±8.0	37.0±26.6	0
	Hydroptilidae	20.0±10.0	10.0±5.0	10.0±5.0
	Leptoceridae	47.0±27.0	28.0±15.0	10.0±5.0
	Philopotamidae	0	10.0±5.0	0
	Polycentropodidae	17.0±9.0	10.0±5.0	0
Coleoptera	Dytiscidae	0	0	10.0±5.0
	Elmidae	25.0±10.0	68.0±53.0	25.0±14.0
	Gyrinidae	15.0±8.0	0±0	10.0±5.0
	Hydrophilidae	10.0±5.0	0±0	0
	Psephenidae	0	10.0±5.0	0
	Ptilodactylidae	0	10.0±5.0	0
	Staphylinidae	10.0±5.0	0±0	0
Diptera	Ceratopogonidae	10.0±5.0	16.0±5.0	40.0±23.0
	Chironomidae	65.0±33.0	180.0±138.0	133.0±117.0
	Simuliidae	0	0	17.0±10.0
	Syrphidae	20.0±10.0	18.0±7.0	0

Table 3. Indicator species analysis: proportion of contribution of order and families by land use group: extensive cattle ranching (CR), intensive agriculture and dairy production (AD) and urban (U).

Order	Family	Land use	Stat	p-value
Ephemeroptera		CR, AD	0.842	0.0126
Littorinimorpha		AD	0.873	0.0003
Amphipoda		U	0.881	0.0064
	Leptophlebiidae	CR	0.883	0.005
	Hydropsychidae	CR	0.803	0.015
	Cochliopidae	AD	0.857	0.0004
	Hyalellidae	U	0.890	0.007
	Glossiphoniidae	U	0.790	0.007

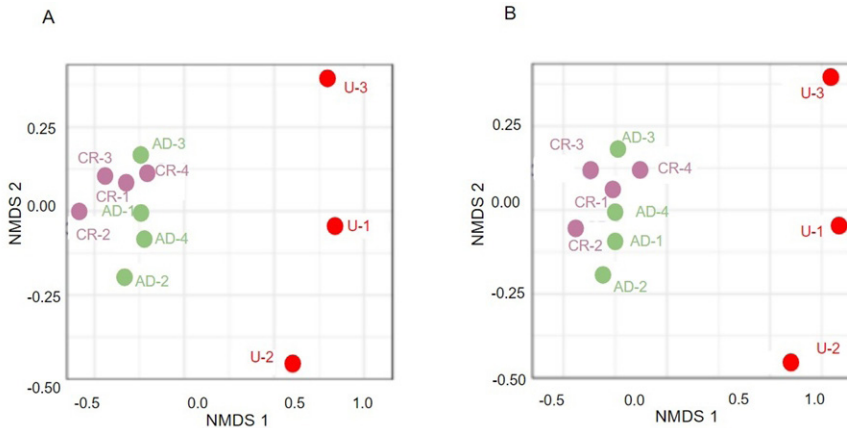


Figure 2. Macroinvertebrate community ordination analysis of the different land use types in the study area using non-metric multidimensional scaling (NMDS). A: order taxonomic level analysis, B: family level. Stress: 0.055 (order level), 0.071 (family level). Sampling sites: CR: extensive cattle ranching sites, AD: intensive agriculture and dairy production sites, and U: urbanization sites.

highest abundance values in CR (CR=13.5 ± 10.8 vs. AD= 5.3 ± 3.6, and U= 0).

4. Discussion

The results demonstrated the potential use of higher taxonomic levels for monitoring lowland streams evaluated in this study. However, it is crucial to expand the number of study sites to include other land uses (e.g., afforestation) and verify the consistency of the findings.

Regarding taxonomic levels, employing macroinvertebrates as bioindicators at the order level offers advantages in terms of speed and ease of implementation in monitoring practices. However, it also highlights the challenge of assigning consistent tolerance categories due to the inclusion of family and genera with different tolerance levels within an order (Hilsenhoff, 1988; Flowers, 2009). To address this issue, several authors have identified certain orders that exhibit greater consistency in their tolerance classification (i.e., they are always classified as tolerant or sensitive regarding the families; Rodrigues Capítulo et al., 2001; Casset, 2013; Hentges, 2019; Restello et al., 2020). As an example, Trichoptera, Ephemeroptera, and Plecoptera, known for their high occurrence in sites with oxygenated and clean water conditions (Domínguez & Fernández, 2009).

Hyaellidae exhibited higher abundance in urban streams, indicating a tolerant response to high-impact conditions. These organisms have demonstrated flexibility in food resource acquisition, particularly feeding on sediment organic matter, which is predominant in urban

streams due to sewage inflow (Suedel & Rodgers Junior, 1994; Saigo et al., 2010). Moreover, within the order Amphipoda found in Uruguayan streams, Hyaellidae is the sole family present, making the use of a coarse taxonomic resolution equivalent to a finer level. A similar situation arises with Glossiphoniidae, the only representative family in the region for Rhynchobdellida, known for its tolerance to pollution and high nutrient concentrations (Arias et al., 2020).

Intensive agriculture (AD) sites had a higher abundance of macroinvertebrates, especially Cochliopidae. These gastropods usually have an adaptive potential for agrochemicals, allowing them to take advantage of the organic matter produced by agricultural activity (Juárez et al., 2018). Another difference between AD and CR land uses is the higher relative abundance of Ephemeroptera and Trichoptera in CR, particularly Hydropsychidae (Trichoptera) followed by and Leptophlebiidae (Ephemeroptera). Families included in Plecoptera, Trichoptera, and Ephemeroptera may indicate varying thresholds for tolerating pollution. Watercourses with high oxygen levels and good water quality are often home to Leptophlebiidae (Domínguez & Fernández, 2009; Springer, 2010). However, in waters with an abundance of nutrients, taxa such as the Hydropsychidae, Baetidae, and Caenidae may have a wider tolerance range or stronger resilience (Chang et al., 2014; Masese & Raburu, 2017; Barrios et al., 2024). Several authors have suggested that family-level resolution could distinguish between unimpaired, moderately impaired, and severely impaired systems (Hewlett,

2000; Lenat & Resh, 2001; Waite et al., 2004; Buss & Vitorino, 2010). However, focusing on conservation, life histories, specific indicator groups, or particular types of disturbance, it is necessary to require genus- or species-level identifications (Buss & Vitorino, 2010).

In this study, the use of a taxonomic resolution at the family level or even coarser (order level) proved to be useful and sufficient in significantly distinguishing between different land uses, consistent with previous studies (Ruellet & Dauvin, 2007; Springer, 2010; Hentges et al., 2021). It is worth noting that for our study sites, some orders (i.e., Amphipoda, Littorinimorpha, and Rhynchobdellida) typically had only one family present, which increases the efficiency of work at the order level.

Order-level identification would be considered a cost-effective method for biomonitoring, as it reduces the time and effort required for identification compared to the family level. However, as we analyzed in this work, it is crucial to assess whether the information obtained at this level is comparable to that obtained at the family level. As evidenced in this study, where macroinvertebrate communities exhibit a weak family-order relationship, it is anticipated that studies conducted considering these two taxonomic levels will exhibit strong congruence, indicating clear taxonomic sufficiency at the order level. Conversely, in regions characterized by a high diversity of families, it is anticipated that this congruence will decrease (Hawkins et al., 2000).

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