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Macroinfaunal assemblages in sandy seabeds of San Blas (SE Tenerife, Canary Islands, NE Atlantic Ocean)

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Riera, R., M. Rodríguez & Ó. Monterroso (2011). Comunidades macroinfaunales en fondos arenosos de San Blas (SE de Tenerife, islas Canarias, océano Atlántico noreste). *Vieraea* 39: 65-76.

RESUMEN: Las comunidades infaunales presentes en las praderas de *C. nodosa* albergan la mayor parte de la biodiversidad presente en estos fondos. En este trabajo se analiza la comunidad macroinfaunal de una pradera de *C. nodosa* presente en una localidad de la costa sureste de Tenerife. La comunidad estuvo dominada por los crustáceos, siendo el anfípodo *Ampelisca brevicornis* y el tanaidáceo *Apseudes talpa* las especies más abundantes. Se registraron diferencias importantes a nivel de abundancias y diversidad, incluso en el mismo punto de muestreo. Las variaciones en las variables ambientales analizadas (granulometría) fueron el factor principal que explica las diferencias en la comunidad macrofaunal.
Palabras clave: Macroinfauna, *Cymodocea nodosa*, Tenerife, islas Canarias, océano Atlántico.

ABSTRACT: The infaunal communities of *C. nodosa* meadows shelter most of the biodiversity associated with these seabeds. We studied macroinfaunal assemblages of a *C. nodosa* meadow from a locality on the south-east coast of Tenerife. Macroinfaunal assemblages were clearly dominated by crustaceans. The amphipod *Ampelisca brevicornis* and the tanaid *Apseudes talpa* were the most dominant taxa in studied stations. Macrofaunal assemblage showed important variations in terms of abundances and diversity, even at the same station. Variations in measured environmental variables (e.g. granulometry) are the main factor to explain these differences in macrofaunal assemblages.
Key words: Macrofauna, *Cymodocea nodosa*, Tenerife, Canary Islands, Atlantic Ocean.

INTRODUCTION

Seagrasses meadows have been used extensively as bioindicators of environmental health in coastal marine areas. The marine phanerogam *Cymodocea nodosa* forms extensive meadows in subtidal sandy seabeds of the Canarian archipelago (Pavón-Salas *et al,* 2000). Benthic communities in coastal areas are highly sensitive to a range of natural and anthropogenic perturbations which occurred at both regional and global (e.g. worlwide) scales. Management requires the integration of previous baseline databases with contemporary ecological conditions to allow stakeholders and/or managers to develop effective tools that can predict changes on certain assemblages and/or particular species, as well as, to preserve natural habitats (Carter, 1990). In addition, detailed taxonomic analysis is a prerequisite in environmental monitoring studies and helps to understand the functioning of a particular assemblage because each species is characterized by an ecological role (Maggiore & Keppel, 2007).

Intertidal and shallow subtidal sedimentary habitats (< 50 m deep) constitute a small proportion of marine soft sediments (Ellis *et al*, 2000). However, they are characterized by having a high production and comprise a wide variety of habitats. In particular, macrofaunal activity influences ecosystem processes (e.g. nutrient cycles, sediments dispersion, etc…) (Snelgrove, 1998). Macrofaunal assemblages structure must be studied in order to determine local and regional diversity patterns (Labrune *et al*, 2008).

An ecological assessment was carried out in San Blas (SE Tenerife) to characterize macroinfaunal assemblage structure of *Cymodocea nodosa* meadows of this area. This environmental study was conducted to coastal pressure from human settlements, because an artificial sandy beach was planned in the study area.

The main objectives of the present work were i) to describe spatial patterns of macrofaunal diversity and dominance in the study area; ii) to identify macrofaunal species that characterized assemblage structure.

MATERIAL AND METHODS

Study area

This study was conducted in San Blas (coordenates: 28º1'22"N/16º36'36"W), a locality on the south-east coast of Tenerife (Canary Islands, NE Atlantic Ocean) (fig. 1). There is no previous information about macrofaunal assemblages of this bay. This bay can be considered as ultradissipative (*sensu* Short, 1999), with an intertidal pebble beach and a semidiurnal 2 m tide range. The study area is characterized by the presence of an important urban settlement ("Amarilla Golf" turistic area), with a marina (Amarilla Golf harbour) on the surroundings. Subtidal seabeds of the study site were characterized by the presence of a dense *Cymodocea nodosa* seagrass meadow from 7 to 20 m depth; at 25 m deep is replaced by *Caulerpa prolifera* and *Halophila decipiens* to 40 m.

All sampling stations were collected in *C. nodosa* seagrass meadows (legislated as an endangered species) in order to determine macroinfaunal biodiversity in these vegetated substrates. A total of seven subtidal sandy stations were sampled (Table 1).

Sediment samples were collected manually by SCUBA divers at a range of 12-27 m depth in October 2004. Sediment cores (20 cm inner diameter) were pushed into the sediment to a depth of 20 cm (volume: 600 cm^3). Three replicates per station were collected for faunistic analysis and an adjacent sample for sediment analysis (granulometry).

Analysis of macrofauna

Samples were preserved in 10% seawater formaldehyde solution and decanted through a 0.5 mm mesh sieve. The fraction remaining on the mesh sieve was separated into different taxonomic groups under a binocular microscope and preserved in 70% ethanol. Posteriorly in the laboratory, macrofaunal specimens were determined to species level, whenever possible, by means of a binocular microscope or even in a LEICA DMLB microscope equipped with Nomarski interference contrast.

Analysis of granulometry

The granulometry of the sediment was obtained from subsamples of 100 g. Samples were dried at air temperature, sieved on a stack of graded sieves ranged from 0.063 mm and 2 mm mesh, and the residue on each weighted (Buchanan & Kain, 1971).

Statistical analysis

Biological descriptors of the community (abundance, Shannon's diversity and Pielou's evenness) were calculated. Differences on univariate indices among stations were tested with non-parametric Kruskal-Wallis test.

The affinities among communities based on species composition were established using a dendrogram and a MDS (non-metric multidimensional scaling), being the abundance data square root transformed and the Bray-Curtis similarity index used. The ANOSIM routine (Clarke, 1993) was used to analyse differences between stations and soft-bottom communities, being identified the macrobenthic species responsible for the observed trends by means of SIMPER routine. Multivariate analyses were carried out using the PRIMER 5.2. Package (Plymouth Routines In Multivariate Ecological Analysis) (Clarke & Warwick, 1994).

RESULTS

Macrofauna

A total of 909 specimens, belonging to 65 species (Table 3), were collected in the sampling stations (M1, M2, M4, M5, M7, M8 and M10). One species was determined to phylum level, four taxa to generic level and the remaining ones to species. The most diverse taxonomic group were molluscs (23 taxa), followed by crustaceans and polychaetes, with 21 and 14 species, respectively.

In terms of abundances, crustaceans were the dominant group representing 73% of the overall macrofaunal densities. Molluscs and polychaetes were the second and third taxonomic group, with 15.3% and 10.6%, respectively.

In terms of species, the most abundant taxa were the amphipod *Ampelisca brevicornis* (269 ind) and the tanaid *Apseudes talpa* (262 ind). The remaining species obtained abundances lower than 50 ind. To the contrary, 22 species were scarce and represented by one single individual (Table 3).

Species richness varied between 14 taxa (sta. M2) and 30 taxa (sta. M4). Macrofaunal abundances fluctuated from 18.33 ind. in M8 to a maximum of 100.33 ind. in M5. Shannon's diversity varied between 0.80 (sta. M7) and 2.40 (sta. M4) (Table 4). In terms of evenness, station M5 was characterized by having the lowest value (0.49), followed by M7 (0.50). The highest values of evenness were found in M8 (0.93) and M4 (0.89). Shannon's diversity varied between 0.80 (sta. M7) and 2.40 (sta. M4) (Table 4).

Granulometry

About environmental variables, all stations were characterized by the dominance of fine and medium sands, with the exception of M8 (52%) and M5 (50%) dominated by coarse sands. Silt and clay content was scarce in all sampling points (0-0.03%). Stations M2 and M4 were characterized as fine sands, and stations M1, M5, M7 and M10 as medium sands. Station M8 was characterized as coarse sands (Table 2).

Multivariate analysis

The heterogenity rate of replicates within one sampling station was calculated with the MDI (Multivariate Dispersion Index). Maximum MDI values were found in the sampling station M7, with 1.36, characterized by having the lowest value of diversity. Stations M4, M8 and M1 obtained high MDI values (> 1), due to the differences in macrofaunal community structure among the three replicates. To the contrary, the lowest MDI value was encountered in station M5 (0.18), showing a high homogeneity among replicates (Table 5).

Sampling stations were divided into two branches at 19% of similarity (Fig. 2). The first group was compound by stations M2, M5, M8 and M10 and the second one the remaining sampling points M1, M4 and M7. This two groups were significantly different in the macrofaunal community structure (one-way ANOSIM, R = 0.62, p = 0.1%). The first group was characterized by the presence of the mollusc *Nassarius cuvierii,* the isopod *Eurydice pulchra* and the polychaete *Armandia cirrhosa*. The stations M2 and M5 were separated from the main group due to their high abundances of the amphipod *Ampelisca brevicornis* and the tanaid *Apseudes talpa*.

The second main branch (M1, M4 and M7) was characterized by high abundances of the tanaid *A. talpa*, the amphipod *Urothoe marina* and the mollusc *Turritella brocchii*. The sampling point M7 was segregated at 36% of similarity due to the presence of the polychaete *Aponuphis bilineata* and the ostracod *Cypridina mediterranea* (fig. 2).

Stations M5 and M7 were clearly dominated by one species, the amphipod *A. brevicornis* in M5 (65% of overall abundance) and the tanaid *A. talpa* in M7 (61% of overall abundance). To the contrary, stations M4 and M8 were dominated by several species with intermediate densities, being the most abundant the mollusc *T. brochii* in M4 (17% of overall abundance) and the amphipod *A. brevicornis* in M8 (20% of overall abundance) (fig. 3).

DISCUSSION

Macrofaunal assemblages in San Blas are characterized by i) a marked variability in abundance and diversity between samples, as well as, ii) the high level of rareness of macrofaunal species in assemblage structure. Both factors established the presence of numerous outliers, species with fluctuated abundances in the same sampling station, and the relationship between macrofaunal assemblage diversity and environmental variables (e.g. granulometry). However, the observed variability can only be partially explained by sedimentary types, and other environmental variables (organic matter, nitrogen or phosphorus content) can shed light on the present results. Although, in the Canary Islands the concentrations of former variables remained low in *Cymodocea nodosa* meadows (Riera, *pers. obs*.). Probably, other parameters, such as, microtopography, permeability and compactness of the sediment could be responsible of the macrofaunal community structure of the sampling stations.

The most abundant species were the amphipods *Ampelisca brevicornis* and *Urothoe marina*, the tanaid *Apseudes talpa* and the mollusc *Turritella brocchii* that are characteristic taxa of subtidal sandy seabeds of the Canary Islands. The former species have been found in non-affected sediments and are considered as typical of ecosystems without natural and/or anthropogenic perturbations (Herrando-Pérez *et al*. 2001).

In contrast with former ecological studies carried out in the Canary Islands (Brito *et al*. 2005, Herrando-Pérez *et al*. 2001), macrofaunal community structure was dominated by crustaceans (73%). Brito *et al* (2005) found a high polychaete diversity in *Cymodocea nodosa* meadows, however, they used a 0.1 mm sieve that can retain small-size specimens (e.g. syllids) and juveniles (e.g. opheliids, paraonids, spionids and sabellids). Brito *et al* (2005) obtained intermediate abundances in *C. nodosa* meadows, with a clear dominance of polychaetes *(Aponuphis bilineata, Chone* sp and *Cirrophorus armatus*) and the amphipod *Ampelisca brevicornis*. Differences in taxa compositions (amphipods vs polychaetes) could be due to differences in environmental variables among *C. nodosa* meadows (mainly organic matter content).

The presence of *Cymodocea nodosa* meadows allows the settlement of fine sediment particles and organic matter in the seabed, as well as, a more complex environment with a high number of microhabitats. Consequently, species abundance and richness is much higher in *C. nodosa* meadows that in sandy bare sediments (Brito *et al*, 2005).

The use of infaunal communities (macro- and meiofauna) should be considered as a crucial tool for the estimation of biodiversity of seagrass meadows in the Canarian archipelago. These ecosystems harbour a diverse assemblage structure of different sizes (macro- and meiofauna) and trophic guilds (detritivorous, carnivores, scavengers, among others) that can occupy different microhabitats, creating a complex system with different interactions among species. In the present study, we checked the importance of analysing the macroinfaunal community as a biodiversity tool to characterize a fragile ecosystem, as it is the *C. nodosa* meadow. This kind of studies should be a complement for the ecocartographic and monitoring studies of *C. nodosa* meadows that characterize this ecosystem with descriptive measures of the phanerogam assemblage (coberture, density and leaf length, among others).

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TABLES AND FIGURES

Stations	Coordinates	Depth (m)	Seabed communities
M1	28º 02' 15"N 16º 59' 83" E	26	*Cymodocea nodosa* meadows + *Caulerpa prolifera* + *Halophila decipiens*
M2	28º 02' 48" N 16º 59' 95" E	11	*C. nodosa* meadows
M4	28º 02' 09" N 16º 59' 78" E	27	*C. nodosa* meadows + *C prolifera* + *H. decipiens*
M5	28º 02' 51" N 16º 59' 87" E	11.8	*C. nodosa* meadows
M7	28º 02' 31" N 16º 59' 73" E	20.7	*C. nodosa* meadows
M8	28º 02' 53" N 16º 59' 75" E	10.5	*C. nodosa* meadows
M10	28º 02' 53" N 16º 59' 61" E	12	*C. nodosa* meadows

Table 1.- Location and seabed communities of sampling stations.

Stations	Gravels (%)	Very coarse sands (%)	Coarse sands (%)	Medium sands (%)	Fine sands (%)	Very fine sands (%)	Silt/clay (%)
M1	5.38	6.31	13.29	66.64	8.35	0.03	0.00
M2	0.03	0.33	1.56	12.99	70.35	14.74	0.00
M4	17.79	6.44	11.15	14.84	37.18	12.57	0.03
M5	0.06	0.98	50.01	37.74	10.53	0.66	0.02
M7	2.17	1.91	32.62	53.78	9.14	0.38	0.00
M8	7.43	12.74	52.2	26.38	1.21	0.04	0.00
M10	0.13	0.19	1.52	51.82	40.23	6.08	0.03

Table 2.- Sedimentary composition of sampling stations.

Group	Species	M1	M2	M4	M5	M7	M8	M10	TOTAL
Chordata	*Parophidion vassali*	0	0	1	0	0	0	0	**1**
Crustacea	*Ampelisca brevicornis*	0	47	0	184	3	9	26	**269**
Crustacea	*Anapagurus laevis*	1	0	0	0	0	0	0	**1**
Crustacea	*Apseudes talpa*	23	24	13	83	119	0	0	**262**
Crustacea	*Bagatus minutus*	0	0	1	0	0	0	0	**1**
Crustacea	*Bathyporeia elegans*	0	5	0	5	0	0	0	**10**
Crustacea	*Cryptosoma cristatum*	0	0	1	0	0	0	0	**1**
Crustacea	*Cypridina mediterranea*	2	1	3	0	7	0	0	**13**
Crustacea	*Erichthonius brasiliensis*	1	0	0	0	0	1	0	**2**
Crustacea	*Eurydice pulchra*	0	0	0	4	0	3	6	**13**
Crustacea	*Harpinia antennaria*	1	6	4	3	4	0	1	**19**
Crustacea	*Iphinoe canariensis*	0	2	0	3	0	1	0	**6**
Crustacea	*Leptochelia dubia*	0	0	0	3	0	0	0	**3**
Crustacea	*Nebalia* aff. *clausii*	0	0	0	1	0	0	0	**1**
Crustacea	*Photis reinhardi*	0	0	1	0	0	2	1	**4**
Crustacea	*Phthisica marina*	1	0	0	0	0	0	0	**1**
Crustacea	*Portunus hastatus*	2	0	0	0	0	0	0	**2**
Crustacea	*Processa canaliculata*	1	0	0	0	1	0	0	**2**
Crustacea	*Pseudoprotella phasma*	0	0	3	0	1	0	0	**4**
Crustacea	*Sunampithoe pelagica*	0	0	1	0	0	0	0	**1**
Crustacea	*Urothoe marina*	19	1	12	3	11	1	1	**48**
Crustacea	*Xantho poressa*	0	0	1	0	0	0	0	**1**
Echinodermata	*Amphipholis squamata*	1	0	1	0	0	0	0	**2**
Echinodermata	*Brissus unicolor*	1	0	1	0	0	0	0	**2**
Mollusca	*Antalis vulgare*	0	0	1	0	0	0	0	**1**
Mollusca	*Atys macandrewi*	0	0	0	0	0	1	0	**1**
Mollusca	*Azorinus chamasolen*	0	0	1	0	0	0	0	**1**
Mollusca	*Bela ornata*	3	0	0	1	0	4	0	**8**
Mollusca	*Bittium incile*	0	0	0	0	0	0	1	**1**
Mollusca	*Bittium latreillii*	2	0	4	0	2	0	0	**8**
Mollusca	*Comarmondia gracilis*	0	0	1	0	0	0	0	**1**
Mollusca	*Ctena decussata*	1	0	0	0	0	0	0	**1**
Mollusca	*Cylichna cylindracea*	0	0	0	0	0	3	0	**3**

Mollusca	*Gouldia minima*	0	0	1	0	0	0	0	**1**
Mollusca	*Jujubinus exasperatus*	1	3	0	0	0	1	2	**7**
Mollusca	*Linga adansoni*	0	0	4	0	0	0	0	**4**
Mollusca	*Lucinella divaricata*	3	0	3	0	0	1	0	**7**
Mollusca	*Monophorus pantherinus*	0	1	1	0	0	0	0	**2**
Mollusca	*Nassarius cuvierii*	0	2	1	0	3	6	12	**24**
Mollusca	*Natica furva*	0	1	0	0	1	0	0	**2**
Mollusca	*Ocinebrina aciculata*	1	0	0	0	0	0	0	**1**
Mollusca	*Parvicardium scriptum*	0	0	0	0	0	0	1	**1**
Mollusca	*Ringicula conformis*	1	0	1	0	0	1	0	**3**
Mollusca	*Rissoa guerini*	0	1	0	0	0	0	0	**1**
Mollusca	*Smaragdia viridis*	3	0	1	0	0	0	1	**5**
Mollusca	*Solemya togata*	0	0	0	0	2	0	0	**2**
Mollusca	*Turritella brocchii*	29	0	20	0	4	1	0	**54**
Nematoda	*Synonchus* aff. *fasciculatus*	0	0	0	0	0	0	1	**1**
Nemertea	Nemertino indet.	0	0	0	2	0	0	0	**2**
Polychaeta	*Aponuphis bilineata*	2	0	1	1	12	3	3	**22**
Polychaeta	*Armandia cirrhosa*	0	0	0	1	0	5	5	**11**
Polychaeta	*Chone duneri*	10	0	4	1	0	4	1	**20**
Polychaeta	*Chone filicaudata*	0	0	2	0	0	1	1	**4**
Polychaeta	*Chone* sp.	1	0	0	0	3	0	0	**4**
Polychaeta	*Eumida sanguinea*	0	0	1	0	0	0	0	**1**
Polychaeta	*Glycera fallax*	0	0	0	0	0	4	2	**6**
Polychaeta	*Malacoceros* sp.	0	0	0	1	0	0	0	**1**
Polychaeta	*Nephthys caeca*	0	0	0	1	0	0	0	**1**
Polychaeta	*Poecilochaetous serpens*	0	0	0	0	0	1	2	**3**
Polychaeta	*Prionospio steenstrupi*	2	2	1	2	1	0	0	**8**
Polychaeta	*Scoloplos (Leodamas)* sp	0	1	0	1	0	2	3	**7**
Polychaeta	*Sigalion squamatum*	5	0	0	1	1	0	0	**7**
Polychaeta	*Streptosyllis campoyi*	0	0	0	0	0	0	1	**1**
Pycnogonida	*Nymphon* sp.	0	0	0	0	1	0	0	**1**
Sipuncula	*Aspidosiphon muelleri*	1	0	0	0	0	0	0	**1**
	TOTAL	**118**	**97**	**91**	**301**	**176**	**55**	**71**	**909**

Table 3.- Species list collected in sampling stations.

Station	Nº species	Nº individuals (0.03 m²)	Evenness (J')	Diversity (H')
M1	26	39.33	0.74	1.84
M2	14	32.33	0.73	1.30
M4	30	30.33	0.89	2.40
M5	19	100.33	0.49	1.12
M7	17	58.67	0.50	0.80
M8	21	18.33	0.93	2.15
M10	19	23.67	0.86	1.93

Table 4.- Macrofaunal assemblage descriptors of the sampling stations.

Stations	MDI
M5	0.18
M10	0.91
M2	0.91
M4	1.03
M8	1.27
M1	1.33
M7	1.36

Table 5.- Multivariate dispersion index (MDI) in sampling stations.

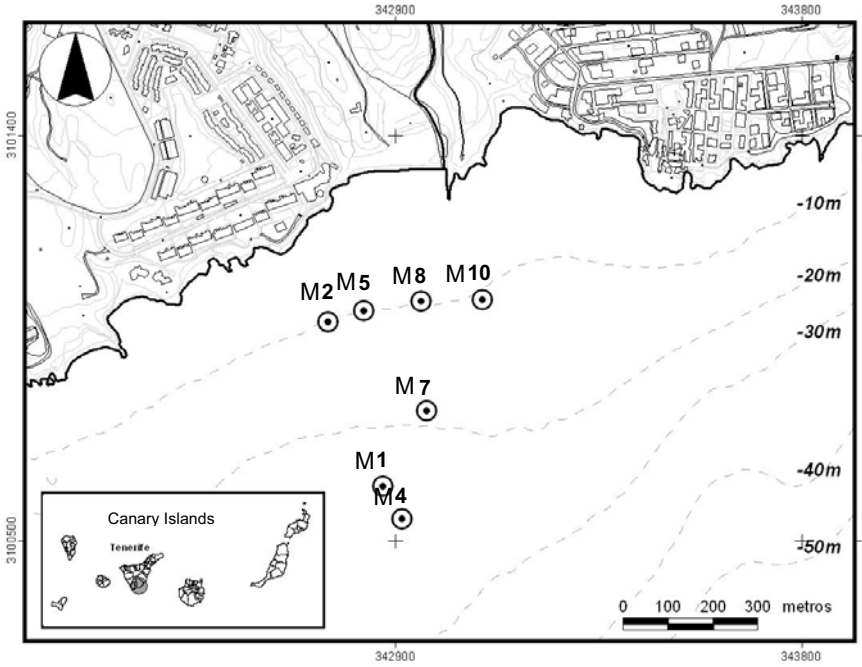

Figure 1.- Location of sampling stations.

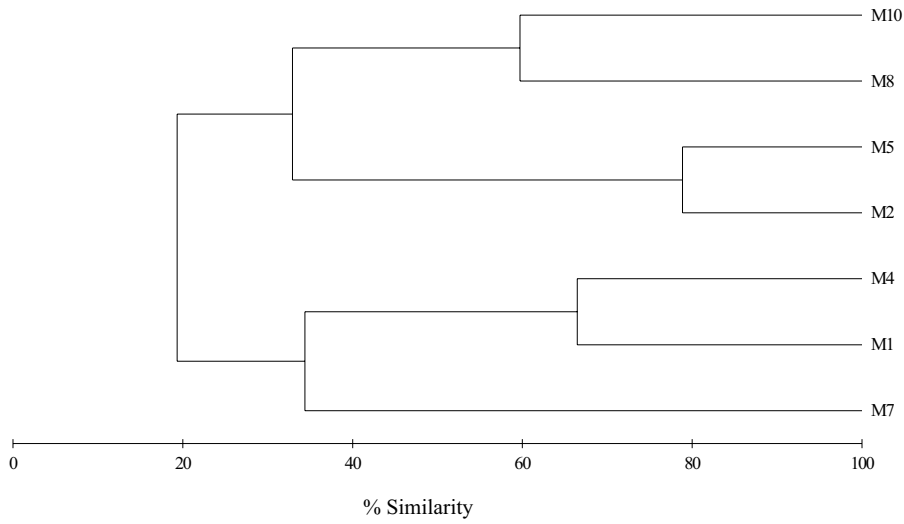

Figure 2.- Dendrogram of similarity of sampling stations.

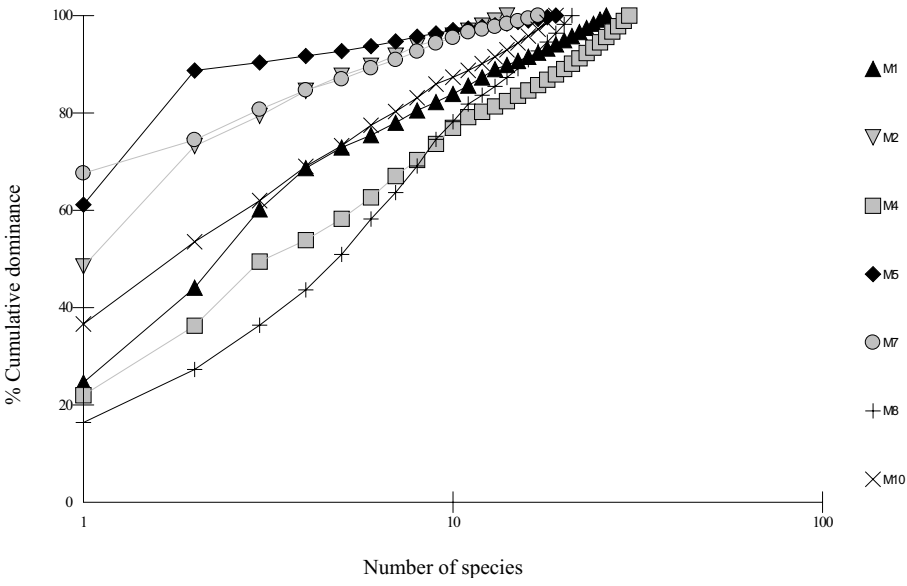

Figure 3.- Dominance curves of sampling stations.

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