

Capítulo 2.
Post larval, short-term,
colonization patterns: the effect
of substrate complexity across
subtidal, adjacent, habitats





Post larval, short-term, colonization patterns: The effect of substratum complexity across subtidal, adjacent, habitats

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ABSTRACT

Benthic habitats are colonized by organisms from the water column and adjacent habitats. There are, however, variations in the 'acceptability' of any habitat to potential colonists. We assessed whether the structural complexity of artificial substrata affected patterns of short-term colonization of post larval faunal assemblages across subtidal habitats within a coastal landscape. Specifically, we tested whether short-term colonization patterns on 3 types of artificial substrata encompassing a range of complexities, including a leaf-like unit, a cushion-shaped leaf-like unit and a cushion-shaped unit, were consistent across 4 adjacent habitats: macroalgal-dominated bottoms, urchin-grazed barrens, seagrass meadows and sandy patches, at Gran Canaria (eastern Atlantic). A total of 16,174 organisms were collected after 4 weeks and 4 taxonomic groups (Crustacea, Chordata, Echinodermata and Mollusca) dominated the assemblage. Despite considerable among-taxa variability being observed in response to habitat effects, the total abundance of colonizers, as well as the abundance of Arthropoda, Chordata and Echinodermata, was affected by the habitat where collectors were deployed, but did not differ among types of collectors. Similarly, the assemblage structure of colonizers was mainly affected by the habitat, but not by the type of collector; habitat contributed to explain most variation in the assemblage structure of the four dominant taxonomic groups (from ca. 5.44–19.23%), and obscured, in all cases, variation explained by the type of collector. As a result, the variation in short-term colonization patterns of faunal assemblages into artificial collectors was mostly affected by variation associated with habitats rather than by differences in the structural complexity of collectors. The largest abundances of colonizers, particularly Echinodermata, were found on sandy patches relative to other habitats, suggesting that the 'availability', rather than any particular attribute related to the 'acceptability' of artificial collectors, e.g. its structural complexity, was the main driver of patterns of faunal short-term colonization.

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1. Introduction

Benthic subtidal habitats are continually colonized by organisms from the water column, mainly as juveniles through larval dispersal, and organisms migrating from adjacent habitats, mainly as sub-adults and adults through crawling, active swimming, rafting on the surface of the water, or being transported passively by wave action (Underwood and Keough, 2001; Chapman, 2002). There are, however, variations in space and time in the suitability or 'acceptability' of a habitat to potential colonizers (Singer, 2000). The selection of any habitat by the potential pool of colonizers depend on, amongst other factors, the physical characteristics, as

the architecture of the habitat (Srinivasan, 2003) and sensory signs (Gardner et al., 2005) that include sensory cues related to the presence of benthic organisms (conspecifics living in the surroundings of any habitat (Lecchini, 2005; Wright et al., 2005)). An understanding of the effects of these factors is needed to explain the spatial and temporal patterns in adult abundances.

The structural complexity of any benthic habitat is a key attribute to explain patterns in the arrival of new colonizers (Bourget et al., 1994; Beck, 2000; Kelaher, 2003; Jenkins et al., 2009). For example, it has long been recognized that benthic habitats with a high structural complexity provide new, small-sized, colonizers with a shelter against predators (e.g. Robertson and Blaber, 1992; Nagelkerken et al., 2000; Hereu et al., 2005). Our understanding, however, is biased towards observational, rather than experimental studies. This precludes a general assessment of the importance of habitat complexity as a factor affecting patterns of colonization of

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ABSTRACT

Benthic habitats are colonized by organisms from the water column and adjacent habitats. There are, however, variations in the 'acceptability' of any habitat to potential colonists. We assessed whether the structural complexity of artificial substrates affected patterns of short-term colonization of post larval faunal assemblages across subtidal habitats within a coastal landscape. Specifically, we tested whether short-term colonization patterns on 3 types of artificial substrates encompassing a range of complexities, including a leaf-like unit, a cushion-shaped leaf-like unit and a cushion-shaped unit, were consistent across 4 adjacent habitats: macroalgal-dominated bottoms, urchin-grazed barrens, seagrass meadows and sandy patches, at Gran Canaria (eastern Atlantic). A total of 16,174 organisms were collected after 4 weeks and 4 taxonomic groups (Crustacea, Chordata, Echinodermata and Mollusca) dominated the assemblage. Despite considerable among-taxa variability was observed in response to habitat effects, the total abundance of colonizers, as well as the abundance of Arthropoda, Chordata and Echinodermata, was affected by the habitat where collectors were deployed, but did not differ among types of collectors. Similarly, the assemblage structure of colonizers was majorly affected by the habitat, but not by the type of collector; habitat contributed to explain most variation in the assemblage structure of the four dominant taxonomic groups (from ca. 5.44 to 19.23 %), and overpowered, in all cases, variation explained by the type of collector. As a result, variation in short-term colonization patterns of faunal assemblages into artificial collectors was mostly affected by variation associated with habitats rather than by differences in the structural complexity of collectors. Largest abundances of colonizers, particularly Echinodermata, were found on sandy patches relative to other habitats, suggesting that the 'availability', rather than any particular attribute related to the 'acceptability' of artificial collectors, e.g. its structural complexity, was the main driver of patterns of faunal short-term colonization.

Keywords: colonization, recruitment, artificial collectors, habitats, Canary Islands.

Patrones de colonización de organismos bentónicos
en hábitats litorales de Gran Canaria

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Capítulo 2

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2.1 INTRODUCTION

Benthic subtidal habitats are continually colonized by organisms from the water column, mainly as juveniles through larval dispersal, and organisms migrating from adjacent habitats, mainly as sub-adults and adults through crawling, active swimming, rafting on the surface of the water, or being transported passively by wave action (Underwood and Keough, 2001; Chapman, 2002). There are, however, variations in space and time in the suitability or 'acceptability' of a habitat to potential colonizers (Singer, 2000). The selection of any habitat by the potential pool of colonizers depend on, amongst other factors, the physical characteristics, as the architecture of the habitat (Srinivasan, 2003) and sensory signs (Gardner *et al.*, 2005) that include sensory cues related to the presence of benthic organisms (conspecifics living in the surroundings of any habitat (Lecchini, 2005; Wright *et al.*, 2005)). An understanding of the effects of these factors is relevant to explain the spatial and temporal patterns in adult abundances.

The structural complexity of any benthic habitat is a key attribute to explain patterns in the arrival of new colonizers (Bourget *et al.*, 1994; Beck, 2000; Kelaher, 2003; Jenkins *et al.*, 2009). For example, it has long been recognized that benthic habitats with a high structural complexity provide new, small-sized, colonizers with a shelter against predators (e.g. Robertson and Blaber, 1992; Nagelkerken *et al.*, 2000; Hereu *et al.*, 2005). Our understanding, however, is biased towards observational, rather than experimental studies. Without a doubt, this is precluding a general assessment of the importance of habitat complexity as a factor affecting patterns of colonization of subtidal biota, particularly across a range of coastal habitats (Underwood and Keough, 2001).

Artificial Substrates (hereafter ASs) provide a unique opportunity to test specific models of colonization patterns into new habitats by faunal assemblages (e.g. Olabarria *et al.*, 2002; Underwood and Chapman, 2006; Cole *et al.*, 2007; Rule and Smith, 2007). These artificial habitats may attract most elements of the mobile fauna in their near vicinity. Our perception of the relative importance of different ecological mechanisms on patterns of colonization into ASs is, however, rather limited (Rule and Smith, 2007; Chapman *et al.*, 2008). Indeed, most studies using ASs have exclusively analyzed patterns of colonization into ASs across a set of spatial and temporal scales, as a way to indirectly infer the relative importance of different ecological mechanisms. Patterns of colonization of faunal assemblages in any AS are likely influenced by the structural complexity of collectors; for example, there are larger numbers of species and individuals on highly-complex artificial substrates than on smooth, low complexity, substrates (Christie *et al.*, 2007). However, differences in complexity between types of ASs can be confounded by differences in the amount of available habitat provided by ASs, because often the more complex an AS is, the larger the amount of provided habitat is. In fact, the potential separate effects of complexity and area on species richness and abundance have rarely been addressed (Johnson *et al.*, 2003) and, therefore, statistical routines that specifically correct this issue should be implemented, for example, through the use of covariates (Kostylev *et al.*, 2005).

In a part of the temperate coasts of the world, habitats occurring at small scales (< 102 m) are arranged in mosaics within large landscapes (>103 m). These habitats can vary substantially in the composition and abundances of their associated biotas (e.g. Taylor and Cole, 1994; Tuya *et al.*, 2008), which may reflect changes in the intensity of ecological mechanisms among habitats, such as the arrival of new individuals. For example, colonization by polychaetes into ASs was notably influenced by the type of biogenic habitat (the 'matrix of habitats') that surrounded ASs in the intertidal (Cole *et al.*, 2007).

This study aimed to assess whether the structural complexity of artificial substrates affected patterns of short-term colonization of post larval faunal assemblages across a range of subtidal habitats arranged in mosaics within a coastal landscape. Specifically, we tested whether short-term colonization patterns in 3 types of ASs, encompassing a range of substratum complexities, were consistent across four subtidal habitats: algal-dominated rocky bottoms, rocky urchin-grazed barrens, seagrass meadows and sandy patches that are arranged in mosaics within landscapes in the eastern Atlantic.

2.2 MATERIALS AND METHODS

2.2.1 Study area

This study was carried out at two localities off the east coast of Gran Canaria (Canary Islands, Spain): Risco Verde (27°51'25.94" N, 15°23'10.26" W) and Playa del Cabrón (27°52'14.43" N, 15°23'00.31" W) (Fig. 2.1). Both localities encompass a mosaic of subtidal, neighboring, habitats, including seagrass meadows constituted by the marine phanerogam *Cymodocea nodosa* and sandy patches on soft substrata, as well as urchin-grazed barrens and macroalgal-dominated beds (mainly dominated by the frondose genera *Cystoseira* and *Sargassum*, as well as *Dyctiota* spp., *Padina pavonica* and *Lobophora variegata*) on adjacent rocky substrata. All habitats are found interspersed at ca. 5-10 meters depth.

2.2.2 Type of collectors

Three types of ASs were designed, based on previous studies (e.g. Phillips and Booth, 1994; Butler and Herrnkind, 2001; Phillips *et al.*, 2006), to encompass a range of substrate complexities (Fig. 2.2). A Leaf-Like Unit (LLU, Fig. 2.2a) consisted of a plastic mesh frame (50 cm², 2 cm of diameter of mesh size) to which artificial leaves (green plastic raffia, 35 cm long and 10 mm wide) were attached every ca. 4 cm. Raffia is positively buoyant underwater and so float upright. The Cushion-shaped Leaf-Like unit (CLLU, Fig. 2.2b) was the same collector as the LLU, but folded as a cushion. A total of 75 cm² of concealment gardening mesh (≤ 1 mm diameter) was included inside, creating small holes and shelters. Finally, the Cushion-shaped Unit (CU, Fig. 2.2c) was morphologically identical to the CLLU, but without the artificial leaves. The amount of habitat provided by each type of collector differed; the LLUs and CLLUs had a similar mean displaced volume (ca. 1.4 l), but larger than the mean volume of CUs (ca. 0.8 l).

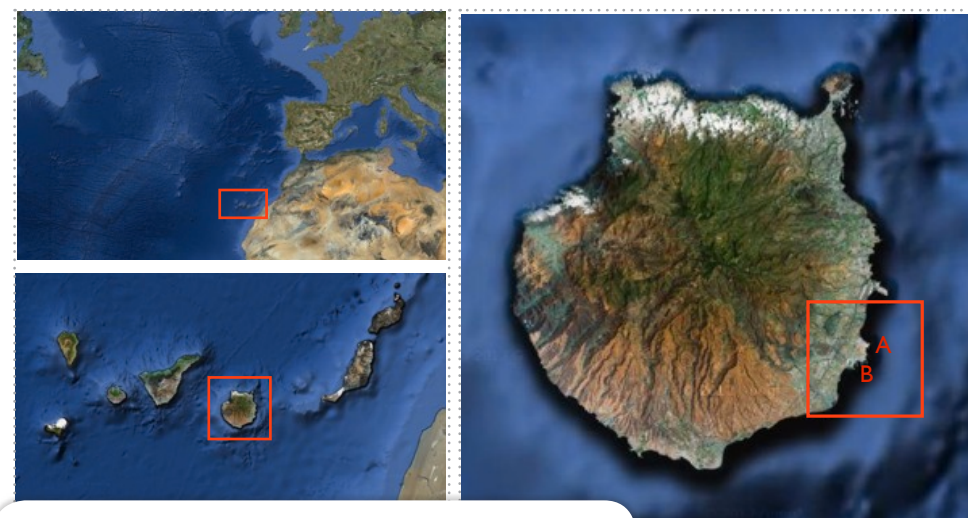


Fig. 2.1 Location of the study area in the eastern Atlantic Ocean; (A) Playa del Cabrón and (B) Risco Verde.

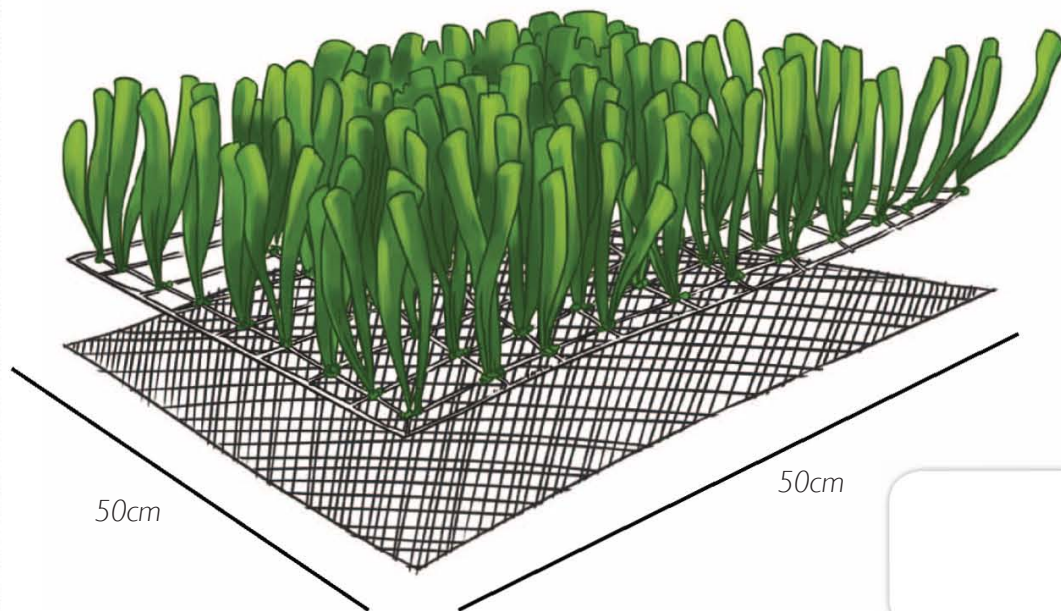
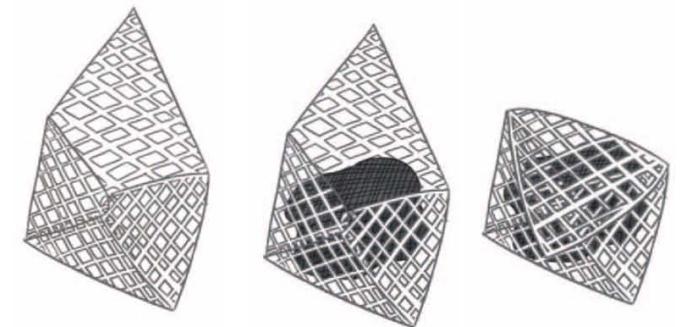
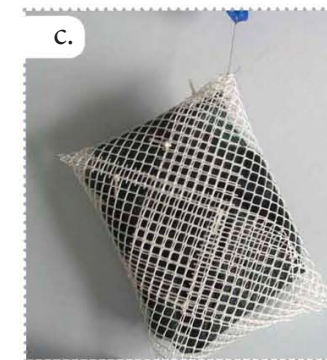
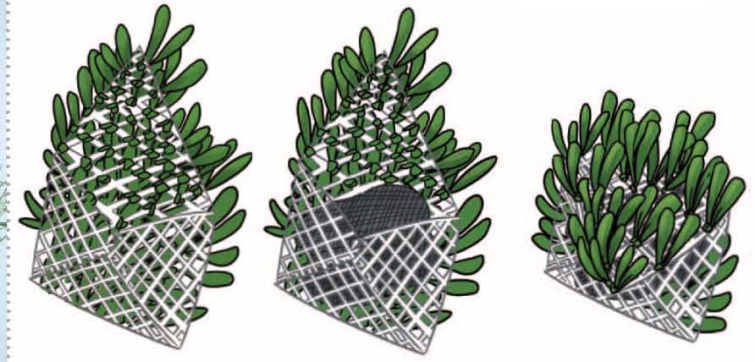
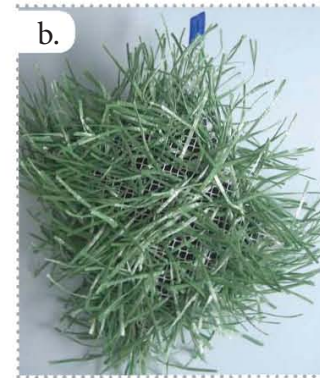


Fig. 2.2 Artificial collectors used in the study: (a) Leaf-Like Unit (LLU), (b) Cushion-shaped Leaf-Like Unit (CLLU) and (c) Cushion-shaped Unit (CU).

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2.2.3. Experimental set up

Four replicates of each type of collector were deployed on each habitat at each locality. Adjacent ASs within each type of habitat were, in all cases, 3e5 m apart; ASs from any two adjacent habitats were 100 s of m apart. ASs were fixed through cable ties on hard substrata and by iron rods (ca. 50 cm long) on soft substrata. In all cases, ASs were in contact with the seabed. A total of 48 ASs were deployed at both localities on the start of August 2008 and were subsequently retrieved on the start of September 2008; this period of time (4 weeks) encompassed an entire lunar cycle. Each AS was removed by divers by carefully enclosing each unit within a cloth bag. The bags were carried to the laboratory, where each collector was cleaned with freshwater, and all organisms retained by a 0.5mm mesh sieve subsequently identified to the lowest possible taxonomic level, mostly to taxonomic identifiable units corresponding to families.

2.2.4. Data analysis

Differences in the total abundance of colonizers, including the total abundance of the 4 dominant phyla: Arthropoda, Chordata, Echinodermata and Mollusca, which accounted for the 96.85 % of individuals, and the abundance of the 16 dominant taxonomic groups (those with a contribution > 1% of the total abundance), among types of ASs and habitats were tested through a 2-way permutation-based ANCOVA, based on euclidian distances from untransformed data. About half of collectors were lost, due to either storms or sabotages. As a result, collectors from the two localities were pooled into their corresponding 'Collector' and 'Habitat' types, irrespective of their origin, to maintain a balanced design. The model, therefore, included the fixed factors: 'Collector' and 'Habitat'. The same model, but in the multivariate context via a permutational multivariate ANCOVA using PERMANOVA through 4,999 permutations under a reduced model (Anderson, 2001), tested for differences in the structure of the entire assemblage of colonizers, as well as in the assemblage structure of each of the four dominant taxonomic groups, among types of ASs and habitats. In these analyses, we accounted for differences in the amount of available habitat provided by different types of collectors by using their volume

as a covariate; the displaced volume of small habitats have been previously used as a proxy for the amount of habitat they provide (e.g. algae, Hacker and Steneck, 1990). Transformations did not render homogeneous variances for the ANOVAs performed on the abundances of the 16 dominant taxonomic groups; as a result, the significance level was fixed at the 0.01 instead of 0.05 to avoid an increase in a type I error. In all cases, we estimated the relative importance of each experimental factor based on the estimation of their variance components (Graham, 2001), and pairwise comparisons were used to resolve differences among levels of factors, whenever appropriate. Canonical Analysis of Principal coordinates (CAP, Anderson and Willis, 2003) was used as a constrained ordination procedure to separately visualize differences in the assemblage structure of colonizers among types of collectors and among habitats. Essentially, CAP finds axes in the multivariate space to maximize the separation among groups (types of collectors and habitats in our case). First, we conducted a Principal Coordinates Analysis (PCO); we then carried out the CAP based on that subset of the PCO axes at which additional PCO axes did not add explanatory power. The CAP routine calculated miscalculation errors for groupings using the 'Leave-one-out Allocation success' (LoA): each collector was removed from the dataset, the CAP analysis rerun using the remaining observations, and then the removed data point classified to the nearest group centroid in the canonical space. Comparison of known with allocated groups provided miscalculation errors (Anderson and Willis, 2003). All multivariate procedures were carried out by means of the PRIMER 6.0 package (Clarke and Warwick, 2001) using Bray-Curtis similarities on untransformed data.

➤ 2.3 RESULTS

Forty eight collectors (from a total of 96) were retrieved (the rest was lost due to either storms or sabotages), corresponding to 4 replicates of each type of AS from each habitat, regardless of the locality. A total of 16,174 organisms were collected, corresponding to 50 taxa (major identifiable groups), including 22 families, 19 orders and 8 phyla (Appendix 1).

2.3.1 Differences in the abundance of colonizers: assemblage-level patterns

The total abundance of colonizers, and the total abundance of Arthropoda, Chordata, Echinodermata and Mollusca, did not differ between the three types of collectors (Fig. 2.3; Table 2.1, ANCOVA: 'Collector': Arthropoda $P=0.4508$; Chordata $P=0.736$; Echinodermata $P=0.9412$; Mollusca $P=0.1452$). The total abundance of colonizers, however, was significantly affected by the habitat where collectors were deployed (Fig. 2.3; Table 1, ANCOVA: 'Habitat': Arthropoda $P=0.0262$; Chordata $P=0.0004$; Echinodermata $P=0.005$), except for Mollusca (Table 2.1, 'Habitat': $P=0.1472$). The abundance of the entire assemblage of colonizers was significantly larger on sandy patches than on the other habitats (Fig. 2.3.a, Table 2.1, pairwise comparisons, 'Barrens' vs. 'Sandy patches': $P=0.0014$; 'Macroalgae' vs. 'Sandy patches': $P=0.041$; 'Seagrass' vs. 'Sandy patches': $P=0.0192$). 'Habitat' contributed to explain 16.22% of total variation in the abundance of Arthropoda, though barely the abundance in collectors deployed on macroalgal beds was significantly larger than abundances on sandy patches (Fig. 2.3.b, Table 2.1, pairwise comparisons, 'Macroalgae' vs. 'Sandy patches': $P=0.0156$). 'Habitat' contributed to explain 33.43% of total variation in the abundance of Chordata; the total abundance of Chordata was significantly larger on sandy patches than on the other habitats (Fig. 2.3.c, Table 2.1, pairwise comparisons, 'Barrens' vs. 'Sandy patches': $P=0.001$; 'Macroalgae' vs. 'Sandy patches': $P=0.0018$; 'Seagrass' vs. 'Sandy patches': $P=0.0074$). 'Habitat' contributed to explain 20.25% of total variation in the abundance of Echinodermata; the total abundance of Echinodermata was significantly larger on sandy patches than on barrens and seagrasses (Fig. 2.3.d, Table 2.1, pairwise comparisons, 'Barrens' vs. 'Sandy patches': $P=0.025$; 'Macroalgae' vs. 'Sandy patches': $P=0.0256$; 'Seagrass' vs. 'Sandy patches': $P=0.052$). The total abundance of Mollusca did not change among collectors deployed on different

habitats (Fig. 2.3e, Table 2.1, 'Habitat', $P=1.8567$). In all cases, variability from collector to collector within each combination of type of collector and habitat accounted for the larger amount of variation in total abundance (from 53.33 to 79.75%, Table 2.1).

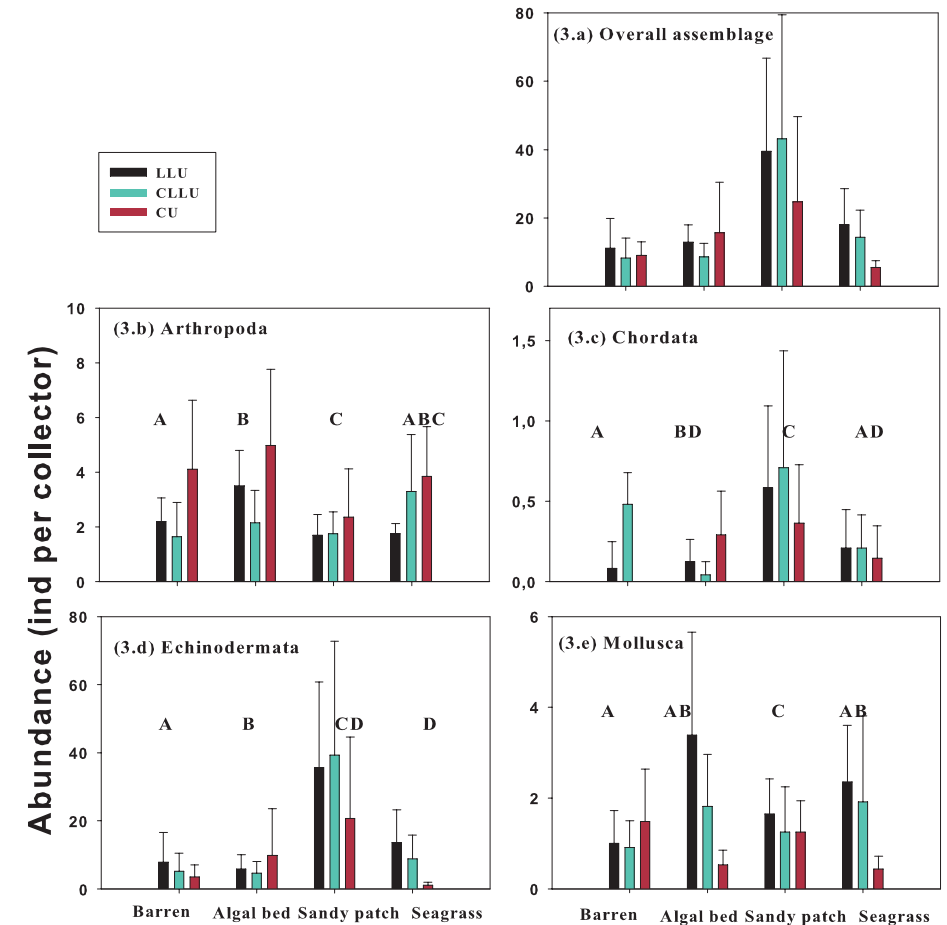


Fig. 2.3 Mean abundance (+SE of means) of organisms colonizing each type of artificial collector deployed on four subtidal, adjacent, habitats within a coastal landscape in the eastern Atlantic. (3a) Overall assemblage, (3b) Arthropoda, (3c) Chordata, (3d) Echinodermata, and (3e) Mollusca. Different letters above bars denote significant differences.

Table 2.1 Results of 2-factor ANCOVA testing for differences in the abundance of colonizers at the assemblage-level between the types of collectors and habitats. Pair-wise comparisons are indicated (B=Barrens; M=Macroalgal beds; SP=Sandy Patches; S=Seagrasses)

	df	MS	F	P	Variance components (%)	Pairwise comparison	P
Overall assemblage							
Covariate	1	1061.1	0.49965	0.4586	0	B vs. M	0.0648
Collector	2	4132.7	1.946	0.153	7.61	B vs. SP	0.0014
Habitat	3	12314	5.7986	0.0012	26.38	B vs. S	0.1736
Collector x habitat	6	1536.9	0.72369	0.6488	0	M vs. SP	0.041
Residual	35	2123.6			66.51	M vs. S	0.6204
						SP vs. S	0.0192
Arthropoda							
Covariate	1	71.837	0.96865	0.3302	0	B vs. M	0.082
Collector	2	58.054	0.7828	0.4508	0	B vs. SP	0.3006
Habitat	3	256.97	3.465	0.0262	16.22	B vs. S	0.6936
Collector x habitat	6	92.16	1.2427	0.3024	4.78	M vs. SP	0.0156
Residual	35	74.162			79	M vs. S	0.1222
						SP vs. S	0.1422
Chordata							
Covariate	1	0.28959	0.16559	0.6622	0	B vs. M	0.4326
Collector	2	0.55038	0.31471	0.736	0	B vs. SP	0.001
Habitat	3	16.083	9.1964	0.0004	33.43	B vs. S	0.1082
Collector x habitat	6	2.5208	1.4414	0.2124	13.19	M vs. SP	0.0018
Residual	35	1.7489			53.33	M vs. S	0.1478
						SP vs. S	0.0074
Echinodermata							
Covariate	1	296.54	0.20428	0.5676	0	B vs. M	0.8652
Collector	2	86.51	5.96E-02	0.9412	0	B vs. SP	0.025
Habitat	3	5875.6	4.0475	0.005	20.25	B vs. S	0.2766
Collector x habitat	6	892.53	0.61484	0.8072	0	M vs. SP	0.0256
Residual	35	1451.7			79.75	M vs. S	0.3608
						SP vs. S	0.052
Mollusca							
Covariate	1	55	0.16397	0.681	0	B vs. M	-
Collector	2	687.16	2.0486	0.1452	9.35	B vs. SP	-
Habitat	3	622.81	1.8567	0.1472	5.21	B vs. S	-
Collector x habitat	6	562.49	1.6769	0.1528	12.36	M vs. SP	-
Residual	35	335.43			73.06	M vs. S	-
						SP vs. S	-

2.3.2 Differences in the abundance of colonizers: taxon-level patterns

Results were similar to those previously reported for the abundance of colonizers at the assemblage-level. For the 16 most conspicuous taxa, the abundance of colonizers did not differ between types of collectors (Table 2.2, ANCOVA: 'Collector': Majidae P=1.7392; Galatheidae P= 1.8081; Grapsidae P=0.124; Paguridae P=0.3626; Diogenidae P=0.0144; Gobiesocidae P=0.707; Ophiodermatidae P=0.0712; Echinidae P=0.9054; Bivalvia P=0.0732; Columbelloidae P=0.6642; Cerithidae P=0.0848; Rissoidae P=0.9576; Naticidae P=2.00E-01; Tricoliidae P=0.53; Trochidae P=0.31; Turridae P=0.0494). However, half of the analyzed taxa showed differences in abundance among habitats where collectors were deployed (Table 2.2, ANCOVA: 'Habitat': Paguridae P=0.002; Gobiesocidae P=0.0004; Ophiodermatidae P=0.0046; Echinidae P=0.002; Columbelloidae P=0.0028; Tricoliidae P=0.0336; Trochidae P=0.0002 and Turridae P=0.0082). Three taxa (Gobiesocidae, Echinidae and Turridae) had, in general, larger abundances on sandy patches than on the other habitats (pairwise comparisons, Table 2.2). In contrast, Paguridae was the only taxon that had lower abundance on sandy patches than on the other habitats. Ophiodermatidae and Tricoliidae had, in general, lower abundances on rocky urchin-barrens than on the other habitats (Table 2.2); in contrast, Columbelloidae had larger abundances on barrens (Table 2.2). Trochidae had larger abundance on macroalgal beds than on the other habitats (Table 2.2).

Table 2.2 Results of 2-factor ANCOVA testing for differences in the abundance of the 16 dominant taxa between types of collectors and habitats. Significant pair-wise comparisons are indicated (B=Barrens; M=Macroalgal beds; SP=Sandy Patches; S=Seagrasses). For the sake of brevity, only of P-values are included.

	df	MS	F	P	Pairwise comparison
Majidae					
Covariate	1	30.055	25.614	0.1354	
Collector	2	20.408	17.392	0.1894	
Habitat	3	91.875	0.78297	0.5256	
Collector x habitat	6	18.958	0.16157	0.9918	
Residual	35	11.734			
Galatheididae					
Covariate	1	0.73558	0.58827	0.4548	
Collector	2	22.609	18.081	0.1764	
Habitat	3	13.889	11.107	0.3642	
Collector x habitat	6	0.74306	0.59425	0.738	
Residual	35	12.504			
Grapsidae					
Covariate	1	30.003	0.54409	0.449	
Collector	2	12.237	22.192	0.124	
Habitat	3	74.722	13.551	0.2642	
Collector x habitat	6	40.347	0.73169	0.6438	
Residual	35	55.143			
Paguridae					
Covariate	1	21.699	11.973	0.2726	
Collector	2	19.063	10.519	0.3626	
Habitat	3	115.94	63.977	0.002	B, M, S > SP
Collector x habitat	6	47.465	26.191	0.0312	
Residual	35	18.123			
Diogenidae					
Covariate	1	14.256	5,97E+02	0.687	
Collector	2	61.465	25.738	0.0144	
Habitat	3	17.856	0.74772	0.5054	
Collector x habitat	6	16.257	0.68076	0.8266	
Residual	35	23.881			

	df	MS	F	P	Pairwise comparison
Ophiidermatidae					
Covariate	1	110.12	42.628	0.0774	
Collector	2	67.84	26.262	0.0712	
Habitat	3	99.743	38.612	0.0046	M, SP, S > B; M > SP
Collector x habitat	6	14.493	0.56104	0.8616	
Residual	35	25.832			
Echinidae					
Covariate	1	768.07	0.54052	0.382	
Collector	2	152.02	0.10698	0.9054	
Habitat	3	6439.5	45.318	0.002	SP > B, M; S > M
Collector x habitat	6	787.85	0.55445	0.8598	
Residual	35	1421			
Bivalvia					
Covariate	1	0.23784	4,62E+02	0.7962	
Collector	2	24.256	47.161	0.0132	
Habitat	3	68.542	13.327	0.2726	
Collector x habitat	6	59.167	11.504	0.3286	
Residual	35	51.432			
Columbellidae					
Covariate	1	9.265	0.45932	0.4808	
Collector	2	82.693	0.40996	0.6642	
Habitat	3	115.13	57.078	0.0028	B, M > SP, S
Collector x habitat	6	12.028	0.59629	0.775	
Residual	35	20.171			
Cerithidae					
Covariate	1	16.837	12.159	0.2684	
Collector	2	57.799	4.174	0.0248	
Habitat	3	33.722	24.353	0.0704	
Collector x habitat	6	31.139	22.487	0.0494	
Residual	35	13.848			
Rissoidae					
Covariate	1	74.219	4,96E+02	0.8246	
Collector	2	82.102	4,97E+01	0.9576	
Habitat	3	295.74	17.892	0.153	
Collector x habitat	6	252.83	15.295	0.1804	
Residual	35	165.3			

	df	MS	F	P	Pairwise comparison
Naticidae					
Covariate	1	20.433	0.36081	0.2626	
Collector	2	7..3573	12.992	0.1996	
Habitat	3	86.875	15.341	0.049	M, SP, S > B; M > SP
Collector x habitat	6	78.333	13.832	0.0576	
Residual	35	5.663			
Tricoliidae					
Covariate	1	0.22172	2,27E+02	0.8742	
Collector	2	62.381	0.63835	0.536	
Habitat	3	31.354	32.085	0.0336	M, SP, S > B
Collector x habitat	6	95.625	0.97854	0.4598	
Residual	35	97.722			
Trochidae					
Covariate	1	31.179	0.34492	0.5176	
Collector	2	11.18	12.368	0.31	
Habitat	3	76.917	8.509	0.0002	M > B, SP, S
Collector x habitat	6	16.938	18.737	0.0956	
Residual	35	90.395			
Turridae					
Covariate	1	7.0701E-3	1,83E+01	0.9568	
Collector	2	12.4	32.031	0.0494	
Habitat	3	18.389	47.501	0.0082	SP, S > B M
Collector x habitat	6	67.431	17.418	0.1192	
Residual	35	38.712			
Gobiesocidae					
Covariate	1	0.38716	0.26254	0.5934	
Collector	2	0.51213	0.34729	0.707	
Habitat	3	13.25	89.852	0.0004	SP > B, M, S
Collector x habitat	6	19.375	13.139	0.2542	
Residual	35	14.747			

2.3.3 Differences in the assemblage structure of colonizers

The CAP analysis efficiently separated the assemblage of colonizers among habitats along the first canonical axis ($\delta_1^2=0.7531$, $P = 0.0002$, Fig. 2.4a). However, the assemblage of colonizers was barely distinguished among types of collectors along its first canonical axis ($\delta_1^2=0.5952$, $P = 0.012$, Fig. 2.4b). In fact, the 'LoA' indicated a larger misclassification for the assemblage of colonizers among types of collectors (43.75%) than among habitats (27.08%). Patterns in the assemblage structure of colonizers were affected, in all cases, by the habitat where collectors were deployed (Table 2.3, 'Habitat': Arthropoda $P=0.0004$; Chordata $P=0.011$; Echinodermata $P=0.0132$; Mollusca $P=0.0002$), but not by the type of collector (Table 2.3, 'Collector': Arthropoda $P=0.7018$; Chordata $P=0.7716$; Echinodermata $P=0.6312$; Mollusca $P=0.1102$). 'Habitat' contributed to explain most variation in the assemblage structure of colonizers (from 5.44 to 19.23%, Table 2.3) and, overpowered, in all cases, variation explained by 'Collector'. Variability from collector to collector within each combination of type of collector and habitat accounted for the largest amount of variation in assemblage structure (from 71.17 to 91.01%, Table 2.3).

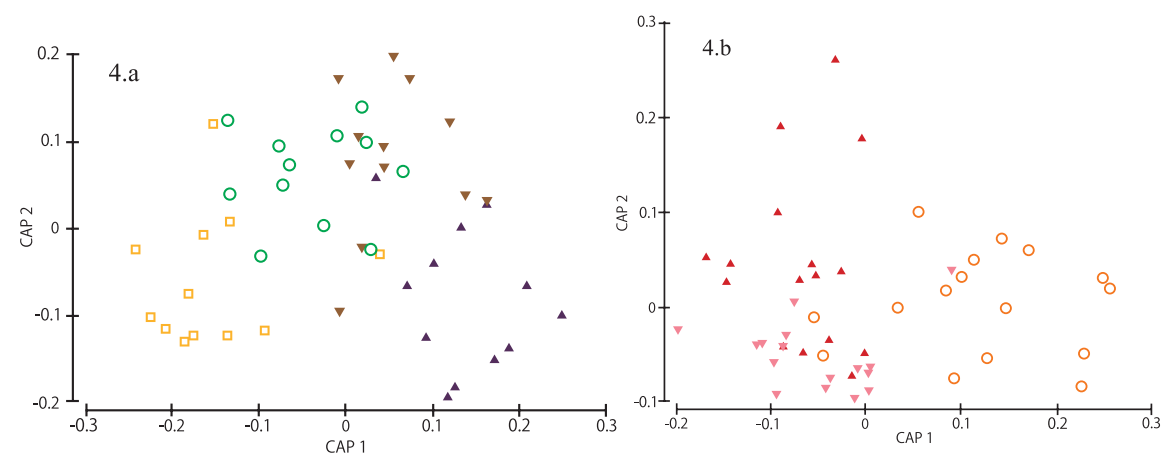


Fig. 2.4 Constrained canonical ordination plots (CAP) to visualize differences in the assemblage structure of colonizers among habitats (4a); ▲: urchin-barrens, ▼: macroalgal beds, □: sandy patches and ○: seagrasses, and types of collectors (4b); ▲: LLU, ▼: CLLU, ○: CU.

Table 2.3 Results of 2-factor multivariate ANCOVA testing for differences in the patterns of assemblage structure of colonizers between types of collectors and habitats. Pair-wise comparisons are included (B=Barrens; M=Macroalgal beds; SP=Sandy Patches; S=Seagrasses).

	df	MS	F	P	Variance components (%)	Pairwise comparison	P
Overall assemblage							
Covariate	1	1817	0.91235	0.523	0	B vs. M	0.0012
Collector	2	2217.3	1.1133	0.3202	1	B vs. SP	0.0002
Habitat	3	8208.4	4.1215	0.0002	19.23	B vs. S	0.0004
Collector x habitat	6	2240.2	1.1248	0.2414	2.39	M vs. SP	0.0002
Residual	35	1991.6			77.38	M vs. S	0.0168
						SP vs. S	0.01
Arthropoda							
Covariate	1	1589.5	0.81216	0.5718	0	B vs. M	0.5372
Collector	2	1487.8	0.76019	0.7018	0	B vs. SP	0.0008
Habitat	3	5964.6	3.0477	0.0004	14.24	B vs. S	0.1524
Collector x habitat	6	2171.5	1.1096	0.3162	2.2	M vs. SP	0.0006
Residual	35	1957.1			83.56	M vs. S	0.042
						SP vs. S	0.0306
Chordata							
Covariate	1	2961.5	0.77002	0.687	0	B vs. M	0.446
Collector	2	2973.2	0.77308	0.7716	0	B vs. SP	0.0016
Habitat	3	7116.7	1.8504	0.011	5.44	B vs. S	0.0688
Collector x habitat	6	4557.7	1.1851	0.163	3.53	M vs. SP	0.0112
Residual	35	3846			91.01	M vs. S	0.4462
						SP vs. S	0.08

	df	MS	F	P	Variance components (%)	Pairwise comparison	P
Echinodermata							
Covariate	1	2005.8	0.79317	0.548	0	B vs. M	0.017
Collector	2	1948	0.77029	0.6312	0	B vs. SP	0.0922
Habitat	3	5929.6	2.3448	0.0132	9.98	B vs. S	0.3208
Collector x habitat	6	2633.6	1.0414	0.4068	0.92	M vs. SP	0.005
Residual	35	2528.9			90	M vs. S	0.092
						SP vs. S	0.2636
Mollusca							
Covariate	1	1676.5	0.80348	0.593	0	B vs. M	0.0048
Collector	2	3061.1	1.4671	0.1102	4.0	B vs. SP	0.0002
Habitat	3	8490.2	4.0691	0.0002	18.18	B vs. S	0.0002
Collector x habitat	6	2867.2	1.3742	0.0696	6.65	M vs. SP	0.006
Residual	35	2086.5			71.17	M vs. S	0.0058
						SP vs. S	0.0674

2.4 DISCUSSION

The present study has demonstrated that variation in short-term colonization patterns of post larval fauna into artificial collectors was mostly affected by variation associated with habitats across a coastal landscape, rather than by differences in the structural complexity of collectors; this was the general pattern observed for a range of organisms, including Arthropoda (mostly decapod crustaceans), Echinodermata, Chordata and Mollusca (majorly prosobranch gastropods). This study, however, was limited to four weeks during summer. Consequently, our results should be taken with cautious and avoid generalizations, particularly because short-term colonization of benthic habitats is largely driven by temporal patterns of larvae availability in the water column (Underwood and Keough, 2001). However, the main finding of this study, i.e. variation in patterns of macrofaunal short-term colonization was majorly explained by variation in habitat types rather than by types of collector, was consistent for a wide range of organisms, providing valid support for this observation.

Sandy bottoms are homogeneous environments that often sustain assemblages with lower diversity and abundance than nearby substrates with a higher structural complexity (e.g. Jenkins and Wheatly, 1998; Guidetti, 2000; Guidetti and Bussoti, 2002; Pihl and Wennhage, 2002; Tuya *et al.*, 2005). In our study, however, collectors deployed on sandy patches showed the largest abundances of colonizers, particularly organisms within the groups Echinodermata (e.g. Echinidae = sea urchins) and Chordata (e.g. the fish family Gobiesocidae). This unexpected result could be explained by the fact that artificial collectors can function as 'oases' on sandy bottoms; organisms settling from the water column into the benthos take advantage of the single available shelter in the benthos. This result suggests that the 'availability', rather than any particular attribute related to the 'acceptability' of artificial collectors, e.g. structural complexity, was a relevant driver of patterns of faunal short-term colonization into collectors for Echinodermata and Chordate, particularly for Echinidae and Gobiesocidae, respectively.

Echinidae have often broad larval dispersal phases; this is particularly the case of the, by far, most abundant sea urchin of the Canary Islands, the long-spined urchin *Diadema antillarum* (Hernández *et al.*, 2006), which has been

previously observed to colonize artificial collectors in the Canaries during summer (Hernández *et al.*, 2006). Recruits of *D. africanum* prefer cryptic habitats and clean surfaces free of algae (Bak, 1985); as a result, artificial collectors are a perfect habitat to settle and recruit into, irrespective of the matrix of habitats that surrounds them. It is plausible then, that the arrival of sea urchins had been similar among habitats, but a post-colonization mechanism, e.g. predation, may have increased survivorship of sea urchin recruits on the habitat where predation pressure is, in theory, lower as a result of the low abundance of small-sized sea urchin predators (e.g. fishes, octopuses, etc), i.e. sandy substrates relative to rocky reefs (Clemente *et al.*, 2007). A similar explanation could be plausible to explain the larger abundances of fish within the Gobiesocidae family on sandy patches. However, this remains open to speculation, in particular since the biology of these cryptic species is largely unknown in the eastern Atlantic.

Arthropods (mostly decapod crustaceans, which accounted for 57.91% of total arthropods), however, showed lower abundances on sandy patches than on hard substrates, i.e. urchin-grazed barrens and macroalgal beds. Larvae and post-larvae of decapod crustaceans are often active swimmers that locate the most suitable coastal habitat (Rothlisberg *et al.*, 1995), particularly those providing food and refuge. At the end of their planktonic stage, most decapod crustaceans can differentiate between different types of habitats during their settlement, possibly by chemoreception (Boudreau *et al.*, 1993; Liu and Loneragan, 1997) and by physical examination of the structure (Herrnkind and Butler, 1986; Liu and Loneragan, 1997). This could help out to explain the avoidance by individuals within the taxon Paguridae (hermit crabs) for substrates devoid of vegetation (sandy patches), and an overall larger abundance on rocky substrates and seagrass meadows, where Paguridae typically find food and shelter in the study area (Espino *et al.*, 2006).

Molluscan assemblages, in particular most species of prosobranch gastropods (which were 96.16% of the molluscs we observed, Appendix 1), frequently live within canopies provided by different types of vegetation (e.g. Kelaher, 2003, Chapman *et al.*, 2008). Dispersion of prosobranch gastropods to new habitats is largely dependent on their larval ecology, particularly according to planktotrophic vs. non-planktotrophic (= direct development within egg capsules) strategies. Despite the larval ecology of prosobranch gastropods is mostly unknown in the eastern Atlantic, gastropods within the family Columbellidae have a typically non-planktotrophic development within

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egg masses until they emerge as crawling juveniles: this pattern has been found in the western Atlantic (Fortunato, 2004). This result could help to explain the larger abundances of Columbellidae on rocky substrates: the environment where the most conspicuous Columbellid gastropod of the Canaries, *Columbella adansoni*, is typically found (Pérez-Sánchez and Moreno-Batet, 1990, Espino *et al.*, 2006) relative to soft bottoms. Prosobranch gastropods living on subtidal rocky substrates, regardless of their prevalent mode of dispersion, can rapidly colonize artificial collectors adjacent to the habitat they inhabit (Jorgensen and Christie, 2003, Tuya *et al.*, 2008). A similar explanation seems plausible to explain the larger abundance of Trochidae on rocky macroalgal beds relative to the other habitats. Trochids often live on hard substrates (Williams *et al.*, 2010), including algal beds, and, at least in the western Atlantic, majorly lack a planktotrophic development (Díaz-Ferguson *et al.*, 2010). Available knowledge to infer the potential reasons the other two abundant prosobranch gastropod taxa (Tricoliidae and Turridae) showed differences among habitats, is, however, mostly lacking, and remains exclusively open to speculation. Individuals of the Turridae family often live in soft bottoms in the study area (Pérez-Sánchez and Moreno-Batet, 1990). If planktotrophic development is limited for this taxon, the larger abundances found on soft bottoms could be explained by the proximity to resident adult populations.

In summary, this study has showed that variation in short-term colonization patterns of faunal assemblages into artificial collectors was mostly affected by variation associated with habitats across a landscape, rather than by differences in the structural complexity of collectors.

Appendix 1. Mean abundance (+SE of means) of organisms colonizing each type of artificial collector deployed on four subtidal, adjacent, habitats within a coastal landscape in the eastern Atlantic.

	Urchin-Barrens			Macroalgal Beds		
	LLU	CLLU	CU	LLU	CLLU	CU
Arthropoda						
Ammotheidae: <i>Achelia echinata</i>	0	0	0.5 + 0.28	0	0	0
Amphipoda	107 + 49.6	42.5 + 15.2	44.3 + 11.04	23.75 + 9.97	55.5 + 24.75	47 + 6.64
Caprellidae	0.75 + 0.5	1.25 + 0.62	0.75 + 0.47	0.75 + 0.47	0.25 + 0.25	0.75 + 0.5
Isopoda	16 + 11.67	41 + 22.85	6.75 + 2.68	35.5 + 18.51	37.5 + 18.4	20.3 + 5.4
Mysidae	0	0	0	0	0	0
Natantia	62.5 + 42	63 + 5.08	59.5 + 13.39	79 + 8.75	117.3 + 29	114.3 + 13
Majidae	2.5 + 0.95	1 + 1	2.25 + 0.75	2.75 + 2.75	2.5 + 1.5	1.75 + 1.4
Galatheidae: <i>Galathea squamifera</i>	0	0.75 + 0.47	0	0.5 + 0.5	1.25 + 0.75	1.25 + 0.9
Grapsidae	0.25 + 0.25	1.25 + 0.47	2.25 + 0.62	0	2.75 + 1.49	3.75 + 0.5
Xanthidae	0	0	0	0	0	0.25 + 0.3
Paguridae: <i>Pagurus anachoretus</i>	8.25 + 3.37	5.25 + 2.28	7.25 + 1.93	14.3 + 3.03	4.25 + 1.65	7.25 + 2.6
Diogenidae: <i>Calcinus tubularis</i>	1.5 + 0.64	0.75 + 0.75	1 + 1	9.25 + 7.63	1.25 + 0.94	4.75 + 2.8
Chordata						
Gobiesocidae: <i>Lepadogaster candollei</i>	0	0.75 + 0.47	0	0	0	0.5 + 0.28
Gobiesocidae: <i>Opeatogeny cadenati</i>	0	0	0	0.5 + 0.28	0	0
Labridae: <i>Coris julis</i>	0	0	0	0	0	0.25 + 0.25
Labridae: <i>Symphodus trutta</i>	0.5 + 0.5	0	0	0	0	0
Apogonidae: <i>Apogon imberbis</i>	0	0.25 + 0.25	0	0	0.25 + 0.25	0
Gobidae	0	0	0	0	0	0
Scorpaenidae: <i>Scorpaena</i> spp.	0	0	0	0.25 + 0.25	0	0.25 + 0.25
Syngnathidae: <i>Syngnathus typhle</i>	0	0	0	0	0	0
Echinodermata						
Ophiordermatidae: <i>Ophioderma longicaudum</i>	0.5 + 0.28	0.25 + 0.25	0.75 + 0.47	8.5 + 3.66	3.25 + 0.85	9.5 + 7.87
Echinidae: <i>Paracentrotus lividus</i>	15.25 + 7.2	10.3 + 3.94	3.25 + 1.88	3.25 + 1.65	6 + 3.48	1.75 + 0.62

	Urchin-Barrens			Macroalgal Beds		
	LLU	CLLU	CU	LLU	CLLU	CU
Mollusca						
Bivalvia	0	0	0	2 + 2	0	0
Columbellidae: <i>Columbella adansoni</i>	5.75 + 2.56	8.5 + 1.7	6.75 + 3.81	7.25 + 5.7	3 + 1.08	1.25 + 0.75
Mitridae: <i>Mitra</i> spp.	0	0	0	0.25 + 0.25	0	0
Cerithidae: <i>Bittium</i> spp.	0.25 + 0.25	1 + 0.57	3.5 + 2.53	0	0.5 + 0.5	0
Cerithidae: <i>Cerithium</i> spp.	0	0	0.25 + 0.25	1.5 + 1.5	0	0.25 + 0.25
Rissoidae: <i>Rissoa</i> spp.	3.25 + 2.35	2 + 0.91	2.75 + 2.42	7.75 + 3.09	8.25 + 3.32	0.5 + 0.5
Rissoidae: <i>Alvania</i> spp.	0.75 + 0.47	0.75 + 0.47	0.5 + 0.28	4.75 + 3.44	5 + 2.12	0.75 + 0.47
Rissoidae: <i>Crisilla</i> spp.	3.75 + 2.49	1.75 + 0.62	0.5 + 0.5	14.5 + 7.59	2.5 + 1.04	0.25 + 0.25
Naticidae	0.25 + 0.25	0	0.25 + 0.25	5 + 4.06	0.25 + 0.25	0
Costellariidae	0	0	0	0.25 + 0.25	0.25 + 0.25	0
Marginellidae	0	0	0	0	0.75 + 0.47	0
Turridae	0	0.25 + 0.25	0	0.25 + 0.25	0.25 + 0.25	0
Volutidae	0	0	0	0	0	0
Conidae: <i>Conus pulcher canariensis</i>	0	0	0	0	0	0
Buccinidae	0.25 + 0.25	0	0	0.75 + 0.47	0.5 + 0.5	0.25 + 0.25
Tricoliidae: <i>Tricolia pullus canarica</i>	1.25 + 0.94	0.5 + 0.28	0	4.25 + 2.32	4.25 + 2.09	0
Trochidae: <i>Osilinus</i> spp.	2.5 + 1.04	0.5 + 0.28	0.5 + 0.5	9.75 + 3.79	7 + 2.51	1.5 + 0.86
Turbinidae: <i>Moelleria costulata</i>	0	0	0.25 + 0.25	0	0	0
Terebridae	0	0	0	0	0	0
Tylodinidae: <i>Tylodina perversa</i>	0	0	0	0	0	0.25 + 0.25
Aplysiidae: <i>Aplysia</i> spp.	0	0.25 + 0.25	0	0.25 + 0.25	0	0.5 + 0.5
Annelyda						
	10.7 + 3.61	2.25 + 0.94	5.25 + 2.01	7.25 + 2.49	2 + 1.22	10.5 + 6.19
Nemertea						
Baseodiscidae: <i>Baseodiscus delineatus</i>	0	0	0	0	0	0
Platyhelminthes						
Pseudoceridae: <i>Thysanozoon brochii</i>	0.25 + 0.25	0	0	0.25 + 0.25	0	0.25 + 0.25
Cnidaria						
Actiniidae	0	0	0	0	0	0

	Sandy Patches			Seagrasses		
	LLU	CLLU	CU	LLU	CLLU	CU
Arthropoda						
Ammonotheidae: <i>Achelia echinata</i>	0	0	0	0	0.5 + 0.28	0.5 + 0.288
Amphipoda	226.25 + 131.09	147.25 + 36.37	42.5 + 13.54	60 + 24.72	94.75 + 49.98	161.75 + 89.38
Caprellidae	6 + 3.48	3.75 + 0.47	1.5 + 0.5	2.75 + 1.37	2.75 + 1.75	1.75 + 0.85
Isopoda	19.25 + 6.28	14.5 + 5.51	3 + 1.08	18.5 + 10.4	58.5 + 21.01	41 + 9.81
Mysidae	5.5 + 3.77	0	1.25 + 1.25	0.5 + 0.28	0	5.75 + 5.75
Natantia	103.25 + 78.25	263.5 + 45.46	86.3 + 39.8	73.3 + 33.6	426.3 + 148	326 + 73.62
Majidae	5.25 + 3.96	2.5 + 1.04	4 + 1.87	2.5 + 0.95	2.25 + 0.25	2.5 + 1.04
Galatheidae: <i>Galathea squamifera</i>	1 + 0.7	1.5 + 0.28	0.25 + 0.25	0.25 + 0.25	1 + 1	1.25 + 0.25
Grapsidae	1.25 + 0.75	2.5 + 0.86	1.25 + 0.47	2.75 + 1.11	4 + 2.82	2.5 + 1.55
Xanthidae	0	0.25 + 0.25	0.25 + 0.25	0	0.25 + 0.25	1.5 + 1.19
Paguridae: <i>Pagurus anachoretus</i>	1 + 0.7	2 + 1.41	1 + 1	3.25 + 0.75	9 + 3	3.25 + 1.65
Diogenidae: <i>Calcinus tubularis</i>	0	0.75 + 0.47	0	0.5 + 0.5	0.25 + 0.25	0.75 + 0.47
Chordata						
Gobiesocidae: <i>Lepadogaster candollei</i>	2 + 1.08	3.5 + 1.65	0.75 + 0.47	1.25 + 0.47	0.75 + 0.47	0.25 + 0.25
Gobiesocidae: <i>Opeatogeny cadenati</i>	1 + 0.7	0	0.25 + 0.25	0	0	0
Labridae: <i>Coris julis</i>	0	0	0	0	0	0
Labridae: <i>Symphodus trutta</i>	0	0.25 + 0.25	0	0	0	0
Apogonidae: <i>Apogon imberbis</i>	0.25 + 0.25	0	0.25 + 0.25	0	0	0
Gobidae	0.25 + 0.25	0	0	0	0.25 + 0.25	0.25 + 0.25
Scorpaenidae: <i>Scorpaena</i> spp.	0	0	0	0	0.25 + 0.25	0
Syngnathidae: <i>Syngnathus typhle</i>	0	0.5 + 0.28	0	0	0	0
Echinodermata						
Ophiodermatidae: <i>Ophioderma longicaudum</i>	2	2 + 0.7	1	4.5 + 2.02	2 + 1.35	1 + 0.41
Echinidae: <i>Paracentrotus lividus</i>	69.25 + 58.63	76.75 + 19.19	17.3 + 13.2	22.75 + 10.8	15.75 + 4.88	0.25 + 0.25

	Urchin-Barrens			Macroalgal Beds			
	LLU	CLLU	CU	LLU	CLLU	CU	
Mollusca							
Bivalvia	2.75 + 1.6	0.25 + 0.25		1.25 + 0.75	5 + 2.79	0	0
Columbellidae: <i>Columbella adansoni</i>	1 + 0.7	0.5 + 0.5		0.25 + 0.25	0.75 + 0.47	0.75 + 0.47	0
Mitridae: <i>Mitra</i> spp.	0	0		0	0	0	0
Cerithidae: <i>Bittium</i> spp.	0.25 + 0.25	0		0.25 + 0.25	6.75 + 3.14	2.75 + 2.13	1.25 + 0.47
Cerithidae: <i>Cerithium</i> spp.	7.25 + 3.75	0		0	2.5 + 1.84	0.25 + 0.25	0.5 + 0.28
Rissoidae: <i>Rissoa</i> spp.	3.25 + 2.35	10.5 + 5.18		1.5 + 0.95	9 + 2.73	21.25 + 9.25	1 + 0.71
Rissoidae: <i>Alvania</i> spp.	0.25 + 0.25	3.5 + 2.21		0.75 + 0.47	3.75 + 3.75	3.75 + 3.75	0
Rissoidae: <i>Crisilla</i> spp.	0	0.25 + 0.25		0.5 + 0.5	1.5 + 0.95	1 + 1	0
Naticidae	0	0		0	0	0	0
Costellariidae	0.5 + 0.5	0.25 + 0.25		0	0.25 + 0.25	0	0
Marginellidae	0	0		0	0	0	0
Turridae	5 + 1.73	0		3.25 + 2.28	2.5 + 1.65	0.25 + 0.25	0.25 + 0.25
Volutidae	0.25 + 0.25	0		0	0	0	0
Conidae: <i>Conus pulcher canariensis</i>	0.25 + 0.25	0		0	0	0	0
Buccinidae	0.5 + 0.5	0		0	0	0	0
Tricoliidae: <i>Tricola pullus canarica</i>	4.75 + 1.88	6 + 2.04		0.75 + 0.75	7.75 + 2.95	3.75 + 0.75	1 + 0.41
Trochidae: <i>Osilinus</i> spp.	0.5 + 0.5	0.5 + 0.28		1.5 + 0.86	2 + 1.35	0.75 + 0.75	0.5 + 0.5
Turbinidae: <i>Moelleria costulata</i>	0	0		0	0	0	0
Terebridae	0.25 + 0.25	0		0	0	0	0
Tylodidae: <i>Tylodina perversa</i>	0	0		0	0	0	0
Aplysiidae: <i>Aplysia</i> spp.	2.75 + 1.6	0.25 + 0.25		0.75 + 0.47	0	0	0
Annelyda							
	44.25 + 19.52	5 + 1.77		21.2 + 11.8	5.5 + 3.4	3 + 1.08	6.25 + 2.35
Nemertea							
Baseodiscidae: <i>Baseodiscus delineatus</i>	0	0		0	1 + 0.71	0	0
Platyhelminthes							
Pseudocercariae: <i>Thysanozoon brochii</i>	0	0		0	0	1	0.75 + 0.75
Cnidaria							
Actiniidae	0.25 + 0.25	0		0.25 + 0.25	0	0	0

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