

Aspects of epizoobiontic mollusc assemblages on *Pinna* shells. II. Does the Mediterranean *P. nobilis* represent an isle of biodiversity?

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Abstract: Epizoic molluscs on 49 specimens of the soft-bottom megabenthic bivalve Pinna nobilis Linné, 1758 sampled in the Straits of Messina (Central Mediterranean), were investigated. Univariate indices of biodiversity, based on richness, abundance/evenness and taxonomic relatedness were calculated on mollusc taxocommunity in accordance with bathymetry and shell size of the *P. nobilis*. Furthermore, a multivariate composition of the characterizing epizoic taxa, and the corresponding functional role were investigated; the contribution of basibionts in increasing mollusc diversity on a small scale (soft bottom habitat/biotope), as well as a large scale (regional biogeography) was also tested. Epizoic mollusc assemblage replicates some major characteristics of hard bottom assemblages which are tied to ephemeral photophilous algae, but also displays some peculiar typological and taxonomic characteristics, probably related to the selective effect of the living substratum. Gastropod to bivalve ratio ranges from 4.0 to 5.6:1 in number of species, and from 5.6 to 12.6:1 in abundance, in accordance to shell size. Bittium reticulatum (Da Costa, 1778), Rissoella inflata Locard, 1892 and Gibbula turbinoides (Deshayes, 1835) are the prevalent species, but percentage similarity analysis and non-parametric correlation emphasize at least two multispecies subsets, which contribute to typologically and functionally characterize the mollusc taxocommunity. The recurrent occurrence of cladistically and functionally related microgastropods may suggest a possible specific redundancy or, alternatively, a functional complementarity depending on the ephemeral macrophytal epigrowth. The peculiar mollusc fauna associated with P. nobilis makes this bivalve a meaningful biodiversity reservoir both on the small and large spatial scale. Estimations of local density of *Pinna* populations, joined with species accumulation curves of associated taxa, allows the assessment of minimal patch of bottom surfaces which may sustain a rich network of epizoites.

Résumé : Les assemblages de mollusques épibiontes des coquilles du genre Pinna. II. L'espèce méditérranéenne Pinna nobilis représente-t-elle un îlot de diversité ? Des mollusques épibiontes vivant sur 49 individus du bivalve mégabenthique de fonds meubles Pinna nobilis Linné, 1758, prélevés dans le détroit de Messine (Méditerranée centrale), ont été étudiés. Les indices univariés de diversité, basés sur la richesse spécifique, abondance/équitabilité et relation taxonomique ont été calculés sur le peuplement de mollusques en fonction du niveau bathymétrique et de la dimension de la coquille de P. nobilis. De plus, la structure multivariée des taxa épibiontes les plus typiques et leur rôle fonctionnel ont été analysés; la contribution des mollusques basibiontes à la diversité à petite échelle (habitat/biotope de fond meuble) ainsi qu'à grande échelle (biogéographie régionale) a été aussi évalué. La faune épibionte de mollusques montre quelque caractéristiques parmi les principales des peuplements de fond rocheux, qui sont liées aux algues éphémères photophiles, mais ce peuple-

ment montre aussi d'autres particularités typologiques et taxonomiques, probablement liées à la sélectivité du substrat coquillier vivant. Le rapport gastéropode:bivalve varie de 4,0 à 5,6:1 en nombre d'espèces, et de 5,6 à 12,6:1 en abondance, selon la taille des basibiontes. *Bittium reticulatum* (Da Costa, 1778), *Rissoella inflata* Locard, 1892 et *Gibbula turbinoides* (Deshayes, 1835) sont les espèces prédominantes, bien que l'analyse de similarité et la corrélation non-paramétrique mettent en évidence au moins deux groupes multispécifiques qui contribuent à caractériser typologiquement et fonctionnellement le peuplement des mollusques épibiontes. La présence fréquente des micro-gastéropodes, qui sont proches en termes de relation cladistique ainsi que de stratégie trophique, peut indiquer une possible redondance spécifique ou une fonctionnalité complémentaire, dépendante des macrophytes éphémères. Le peuplement caractéristique de mollusques épibiontes vivant sur *P. nobilis* donne à ce bivalve un rôle de réserve de biodiversité aussi bien à petite qu'à grande échelle. Des estimations de densité locale des peuplements de *Pinna nobilis*, couplés à des courbes cumulées d'espèces, permettent le calcul des superficies minimales d'agrégations de *Pinna nobilis* permettant l'existence d'un riche réseau d'espèces épibiontes.

Keywords: Pinnidae • Associated assemblages • Diversity • Mediterranean • Biogeography.

Introduction

Eco-biological diversity has been widely investigated in recent years, with special focus on indices and measurements (Gray, 2000; Izsák & Papp, 2000; Magurran, 2004). Diversity, which is strictly tied to biotope heterogeneity (Levin, 1992; Barnes, 2001) and to related ecosystem functioning (Cardinale et al., 2000), arises from habitat complexity and is supported by hierarchical space partitioning. Marine macrophytes and macrofauna provide large additional living surfaces, available for colonization by several organisms (Wahl, 1989; Wahl & Mark, 1999), and increasing complexity at different scales (Vance, 1978; Harlin, 1980; Karlson & Shenk, 1983; Russell, 1983; Davis & White, 1994; Barnes & Clarke, 1995; Thompson et al., 1996; Parapar et al., 1997; Olabarria, 2000). Fan shells, large Bivalvia Pteriomorpha which inhabit sublittoral soft bottoms along warm and temperate oceans, support a rich epizoobiontic (sensu Taylor & Wilson, 2002) fauna and flora, representing a secondary hard substratum that increases space heterogeneity on a meso-scale (Kay & Keough, 1981; Keough, 1984a). In this respect, previous investigations concerned the Indo-Pacific Pinna bicolor Gmelin, 1791 (Keough, 1984b), the Atlantic Atrina rigida (Lightfoot, 1786) (Munguia, 2004), the Atlanto-Mediterranean P. rudis Linné, 1758 (Cosentino & Giacobbe, 2007) and the Mediterranean endemic P. nobilis Linné 1758. In this latter species, whose length may exceed 100 cm, the wide valvar surface, further increased by the peculiar scale sculpture (Cosentino & Giacobbe, 2006), plays a prominent role in hosting a large number of epizoic

species (Zavodnik, 1967; Corriero & Pronzato, 1987; Šiletić & Peharda, 2003), especially molluscs (Cosentino & Giacobbe, 2007).

The aims of this study are to:

- describe the diversity of epibiont mollusc assemblages in shells of *P. nobilis*, with particular regard to shell size;
- determine whether pen-shells really act as "biodiversity isles" with respect to both habitat type and regional mollusc biogeography;
- evaluate functional patterns and potential redundancy/ complementarity of the composition of mollusc multispecies by means of multivariate analysis.

Materials and Methods

A total of 49 specimens of the bivalve *Pinna nobilis* were examined from a 0.8 km² sampling area, during June-July 1986, in the Strait of Messina. Samples were taken at depth levels of 5-10 m (26 specimens) and 11-20 m (23 specimens). Sampling was carried out by scuba divers, who placed each shell into a sealed labelled plastic container to avoid any accidental removal of the epizoic fauna. The main axis length of each specimen, from umbo to the mean ventral valvar opening (Le.), was measured by means of millimetric steel calliper (\pm 0.5 mm). This measurement allowed us to arrange the basibionts according to the three size classes: Le. \leq 250 mm, defined as "Small" (7 specimens); 250 mm < Le.< 350 mm, "Medium" (29 specimens); Le. \geq 350 mm, "Large" (13 specimens).

Both the valvar surfaces were lightly scraped to remove macroalgae as well as motile and sessile fauna from the outer surface of the valve, and washed with a jet of water into a 0.1 mesh sieve (ASTM-USA). All the fauna was stored in ethanol 70% for each *Pinna* specimen; mollusc fauna was sorted and determined up to specific or subspecific taxonomic levels. Functional groups concerning motility with respect to the substrate (motile/sessile) and regarding trophic guilds, were defined as follows: browser ("Br", microphytophagous of bacterial and algal film); suspension feeder ("Sf", microphagous of suspended particulate matter); carnivore ("Ca", macrophagous predator); parasite ("Pa", ectoparasitic); omnivore ("Om", non-selective microphage/scavenger). Macrophagous herbivores and omnivores (scavengers) were virtually absent in this assemblage.

Data analysis

Abundances N and relative frequencies fq_i (fraction of basibionts which host the *i*-th species) were assessed for each epizoite in order to evaluate the distribution of the most recurrent species with respect to shell size. Speciesaccumulation curves were also plotted for every size class as well as for the total assemblage to assess the average dimension of a sample of living Pinna which was representative of the associated mollusc assemblages. The multivariate matrix (Epizoites x Basibionts) was converted to a triangular similarity matrix (Bray-Curtis index; not transformed data) and analysed by a one-way permutation test. An ANOSIM (Analysis of Similarity; 9999 permutations) for the factors i) bathymetric level and ii) size class was performed. A dissimilarity percentage analysis (SIMPER) was used to point out the specific contribution of each epizoic mollusc species in the differentiation of the assemblages related to the size category of basibionts. The whole assemblage was reduced to those epizoobionts which contributed at least 3%; species abundances were standardized per total of each species in order to reduce noise interference due to accidental loss of specimens and differences in sample size; data was square root transformed to moderately normalize species distributions among samples of Pinna nobilis. In order to quantify diversity in the assemblages, two categories of indices were calculated: i) traditional indices of biodiversity/evenness (Margalef's d; Shannon-Wiener's H', ln-based; Pielou's J') and ii) indices based on taxonomic relatedness (average taxonomic distinctness, AvTD or Δ^+ ; variation in taxonomic distinctness, VarTD or Λ^+ ; average phylogenetic diversity, AvPD or Φ^+). These indices were assessed on the faunistic data cumulated within each size class of Pinna. Indices Δ^+ , Φ^+ and Λ^+ were based on the presence/absence of data (Clarke & Warwick, 1998 & 2001a; Warwick & Clarke, 2001); taxonomic weights or distances (ω_i) were calculated using taxon richness (Clarke & Warwick, 1999)

from the master data aggregation file. Epizoic species were taxonomically aggregated according to the following categories: species ($\omega_i = 10.21$); sub genus (10.94); genus (14.33); sub family (22.04); family (32.11); super family (43.25); sub order (52.53); order (54.85); super order (67.51); sub class (86.08); class (100). Only three sub species were included to species level. The taxonomic distinctness test (TAXDTEST procedure), with no taxon frequencies (Clarke & Warwick, 2001b), allowed us to evaluate the representativeness of the epizoic assemblage of P. nobilis with respect to the local mollusc fauna living in the Straits of Messina, by means of expected univariate $(\Delta^+; \Lambda^+)$ or bivariate (Δ^+/Λ^+) distributions, which are substantially unaffected by sampling effort (Clarke & Warwick, 1998 & 2001a). In particular, two different master-lists of molluscs were considered: the first list consisted of 109 selected species, which were found from 1984 up to 2001 (small-scale diversity) living in sand/gravel soft bottoms of the Strait where the Pinna dwells,; the second list included the 711 species and nine sub species, reported in the SIBM Checklist (2006) for the biogeographic "sector" of the Strait of Messina, central Mediterranean (large-scale biodiversity or γ-diversity).

Functional patterns within the whole assemblage were assessed ascribing each epizoobiont to a particular trophic guild and motility group; the resulting subsets were converted into the relative matrix and compared to the total epizoic assemblage (RELATE procedure; not transformed data). Similarly, the stepwise algorithm (BVSTEP) was employed to point out the subsets of associated species which best matched the total fauna in terms of non-parametric rank correlation ρ (BIO-BIO procedure; Clarke & Warwick, 2001b). The STATISTICA v.5 (StatSoft Italia) package and PRIMER-E v.6 (Plymouth Marine Laboratory, UK) were employed for statistical uni-/multivariate computations.

Results

Distribution of epizoites

The epizoic molluscs found on the valvar surfaces of *Pinna nobilis* amounted to 120 species, grouped in 76 sub genera, 74 genera, 65 sub families, 47 families, 30 super families, 18 sub orders, 12 orders, 11 super orders and 6 sub classes. Overall they comprised two classes: gastropods (101 species; 2940 specimens; 91.16%) and pelecypods (19 species, 285 specimens; 8.84%). In particular, seven small sized basibionts had a total of 40 species (32 gastropods, 237 specimens; 8 bivalves, 42 specimens), equal to 8.65% of the whole abundance; twenty-nine medium sized basibionts had 99 species (84 gastropods, 1313 specimens; 15

bivalves, 134 specimens), equal to 44.87 %; thirteen large sized basibionts had 79 species (67 gastropods, 1389 specimens; 12 bivalves, 110 specimens), equal to 46.48 %. Rank/abundance distribution (Fig. 1A) showed a well structured assemblage, characterized by three prevalent species (323 \leq N \leq 705; 0.67 \leq fq_i \leq 0.90), forty-nine frequent species ($5 \le N \le 140$; $0.07 \le fq_i \le 0.65$) and sixtyeight rare species (1 \leq N \leq 4; 0.02 \leq fq_i \leq 0.06). The species-accumulation curve as a function of shell size (Michaelis-Menton index; Fig. 1B) showed that the number of sampled epizoites on the total number of Pinna reached almost the asymptote, as observed for small ($S_{max} = 51.84$) and large basibionts ($S_{max} = 88.84$); on the other hand, sampled species exceeded the expected threshold of S_{max} = 90.55, for medium sized basibionts. We inferred that a representative sample of mollusc epifauna would therefore be found by examining at least 25-30 specimens of P. nobilis for each size class.

Within the three size classes, twenty-three of the most frequent species (fq_i \geq 0.18), with 2835 individuals comprising 88% of the total fauna were selected (Fig. 2). Eighteen of these species were found on small bivalves, showing clear lower abundances, even though the number of basibionts was lower. Risoella inflata Locard, 1892 (fq = 0.71), Arca noae (Linné, 1758) (0.57), Gibberula philippi (Monterosato, 1878) (0.57), Jujubinus striatus depictus (Deshayes, 1835) (0.57), Sinezona cingulata (Costa O.G., 1861) (0.57), Gibbula turbinoides (Deshayes, 1835) (0.43) and Hiatella rugosa (Linné, 1767) (0.43) occurred constantly, whereas Bittium reticulatum (Da Costa, 1778) (1.00) and Pisinna glabrata (Von Muehlfeldt, 1824) (0.43) were prevalent in terms of abundance. Basibionts of medium size showed a significant increase in both abundances and frequencies for all the species, in accordance with their larger size; R. inflata was the prevalent epizoite (0.97), followed by B. reticulatum (0.90), G. philippi (0.69), G. turbinoides (0.66) and Vitreolina philippi (Rayneval & Ponzi, 1854) (0.55), although the former and the latter species were the most frequent (0.90 and 0.97 respectively). In the big sized basibionts Ammonicera fischeriana (Monterosato, 1869) (0.77), Omalogyra atomus (Philippi, 1841) (0.69) and Odostomia eulimoides Hanley, 1844 (0.46) increased with respect to the other size classes, besides the cited species B. reticulatum (0.92), R. inflata (0.85), G. turbinoides (0.85) and V. philippi (0.54); finally, J.s. depictus (0.92), A. noae (0.62), P. glabrata (0.62), S. cingulata (0.56), H. rugosa (0.54), Musculus costulatus (Risso, 1826) (0.54), Eatonina ochroleuca (Brusina, 1869) (0.46) and G. philippi (0.46) did not show high abundances but occurred in almost half of the basibiont number. The permutation test of similarity provided a low Global R of 0.23 (p < 0.001) for the bathy-

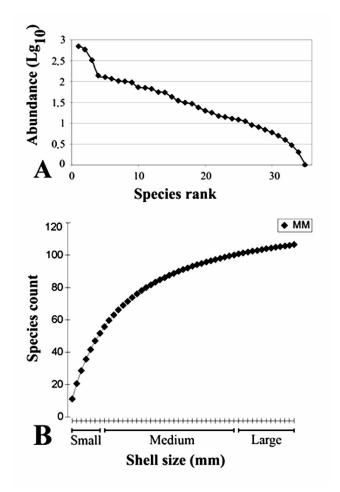


Figure 1. A. Species rank distribution of all mollusc epizoites on *Pinna nobilis*. The similar "broken stick" type trend refers to a long established and structured assemblages. **B.** Species accumulation curve of epizoites (Michaelis-Menton index). All basibionts are arranged according to increasing shell size; asymptote is reached at $S_{max} = 129.38$.

Figure 1. A. Distribution du rang des espèces de tous les mollusques épizoobiontes sur *Pinna nobilis*. La courbe similaire au modèle "bâton brisé" se rapporte aux peuplements établis depuis longtemps et bien structurés. **B.** Courbe de l'accumulation des espèces épizoobiontes (indice de Michaelis-Menton). Tous les basibiontes sont disposés selon l'augmentation de la taille de la coquille; l'asymptote est située à $S_{max} = 129,38$.

metric level and a similar value of 0.21 (p < 0.01) for size factor. Once the early mollusc assemblage settled on juvenile *P. nobilis* specimens, it maintained a high internal similarity, and was also unaffected by depth gradient within the first 20 m of the sublittoral environment.

Notwithstanding the reduced influence of shell size, the dissimilarity percentage analysis, carried out on 82 of the most abundant epizoites, equal to 97.60% of total fauna, highlighted subtle differences according to the size *Pinna*

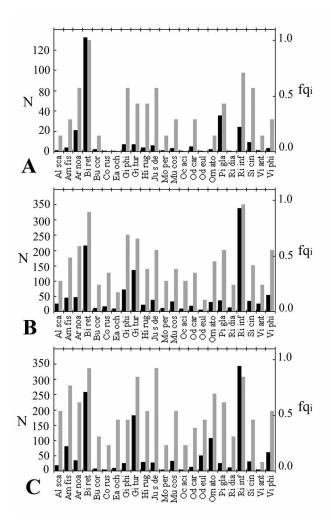


Figure 2. Bar diagrams of twenty-three most characterizing epizoobiontic molluscs in terms of total abundance (N, black bars) and frequency (fq $_i$, grey bars). **A.** Small sized basibionts. **B.** Medium sized basibionts. **C.** Large sized basibionts. Despite non equal sample size, major differences occur between small *Pinna* and the other two classes. For the abbreviation of species names see Table 1.

Figure 2. Abondance totale (N, barres noires) et fréquence relative (fq_i , barres grises) des vingt-trois mollusques les plus caractéristiques. **A.** Basibiontes de petite taille. **B.** Basibiontes de taille moyenne. **C.** Basibiontes de grande taille. Malgré la différence de taille des échantillons de basibiontes, les différences majeures sont entre les petites *Pinna* et les deux autres classes. Pour les abréviations des noms d'espèces, voir le Tableau 1.

nobilis (Table 1). Within the groups similarity progressively increased with size, showing the constitution of a more homogeneous assemblage on the large sized basibionts. As expected, average between-group dissimilarities did not show marked differences among size classes, with the highest value between small and medium basibionts and the

lowest between medium and large basibionts. A total of thirteen epizoites contributed significantly to the intergroup discrimination with a single contribution of 1.35 to 2.54% and a cumulative discrimination of 12.80% in the small-medium comparison, 18.46% in the small-large comparison and 19.64% in the medium-large comparison. Among these epizoic molluscs *B. reticulatum*, *G. philippi*, *G. turbinoides*, *J. striatus depictus*, *R. inflata* and *S. cingulata* were discriminating in all the comparisons, whereas the remaining sixty-nine species contributed secondarily to discriminate the assemblages according to the different growth stages of the *Pinna*, showing an average δ equal to 1.52% (min. = 0.72%; max. = 3.54%).

The computation of biodiversity indices for all the species (Fig. 3) confirmed the increase of abundances with the size of the basibiont, whilst richness showed a slight decrease in the last class. H' reached the highest value in medium shells, only slightly decreasing in large shells, the J' index showed its maximum in the intermediate class and its minimum in the third class. With respect to the relatedness indices, Δ^+ and Φ^+ had higher values in small basibionts, decreasing in medium sized shells; in the third class these two indices showed an opposite trend, the former moderately decreasing with respect to the latter. Higher values of these last two indices emphasized how an immature assemblage, with both low abundance and frequency, may settle precociously on juvenile individuals of P. nobilis but offer a high potential contribution to biodiversity, in terms of taxonomic breadth and phylogenetic "distinctiveness" (Warwick & Clarke, 2001). Λ^+ showed lower values at the extremes of shell sizes with respect to the middle size class, which showed a more uneven taxonomic tree with some taxa overrepresented in comparison to others.

Biogeographic comparison

The associated mollusc epifauna on *P. nobilis* showed a Δ + value of 72.73 (p < 0.01), significantly lower than the species pool living in the same soft bottom habitat as the *Pinna* (74.5 < Δ ⁺ < 83.0), whereas Λ ⁺ was equal to 540.12 (p >> 0.05) and not significantly different from simulated values (470 < Λ ⁺ < 610). Comparisons of each taxonomic class of molluscs (Fig. 4A & B) showed that both distinctness and variation in taxonomic distinctness of gastropods were notably under the lower simulated confidence limit, notwithstanding the higher number of species, whilst pelecypods, less rich in species, fell within the funnel contours. As regards individual basibionts (Fig. 4C & D), the Δ^+ of nine specimens was above the expected mean, thirtytwo specimens were below and three specimens coincided with the mean, whereas five basibionts were below the lower limit. Λ^+ values of five specimens were higher than

Table 1. Dissimilarity percentage analysis (SIMPER, one-way factor) among the three size classes (main axis length in mm) of *Pinna nobilis* basibionts. Most recurrent epizoic molluscs, which contributed at least 3% of abundance, have been selected. Bold numbers indicate highly significant epizoobionts in inter-group comparisons. 76 out of 81 selected species are shown (cut-off for low contribution 90.00 %). The Bray-Curtis dissimilarity (δ) and percentages of dissimilarity (%) have been assessed for each epizoic species; δ to standard deviation (SD) ratio highlighted the most contributing species.

Tableau 1. Analyse de la dissimilarité en pourcentage (SIMPER, un facteur) parmi les trois classes de taille (longueur de l'axe principal en mm) du basibionte *Pinna nobilis*. Les mollusques épizoobiontes plus fréquents, qui contribuent au moins à 3% de l'abondance, ont été sélectionnés. Les numéros en gras indiquent les épizoobiontes les plus significatifs dans la comparaison intergroupe. 76 sur 81 espèces sélectionnées sont montrées (limite du contribution 90.00%). La dissimilarité de Bray-Curtis (δ) et les pourcentages de dissimilarité (%) ont été mesurés pour chaque espèces épizoobionte; le rapport entre δ et l'écart-type (SD) met en évidence les espèces les plus significatives.

SIMPER ANALYSIS Size-group comparison		Small - Medium			Small - Large			Medium – Large		
Average dissimilarity (δ)		83.90			82.30			80.64		
Average group similarity (S')	Small = 17. 65				Medium = 18.46			Large = 23.25		
<u>GASTROPODA</u>	δ	δ/SD	%	δ	δ/SD	%	δ	δ/SD	%	
Alvania cancellata (Da Costa, 1778)	/	/	/	1.19	0.40	1.44	1.01	0.40	1.25	
Alvania cimex (Linné, 1758)	0.71	0.33	0.84	/	/	/	0.91	0.42	1.12	
Alvania discors (Allan, 1818)	0.75	0.26	0.89	/	/	/	/	/	/	
Alvania peloritana Aradas & Benoit, 1844	0.98	0.38	1.17	/	/	/	1.12	0.50	1.39	
Alvania scabra (Philippi, 1844)	1.22	0.57	1.46	1.46	1.07	1.77	1.50	0.88	1.87	
Ammonicera fischeriana (Monterosato, 1869)	1.11	0.95	1.33	2.18	0.84	2.65	1.71	0.86	2.12	
Anisocycla pointeli (De Folin, 1867)	/	/	/	/	/	/	0.82	0.33	1.02	
Bittium reticulatum (Da Costa, 1778)	1.45	1.24	1.72	1.47	1.14	1.78	1.18	1.24	1.46	
Buccinulum corneum (Linné, 1758)	1.49	0.65	1.78	1.69	0.70	2.05	1.42	0.75	1.77	
Cerithiopsis minima (Brusina, 1865)	/	/	/	1.40	0.53	1.70	1.36	0.58	1.69	
Cerithiopsis tubercularis (Montagu, 1803)	0.69	0.18	0.82	/	/	/	/	/	/	
Cerithium vulgatum Bruguière, 1792	0.89	0.39	1.06	/	/	/	0.71	0.38	0.88	
Chauvetia brunnea (Donovan, 1804)	/	/	/	/	/	/	0.75	0.38	0.93	
Chauvetia ventrosa Nordsieck, 1976	/	/	/	1.40	0.42	1.70	1.16	0.41	1.44	
Chrysallida emaciata (Brusina, 1866)	0.80	0.26	0.96	/	/	/	0.62	0.25	0.77	
Chrysallida monozona (Brusina, 1869)	1.82	0.63	2.16	2.36	0.70	2.87	1.20	0.55	1.49	
Clathromangelia quadrillum Dujardin, 1837	/	/	/	0.97	0.41	1.18	0.99	0.44	1.23	
Columbella rustica (Linné, 1758)	1.57	0.66	1.87	1.03	0.47	1.25	1.49	0.74	1.84	
Conus mediterraneus Hwass in Bruguière, 1792	0.76	0.33	0.91	/	/	/	0.82	0.41	1.02	
Coralliophila meyendorffii (Calcara, 1845)	/	/	/	1.19	0.41	1.44	1.26	0.47	1.57	
Crepidula gibbosa De France, 1818	0.92	0.33	1.09	/	/	/	0.98	0.40	1.21	
Dendrodoris grandiflora (Rapp, 1827)	/	/	/	0.92	0.41	1.12	1.06	0.40	1.32	
Dikoleps nitens (Philippi, 1844)	1.39	0.53	1.66	1.43	0.50	1.73	0.97	0.56	1.20	
Eatonina cossurae (Calcara, 1841)	/	/	/	2.11	0.71	2.56	1.85	0.70	2.30	
Eatonina fulgida (Adams J., 1797)	2.97	0.60	3.54	2.89	0.56	3.51	/	/	/	
Eatonina ochroleuca (Brusina, 1869)	0.69	0.42	0.82	1.81	0.76	2.20	1.61	0.86	2.00	
Fasciolaria lignaria (Linné, 1758)	1.43	0.42	1.70	1.83	0.49	2.22	0.88	0.43	1.09	
Fusinus rudis (Philippi, 1844)	0.82	0.25	0.97	/	/	/	0.95	0.33	1.18	
Gibberula oryza (Lamarck, 1822)	0.86	0.33	1.03	/	/	/	0.68	0.32	0.84	
Gibberula philippi (Monterosato, 1878)	1.71	1.11	2.03	1.43	1.07	1.74	1.54	1.05	1.91	
Gibbula ardens (Von Salis, 1793)	1.35	0.36	1.61	1.02	0.47	1.24	0.73	0.26	0.90	
Gibbula racketti (Payraudeau, 1826)	/	/	/	1.05	0.28	1.27	0.87	0.28	1.07	
Gibbula turbinoides (Deshayes, 1835)	1.14	1.20	1.35	2.09	1.82	2.54	1.59	1.52	1.98	
Gibbula varia (Linné, 1758)	1.90	0.43	2.27	1.62	0.36	1.96	/	/	/	
Granulina clandestina (Brocchi, 1814)	1.93	0.46	2.30	1.53	0.35	1.86	/	/	1.42	
Haminoea hydatis (Linné, 1758)	/	/	/	1.05	0.42	1.28	1.15	0.52	1.43	
Haminoea navicula (Da Costa, 1778)	/	/	/	/	/	/	0.87	0.37	1.08	
Hexaplex trunculus (Linné, 1758)	0.90	0.38	1.07	/	/	/	0.97	0.45	1.21	
Jujubinus striatus depictus (Deshayes, 1835)	1.56	1.06	1.86	1.61	1.00	1.95	1.37	1.19	1.70	
Lamellaria perspicua (Linné, 1758)	1.08	0.33	1.29	/	/	/	0.82	0.31	1.02	
Mitra cornicula (Linné, 1758)	0.65	0.19	0.78	/	/	/	/	/	/	

Mitrella scripta (Linné, 1758)	1.45	0.48	1.73	/	/	/	1.11	0.45	1.37
Monophorus perversus (Linné, 1758)	1.53	0.67	1.82	1.32	0.57	1.61	1.26	0.72	1.57
Muricopsis cristata (Brocchi, 1814)	1.52	0.54	1.82	1.14	0.43	1.39	0.82	0.46	1.01
Ocinebrina aciculata (Lamarck, 1822)	1.28	0.58	1.52	1.45	0.45	1.76	1.53	0.65	1.89
Ocinebrina edwardsii (Payraudeau, 1826)	1.72	0.47	2.05	1.11	0.37	1.35	/	/	/
Odostomia carrozzai Van Aartsen, 1987	1.65	0.85	1.97	1.64	0.85	1.99	1.35	0.85	1.67
Odostomia eulimoides Hanley, 1844	/	/	/	1.64	0.76	1.99	1.46	0.80	1.81
Odostomia turrita Hanley, 1844	0.61	0.33	0.72	1.43	0.35	1.74	1.34	0.46	1.67
Omalogyra atomus (Philippi, 1841)	0.87	0.85	1.04	1.98	1.21	2.40	1.59	1.21	1.97
Parvioris microstoma (Brusina, 1864)	0.96	0.46	1.14	/	/	/	1.13	0.58	1.40
Pisinna glabrata (Von Muehlfeldt, 1824)	2.83	0.86	3.37	2.92	0.71	3.54	1.18	1.10	1.46
Pollia dorbignyi (Payraudeau, 1826)	0.77	0.27	0.92	/	/	/	/	/	/
Raphitoma linearis (Montagu, 1803)	/	/	/	/	/	/	0.76	0.37	0.94
Rissoella diaphana (Alder, 1848)	0.84	0.54	1.00	1.27	0.54	1.54	1.41	0.72	1.74
Rissoella inflata Locard, 1892	1.18	1.20	1.41	1.71	1.45	2.08	1.31	1.48	1.63
Scissurella costata D'Orbigny, 1824	1.64	0.55	1.95	/	/	/	1.25	0.51	1.55
Sinezona cingulata (Costa O.G., 1861)	1.67	1.13	1.99	1.85	1.15	2.24	1.35	1.05	1.68
Tricolia deshampsii Gofas, 1993	1.85	0.59	2.20	2.18	0.65	2.65	1.17	0.48	1.45
Tubbreva micrometrica (Aradas & Benoit, 1876)	/	/	/	/	/	/	0.85	0.46	1.06
Vexillum ebenus (Lamarck, 1811)	0.65	0.27	0.77	/	/	/	/	/	/
Vexillum savignyi (Payraudeau, 1826)	0.82	0.38	0.98	0.99	0.50	1.21	1.25	0.59	1.55
Vitreolina antiflexa Monterosato, 1884	1.46	0.63	1.74	/	/	/	1.01	0.54	1.26
Vitreolina philippi (De Rayneval & Ponzi, 1854)	1.44	0.97	1.72	1.53	0.92	1.86	1.56	1.03	1.93
BIVALVIA									
Arca noae (Linné, 1758)	2.04	1.10	2.44	2.15	0.89	2.61	1.41	0.90	1.75
Barbatia barbata (Linné, 1758)	/	/	/	/	/	/	0.84	0.33	1.04
Chama gryphoides Linné, 1758	1.62	0.54	1.94	1.20	0.53	1.46	1.12	0.50	1.39
Chlamys multistriata (Poli, 1795)	1.53	0.42	1.83	1.68	0.41	2.04	/	/	/
Glans trapezia (Linné, 1767)	0.68	0.26	0.81	/	/	/	/	/	/
Hiatella rugosa (Linné, 1767)	1.39	0.95	1.66	2.17	0.97	2.64	1.72	1.04	2.13
Kellia suborbicularis (Montagu, 1803)	0.72	0.33	0.86	/	/	/	0.80	0.41	0.99
Modiolarca subpicta (Cantraine, 1835)	1.83	0.50	2.18	1.31	0.38	1.59	/	/	/
Modiolus barbatus (Linné, 1758)	1.16	0.50	1.38	1.40	0.64	1.70	1.18	0.59	1.47
Musculus costulatus (Risso, 1826)	1.22	0.87	1.45	1.61	1.10	1.96	1.44	1.14	1.79
Pseudochama gryphina (Lamarck, 1819)	0.78	0.26	0.93	/	/	/	0.60	0.25	0.74
Striarca lactea (Linné, 1758)	0.72	0.18	0.86	/	/	/	/	/	/

the expected means, nine values were equal to mean, thirtyfour values were lower than the mean, but no values fell outside the simulated probability funnel. These plots also showed that sample-points of shell size class and depth level were randomly arranged, confirming the taxocommunity as independent of these factors. The bivariate distribution Δ^+/Λ^+ (Fig. 4E) of all basibionts, compared to the simulated m-species contours, showed that the mollusc epizoic species pool was mainly distributed from the lowcentre to low-left of the probability area. Eleven specimens (one small, seven medium, three large) fell outside the contour of 15-species, whilst most of the sampled Pinna nobilis fell between the contour of 15 to 30/50 typical for soft bottom molluscs. A wide scattering of taxonomic distinctness contrasted with a reduced dispersion of Λ^+ values; this latter index in particular was below the simulated distribution. All three size classes showed a great variation in terms of Δ^+ , whilst the observed scattering of Λ+ was mainly due to medium sized basibionts. In a comparison of the mollusc fauna recorded in the regional checklist sixteen species and two sub species found on the *Pinna nobilis* shells in this study constituted new records for the Straits of Messina. The bivariate plot (Fig. 4F) showed a good level of representativeness of observed taxonomic richness associated to the *Pinna* with respect to the regional species pool, with most of the basibionts falling into the central area of the simulation. Since many species of the regional list are characteristic of hard bottom habitats, widespread in the Strait of Messina, the consequent taxonomic spectrum had broadened and included most of the microgastropods which also dwell on the *P. nobilis*.

Functional groups

The RELATE procedure (Table 2) highlighted an epizoic assemblage mainly characterized by microphagous

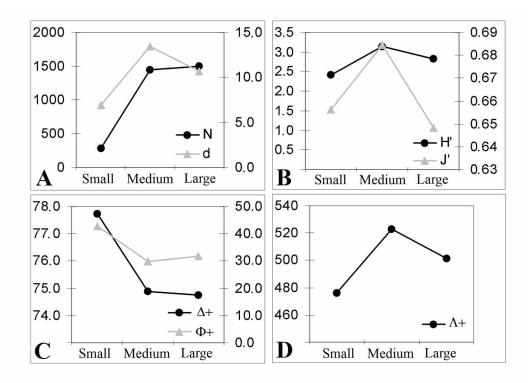


Figure 3. Differential trends of diversity and taxonomic relatedness indices, calculated on mollusc epifauna, cumulated for every basibiont, in each size class. **A.** Abundance N and Margalef's richness d. **B.** Shannon-Wiener's biodiversity H' and Pielou's evenness J'. **C.** Average taxonomic distinctness Δ^+ and average phylogenetic diversity Φ^+ . **D.** Variation in taxonomic distinctness Δ^+ . Figures **A, B** and **D** show the higher biodiversity and variation of the taxonomic tree in medium sized *Pinna*, with respect to the higher relatedness indices of small sized *Pinna* in the figure **C**.

Figure 3. Différents indices de diversité et de relation taxonomique, calculés sur la totalité de l'épifaune à mollusques pour chaque basibionte, dans chaque classe de taille. A. Abondance N et richesse de Margalef d. B. Biodiversité de Shannon-Wiener H' et équitabilité de Pielou J'. C. Spécificité taxonomique moyenne Δ^+ et diversité phylogénétique moyenne Φ^+ . D. Variation de la spécificité taxonomique Δ^+ . Les figures A, B et D montrent la plus grande biodiversité et variation taxonomique dans les *Pinna* des dimensions intermédiaires, par rapport aux plus forts indices dans les *Pinna* de petites taille de la figure C.

Table 2. Functional groups analysis of total mollusc fauna associated to *Pinna nobilis* and of three most representative subsets in terms of Spearrman's rank correlation ($\rho > 0.20$). Matrix of each guild has been compared to both the total species matrix (RELATE) and to the three best-matching subsets, which stepwise algorithm (BVSTEP) has been selected. Number of species are shown in brackets. See text for explanation of data. * p < 5%; *** p < 1%; **** p < 0.1%; n.d., not detectable

Tableau 2. Analyse des groupes fonctionnels de la faune entière des mollusques associés à *Pinna nobilis* et des trois sous-groupes plus représentatifs, basées sur la corrélation du rang de Spearrman ($\rho > 0.20$). La matrice de chaque groupe a été comparée avec la matrice totale des espèces (RELATE) et avec les trois sous-groupes les mieux corrélés (BVSTEP). Le nombre d'espèces est donné entre parenthèses. Voir le texte pour les explications. * p < 5%. ** p < 1%. *** p < 0.1%. n.d., non décelable.

Non-parametric									
rank correlation, ρ	Browsers	Omnivores	Carnivores	Parasites	Suspension feeders	Motile	Sessile		
Total epifauna (120)	(24)	(15)	(42)	(17)	(22)	(101)	(19)		
[RELATE]	0.70***	0.67***	0.30***	0.24**	0.26***	0.98***	0.26***		
1st subset (14)	(3)	(3)	(2)	(3)	(3)	(11)	(3)		
[BVSTEP/RELATE]	0.69***	0.64***	0.24**	0.18*	0.18*	0.98***	0.18*		
2 nd subset (27)	(5)	(3)	(8)	(6)	(5)	(23)	(4)		
[BVSTEP/RELATE]	0.67***	0.45***	0.31***	0.36***	0.35***	0.93***	0.36***		
3rd subset (21)	(7)	(1)	(8)	(0)	(5)	(17)	(21)		
[BVSTEP/RELATE]	0.87***	0.08	0.52***	n.d.	0.22***	0.99***	0.23***		

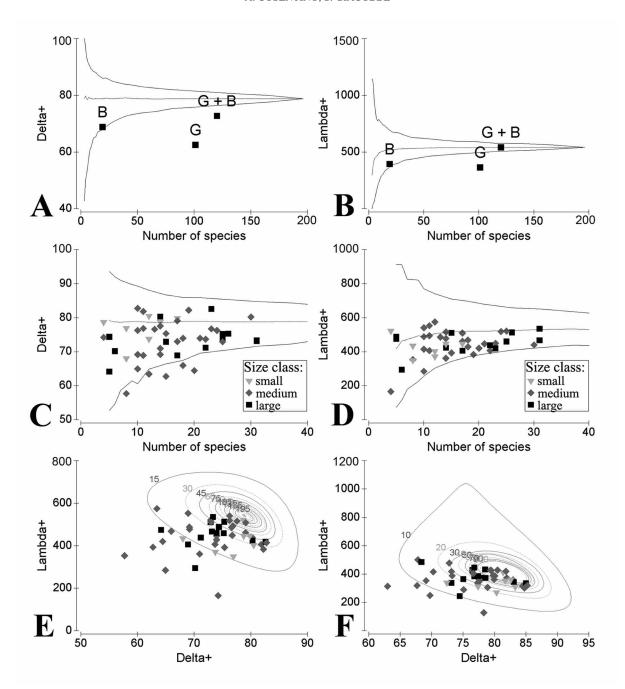


Figure 4. TAXDTEST analysis of the epizoic mollusc assemblage compared to both local soft-bottom species pool (**A-E**) and regional inventory of molluscs up to date recorded in the Strait of Messina (**F**). **A-B**. Funnel plots of taxonomic distinctness and variation in taxonomic distinctness assessed separately for bivalves (B), gastropods (G) and for both. **C-D**. Funnel plots of the same indices assessed for every individual of *Pinna nobilis*. **E**. Δ^+/Δ^+ ellipse plot of investigated epifauna and simulated subsets from 15 to 110 species living in the same habitat of *Pinna*. **F**. Δ^+/Δ^+ ellipse plot of investigated epifauna and simulated subsets from 10 to 720 recorded species (γ-diversity).

Figure 4. Analyse taxonomique du peuplement de mollusques épizoobiontes (TAXDTEST) entre la faune vivant localement dans les fonds meubles (A-E) et l'inventaire régional des tous les mollusques signalés jusqu'à présent dans le Détroit de Messine (F). A-B. Graphiques à entonnoir des indices de la spécificité taxonomique et de la variation de la spécificité taxonomique, calculés séparément pour les bivalves, les gastéropodes et pour les deux. C-D. Graphiques à entonnoir des mêmes indices calculés pour chaque individu de *Pinna nobilis*. E. Graphique à ellipse Δ^+/Λ^+ du peuplement épizoobiontes avec simulations de 15 à 110 espèces vivant dans le même biotope de *Pinna*. F. Graphique à ellipse Δ^+/Λ^+ du peuplement épizoobiontes avec simulations de 10 à 720 espèces signalées (γ-diversité).

browsers (Spearman's ρ = 0.70, p < 0.001) and omnivores (ρ = 0.67, p < 0.001), followed by macrophagous carnivores (Ca: ρ = 0.30, p < 0.001), microphagous suspension/filter feeders (ρ = 0.26, p < 0.001) and parasites (ρ = 0.24, p < 0.01). Motile species (ρ = 0.98, p < 0.001) prevailed on sessile species (ρ = 0.26, p < 0.001).

The BVSTEP (BIO-BIO) analysis carried out on total epifauna, selected a first subset of fourteen species (Sperman's $\rho>0.95$), excluding a second best matching subset of twenty-seven epizoobionts ($\rho>0.5$), and a third subset of twenty-one species, with a notable breakdown of correlation ($\rho>0.2$). All three subsets were characterized by motile browsers and primary consumers; motile omnivores represented the second main guild of the first two subsets, whereas their presence was negligible in the third. Active predators were not abundant, although they were constantly present as much in the total assemblage as in the single subsets. Ectoparasites were less represented, whilst sessile filter feeders showed low rank correlation compared to the total assemblage and to the first subset, and showed a higher correlation to the other two subsets.

Discussion

The Strait of Messina connects the western and eastern Mediterranean basins. The area is characterised by a peculiar tidal-hydrodynamic and sedimentary environment (Colantoni, 1995; Mosetti, 1995) and hosts a wide variety of soft as well as hard-bottom patchy biotopes in a narrow geographic area (Di Geronimo & Giacobbe, 1987), which support a high level of floristic and faunistic biodiversity (SIBM checklist, 2006). The megabenthic bivalve Pinna nobilis, which dwells in photophilous sublittoral softbottoms, significantly contributes to the colonization of hard substrates, behaving as an "erect isle" surrounded by sand and gravel extents (Wahl, 1989; Wahl & Mark, 1999). Due to the prominent role of the tidal and upwelling currents in the Strait, which permit deeper coenosis to distribute at shallower depths (Giaccone, 1987), a close relationship between epizoic assemblage and depth is absent. Furthermore, young basibionts of *P. nobilis* are soon colonized by a taxonomically differentiated assemblage while a greater faunistic similarity characterizes the medium and large sized shells. Some groups of microgastropods, such as the Gibberula and Chrysallida genera or the Eulimidae and Columbellidae families, are overrepresented compared to other taxa in the medium sized basibionts in terms of multi-specific radiation, and notably contribute to variation in the taxonomic tree. In contrast, the higher evenness of the taxonomic structure in the younger shells is a consequence of immature assemblages, mainly caused by physical/environmental constraints and by the shortage of sufficient algal coverage. This leads to a

reduced number of species/individuals which, however, shows a diversified (high Δ^+) and balanced (low Λ^+) taxonomic structure. Congeneric species, in particular within the radiated taxa such as Rissoidae (Alvania genus), Cingulopsidae (Eatonina, Tubbreva), Cerithiopsidae (Cerithiopsis), Costellariidae (Vexillum), Conoidea (Turridae and Conidae families), Piramidellidae (Odostomia genus), are less frequent compared to other taxa such as Trochidae (Jujubinus, Gibbula) or to the Chrysallida and Vitreolina genera. Opistobranchia, which are tied to sponges and hydrozoans, are scanty, whilst pelecypods are equally represented with the exception of Noetidae (Striarca) and Carditidae (Cardita, Glans, Venericardia). Diversely, in the medium sized and largest basibionts, the mollusc fauna shows a clear increase of taxa which is higher than the generic level. This is also favoured by the constitution of a rich epizoobiontic coverage (canopy of Phaeophyceae, incrusting Porifera, Hydrozoa, Bryozoa) which supports species with specialized trophism (Opistobranchia, some ectoparasitic taxa). The advanced successional sere determines the prevalence of biotic constraints which successively reduce some of the less frequent epibiontic molluscs in these shells, producing a tendential reduction of the taxonomic variation. This is likely in the case of the Bittium, Chrysallida, Arca and Striarca genera and in the Columbellidae, Eulimidae, Marginellidae, Philinidae and Retusidae families, even though some other genera show a moderate taxonomic increase (Alvania, Monophorus, Tubbreva, Lima, Venericardia). These different patterns confirm the hypothesis of a tendential "simplification" of the taxonomic structure, either due to an early associated assemblage (physically-regulated) or related to an advanced successional stage (biologically-regulated).

Regarding functional guilds, numerous species are necessary to characterize the whole ensemble (sensu Fauth et al., 1996); many of the observed epizoic molluscs perform almost the same feeding strategy (motile specialized primary consumers and microphagous generalistic browsers), whereas sessile suspension/filter feeders (bivalves) are less representative of the associated ensemble. This data confirms our preliminary results for part of the sampled Pinna population (Cosentino & Giacobbe, 2007) permitting us to generalize towards associated mollusc fauna the "sorting effect" exerted by the basibiont P. nobilis, whose shell may facilitate the settlement of an enriched ephemeral phytocoenosis. The algal covering provides niche-space for browsers and omnivores, but the active filtering of the Pinna in a highly hydrodynamic environment such as the Strait, could monopolize the trophic source, to the detriment of epizoic sessile bivalves. It is worth noting that in more sheltered habitats along the Croatian (Šiletić & Peharda, 2003), Sicilian, Sardinian (Giacobbe pers. ob.) and Tunisian coasts (Rabaoui et al., submitted paper), epibiontic fauna of *P. nobilis* is often dominated by large filter feeder bivalves such as *Arca noae*, *Modiolus barbatus* (Linné, 1758), *Ostrea edulis* (Linné, 1758), *Pinctada radiata* (Leach, 1814), as well as big sponges and colonial Ascidians. Sessile filter feeders are therefore likely to be prevalent in an environment with increased carrying capacity and where the food supply is virtually unlimited, as discussed by de Montaudouin et al. (1999) for the oyster *Crassostrea gigas* (Thunberg, 1793) and its epizoic gastropod *Crepidula fornicata* (Linné, 1758).

The observed mollusc assemblage is rich in small sized phylogenetically related taxa (i.e. Rissooidea, Cerithioidea, Ptenoglossa, Trochoidea and Heterostropha) with a potentially similar adaptive path. Many of these taxa constitute an ensemble of species with overlapping niches. The resulting biodiversity refers to the hypothesis of coexisting and functionally redundant species within the community (Lawton & Brown, 1993). However, the variability provided on a small spatial scale (roughness and shell scars, microhabitat heterogeneity) as well as on a temporal scale (seasonality tied to phytocoenosis) may avoid competitive exclusion (Mc Arthur & Levins, 1967) and lend support to the alternative hypothesis of functional complementarity and species coexistence on a local scale (Loreau & Mouquet, 1999; Loreau & Hector, 2001; Mouquet & Loreau, 2002; Loreau, 2004). The shell surface of the Pinna represents a particular hard bottom habitat and hosts a specialized epifauna particularly from the Gastropoda class of which a significant number of species are present. However, Scaphopoda is absent on Pinna nobilis as well as in its habitat, and Polyplacophora is not found on P. nobilis. In contrast, the associated Pelecypoda also include soft bottom species, which may be sustained by the presence and accumulation of detritus.

The whole epizoic assemblage seems to be a good surrogate of taxonomic diversity on a regional scale, because the biogeographic district of the Strait of Messina comprises other shallow and deep habitats of both hard and soft bottom (Warwick & Light, 2002). From this perspective, active or passive immigration from the regional species pool (biogeographic source) and also from nearby basibionts (local source) may be the key-phenomenon to feed and maintain such a high level of mollusc diversity (Loreau & Mouquet, 1999; Schejter & Bremec, 2007). The secondary substrate provided by *P. nobilis* is therefore able to enrich the local contingent of species, and may constitute a "peculiar" emerging hard substrate which supports a taxonomically and functionally specialized taxocommunity.

The medium sized basibionts represent a potentially higher source of biodiversity. They are richer in terms of

diversity/evenness than juvenile individuals and less "simplified" in terms of taxonomic relatedness than larger specimens. Individuals of intermediate size are the best target for protection, through the constitution of protected bottom surfaces which host patches of *P. nobilis*. Current investigations carried out in the same area (Giacobbe, unpublished data) allowed us to ascertain an average density of P. nobilis of not less than 7 ind.100 m⁻², with a proportion of 0.1:0.6:0.3 for small, medium and large individuals, respectively. If we infer the mean density of medium sized specimens is equal to 4.20 ind.100 m⁻², and consider that the lowest number of basibionts capable of supporting a representative mollusc epifauna is equal to almost thirty specimens, we should infer a unitary patch surface of not less than 700 m² of soft bottom to guarantee the tenability of enough medium sized specimens. The employment of a more sophisticated methodology of population census (Katsanevakis, 2007) would allow a more accurate assessment of this target species, with particular interest in each size class.

Regarding the related *Atrina rigida*, Munguia (2004) has demonstrated how the "species-sorting" mainly affects the motile epifauna, whilst the "priority effect" is more implicated in the distribution of sessile taxa. The protection of a number of these *Pinna*-patches would positively influence the maintenance of taxonomic variability of the epizoic meta-assemblage and may constitute a regional network which supports the genetic flux of associated species. The real "isle of biodiversity" should not therefore be considered the basibiont alone, but rather the whole of its consistent population together with the minimal surface of sandy biotope which supports the basibiontic species as well as its associated biota.

In conclusion, the epizoic mollusc taxocommunity, associated to the megafaunal bivalve Pinna nobilis, revealed a high biodiversity both in terms of specific richness and of taxonomic relatedness, which was in contrast to the general monotony of its trophic-functional structure. The taxonomic distinctness and the related variation index are affected finely by size factor. These basibiontic bivalves increase the local spatial heterogeneity and favour the settlement of mollusc assemblages which are typologically and functionally specialized with respect to a generic sublittoral hard bottom covered by photophilous algae. Juvenile individuals of Pinna nobilis hosted an early and less structured but still diversified assemblage, whereas large sized individuals showed an enriched mollusc epifauna, which was also more uneven and "simplified" by biotic constraints. On the other hand, medium sized shells represented a trade-off between the two stages, since they hosted a rich and well structured assemblage which was more variable in terms of taxonomic relatedness. Due to the peculiar role of P. nobilis as a potential "isle" and "source" of biodiversity on the local spatial scale as well as on the wider regional scale, the authors proposed the medium sized basibionts as a particular target for protection, within the general aim of preserving the Mediterranean populations of this endangered species.

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