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COMUNITÀ SUPRABENTONICHE E ZOOPLANCTONICHE PROFONDE DI DUE CANYON SOTTOMARINI DEL SUD ITALIA

DEEP-SEA SUPRABENTHIC AND ZOOPLANKTONIC COMMUNITIES OF TWO SUB-MARINE CANYONS OF SOUTHERN ITALY

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Questo lavoro si è prefisso come obiettivo lo studio della biodiversità delle comunità di suprabenthos e zooplancton profondo lungo due canyon sottomarini del sud Italia (mar Ionio): il canyon di Amendolara ed il canyon di Squillace. Questi due canyon sono attivi dal punto di vista idrogeologico e, pertanto, contribuiscono significativamente all'apporto di sostanza organica di origine terrestre nelle profondità marine. I canyon di Amendolara e Squillace sono anche siti in cui grava un'intensa attività umana, e ciò li rende particolarmente vulnerabili all'impatto antropico.

I campioni analizzati in questo studio, sono stati raccolti durante la campagna oceanografica Anomcity, nel Giugno 2016, a profondità di circa 400 m, 600 m, 1500 m, nel caso del suprabenthos, per ciascun canyon. I campioni di zooplancton sono stati raccolti, invece, in prossimità di queste profondità ma sempre in corrispondenza del *Deep Scattering Layer*, localizzato a circa 500 m di profondità. Il suprabenthos è stato campionato con una slitta Macer-Giroq (maglia della rete da 0,5 mm), mentre lo zooplancton usando un retino di tipo Nansen (maglia da 0,2 mm). Gli animali sono stati indentificati al livello

tassonomico più basso possibile, contati per stimare l'abbondanza e pesati (peso umido) per stimare la biomassa.

In seguito, per le specie più abbondanti, si è proceduto con l'analisi degli isotopi stabili del carbonio e dell'azoto ($\delta^{13}C$, $\delta^{15}N$) al fine di studiare il funzionamento delle reti trofiche marine profonde suprabentoniche e zooplanctoniche.

Nel canyon di Amendolara sono stati contati ed indentificati 1650 animali suprabentonici, con prevalenza di anfipodi (*Rhachotropis* spp. tra i generi più abbondanti), e 2770 animali zooplanctonici, con prevalenza di copepodi calanoidi (*Calanus helgolandicus*, *Euchaeta* spp., *Pleuromamma gracilis*, ecc.). Nel canyon di Squillace sono stati contanti ed identificati 910 animali suprabentonici, con prevalenza di anfipodi, e 1978 animali zooplanctonici, con prevalenza di copepodi calanoidi.

Il suprabenthos ha mostrato, in generale lungo entrambi i canyon, un aumento sia delle abbondanze che della biodiversità scendendo progressivamente verso la batimetria maggiore (1500 m). Lo zooplancton ha mostrato un trend opposto, con abbondanze e biodiversità maggiori in corrispodondenza delle profondità minori dei due canyon (tra 400 e 600 m). La biodiversità sia del suprabenthos che dello zooplancton ha mostrato valori maggiori lungo il canyon di Amendolara rispetto a quello di Squillace (in Amendolara la concentrazione di

Clorofilla *a* (Chl*a*) ottenuta da dati satellitari, e usata come proxy della produzione primaria, è risultata essere maggiore rispetto a quella di Squillace). Tuttavia, il test PERMANOVA ha messo in evidenza che le differenze tassonomiche riscontrate tra i due canyon non sono significative.

Lo studio delle reti trofiche ha messo in evidenza, nel caso del suprabenthos, la presenza di un elevato numero di specie detritivore e di diverse specie carnivore. Le specie carnivore analizzate sono state gli anfipodi *Rhachotropis* spp. e i decapodi *Richardina fredericii* e *Aristaeus antennatus*. L'elevata eterogeneità tassonomica e trofica del suprabenthos è giustificata dalla notevole quantità di detrito vegetale trascinato dal canyon alle diverse profondità. Lo zooplancton ha mostrato una netta prevalenza di carnivori, riscontrabili sia tra i copepodi (es. *Euchaeta* spp., *Heterorhabdus papilliger*) che tra gli anfipodi iperidi (es. *Streetsia challengeri*, *Primno macropa*). Le notevoli abbondanze di zooplancton carnivoro sono state riscontrate in corrispondenza dei siti meno profondi dei due canyon (400-600 m) in cui si è registrata una maggiore concentrazione di Chl*a*. La presenza di elevate concentrazioni di fitodetrito ha permesso di dedurre la possibile presenza, in corrispondenza di questi siti, di piccoli organismi erbivori predati dallo zooplancton carnivoro; portando ad avere abbondanze e biodiversità maggiori dove queste prede sono maggiormente concentrate.

Le comunità suprabenthoniche, appartenenti al *Benthic Boundary Layer* (BBL) sono, quindi, maggiormente condizionate dall'azione del canyon che, grazie al trasporto di sostanza organica, rende tali comunità più eterogenee sia sul profilo tassonomico che trofico. Le dinamiche delle comunità zooplanctoniche, appartenenti al *Deep Scattering Layer* (DSL), sono invece maggiormente condizionate dall'input di materia organica proveniente dalla superficie.

Chapter one

INTRODUCTION

1.1 The deep Mediterranean sea

Deep marine ecosystems occupy the largest areas of the marine environment, which includes waters and sediments below approximately 200 m depth (Danovaro et al., 2010). They represent the world's largest biome, covering more than 65% of the Earth's surface and including more than 95% of the global biosphere (Danovaro et al., 2010).

The geology of deep-sea floor is complex. It includes regions characterized by complex sedimentological and structural features: continental slopes, submarine canyons, base-of-slope deposits bathyal or basin plains with abundant deposits of hemipelagic and turbidity muds (Danovaro et al., 2010).

The Mediterranean Sea is traditionally one of the most intensively investigated areas of the world in both terrestrial and coastal marine biodiversity. Nevertheless its deep-sea fauna has not yet been satisfactorily studied compared to the other regions of the world (Danovaro et al., 2010).

The Mediterranean Sea is divided into western and central-eastern basins, separated by the Strait of Sicily (Danovaro et al., 2010). The eastern basin is considered to be one of the most oligotrophic areas of the world (Psarra et al.,

2000; Tselepides et al., 2000) (**Fig. 1.1.a).**

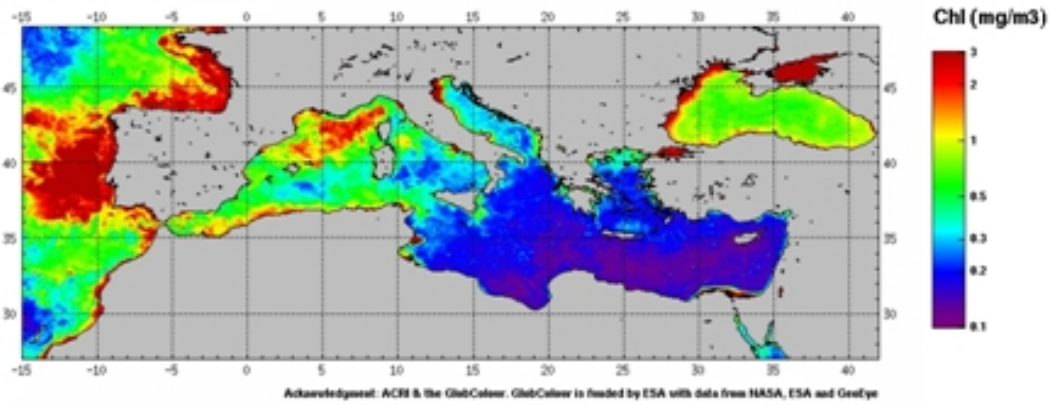

Fig. 1.1.a: GlobColour Weekly Chlorophyll Product (March 2009 - from a high concentration of 3 mg/m^3 in red to 0.1 mg in purple), (image courtesy of ACRI-ST).

The Mediterranean exhibits low concentrations of the potentially limiting organic nutrients (such as proteins and lipids) that significantly decline with increasing distance from the coast and depth within the sediment (Danovaro et al., 2010).

In the highly ologotrophic deep envrironments of the Mediterranean, the role of Bacteria is essential, for example through decomposition of particulate organic matter derived from the upper layers (Danovaro et al., 1993).

The average depth of the Mediterranean basin is about 1,450 m, much shallower than the average depth of the world oceans (about 3,850 m) (Danovaro et al., 2010). This fact has several implications for the deep-water turnover (roughly 50 years) and the vulnerability to climate change and deep-water warming (Danovaro et al., 2010) (**Fig. 1.1.b**).

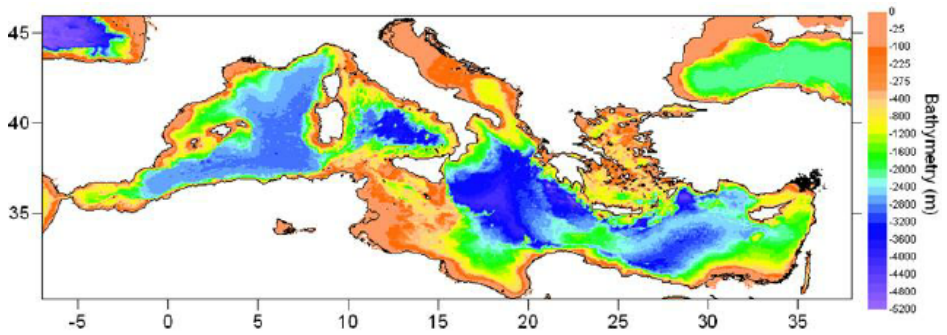

Fig. 1.1.b: Map of the Mediterranean showing main bathymetries (website: *researchgate.net*).

Like all temperate seas, the Mediterranean Sea is affected by seasonality. During late spring and summer, the whole Western Mediterranean is strongly stratified, the seasonal thermocline being 20-50 m deep. In winter, the water column is more homogeneous, especially in the open sea. High oxygen concentrations are present across the water column down to the seafloor (Stanley and Wezel, 1985).

In terms of hydrological features, the Mediterranean Sea is characterized by: 1) high homeothermy from about 300-500 m to the bottom, and bottom temperatures of about 12.8°C to 13.5°C in the western basin and 13.5°C to 15.5°C in the eastern basin (compared to Atlantic Ocean, the Mediterrean Sea is not characterized by thermal boundaries, and the temperature decreases with depth), (Emig and Geistdoerfer 2004); 2) high salinity, from roughly 38 to 39.5 by the stratification of the water column; 3) limited freshwater inputs (the freshwater deficit is equivalent to about 0.5–0.9 m y^{-1}, compensated by the

Atlantic inflow of surface water); 4) a microtidal regime; 5) high oxygen concentrations; 6) oligotrophic conditions, with strong energetic gradients and low nutrient concentrations in the eastern basin (Danovaro et al., 1999).

Regarding deep and bottom currents, these are largely unexplored, but episodic intensification of current speed up to 1 m s^{-1} has been documented (Canals et al., 2006).

The Mediterranean basin is a hot spot of biodiversity with a high percentage of endemic species (Myers et al., 2000), and hosts more than 7.5% of global biodiversity (Bianchi and Morri, 2000).

Data on deep-sea assemblages are still limited (Danovaro et al., 2010; WWF/IUCN, 2004; Ramirez-Llorda et al., 2009).

During the second half of the twentieth century, little deep-sea sampling was conducted in the deep Mediterranean, providing scattered information on macrofauna (Danovaro et al., 2010; Pèrès et al., 1958; Tchukhtchin, 1964; Vamvakas, 1970).

The biodiversity of fauna associated with hot spot ecosystems (like seamounts, cold seeps, and deep corals) has been investigated only in the last three decades (Danovaro et al., 2010; Galil and Zibrowius, 1998; Tursi et al., 2004; Taviani et al., 2005; Taviani, Remia et al., 2005; Freiwald et al., 2009).

1.2 The Benthic Boundary Layer fauna (suprabenthos)

The Benthic Boundary Layer (BBL) is a transitional zone (ecotone or ecocline) between pelagic and benthic domains (Dauvin and Vallet, 2006). An interesting ecological component of the BBL is represented by suprabenthos.

The Suprabenthos fauna, or BBL macrofauna, consists of a set of small-sized animals (generally around 500 μm in size) predominantly crustaceans, living immediately above the seabed, which have good swimming ability and perform, with varying amplitude, intensity and regularity, seasonal or daily vertical migrations above the seabed (Brunel et al., 1978).

Some authors use two different terms to describe subraprabenthic organisms: *holohyperbentos* which rapresents the permanent suprabenthos and *merohyperbenthos* consisting of non-permanent suprabenthos, that partially overlaps in terms of taxon composition with macro-mesozooplankton (Mees and Jones, 1997; Cartes et al., 2008a,b,c).

The animals that belong to this ecological group are part of different taxa: amphipods, cumaceans, mysids, isopods etc. (= *Peracarida*, which constitute the permanent suprabenthos); euphausiids, natantian decapods (= *Eucarida*, also called *near-bottom zooplankton,* which thanks to vertical or ontogenetic migrations, have more probability to be related with the water-sediment interface; Brunel et al., 1978) (**Fig. 1.2**).

The variability of suprabenthos is probably due to changes in sediment type

associated to hydrodynamism (Cartes et al., 2003), or the arrival of fresh organic matter to the bottom (Cartes et al., 2002; Rochoux et al., 2004 a,b).

Food supply is generally considered the main limiting factor in deep sea communities (Gage and Tyler, 1991). Consequently marine snow constitutes a valuable food resource of deep-sea microbes, metazoans and bathyal detritivores (Smith et al., 1996). Marine snow is a flocculent material composed by aggregated detritus (e.g. exopolymers, mucus, phytoplankton, plankton exoskeletons, faecal pellets and bacteria: Fanelli et al., 2013). In particular periodic phytodetritus deposition, associated with marine snow, is an important source of food that reaches the deep-sea bottom (vertical flux: Richoux et al., 2004).

Nevertheless, there has been little attempt to assess the diversity of source materials consumed by organisms in deep-sea ecosystems (Fanelli et al., 2010a). Communities in proximity to canyon systems, where strong advective fluxes channeling terrestrial material or marine macrophyte remains to the deep-seafloor are frequent, may derive food from different sources (Vatter and Dayton, 1998, 1999).

The information about the diet of suprabenthic animals is limited (Svavarsson et al., 1993; Elizalde et al., 1999; Cartes et al., 2002), but their feeding habits appear to be highly diversified. They belong to different “trophic groups” (carnivores, herbivorous, omnivorous etc; Fanelli et al. 2009a,b).

Suprabenthic crustaceans (e.g. amphipods and cumaceans), occupy 2–3 trophic levels with some species exploiting detritus and others being carnivores on meiofauna and small zooplankton (Madurell et al., 2008; Fanelli et al., 2009a,b). As an example, considering amphipods, *Lyssianassidae* are generally considered to be scavengers (Sainte-Maire, 1992), while *Eusiridae* appear to be carnivores because they have large gnathopods (Enequist, 1949) and contain animal lipid biomarkers (Nyssen et al., 2005).

The majority of species are reported to be deposit feeders, ingesting and reworking great amounts of sediments. Consequently, competition for food is expected to be extremely high (Fanelli et al., 2011), consequently in a severely food-limited system the most common feeding strategy will be aimed at reducing, as much as possible the competition, or even to eliminate it, through the consumption of different food sources (Jumars et al., 1990).

The main adaptive biological features of the permanent suprabenthos consists of the direct developement of embryos in marsupial bags (called oosteguites), developed by adult females of peracarid crustaceans (Fanelli, 2007).

The interest towards the study of this fauna is increasing in recent years. In fact, the knowledge of this type of fauna and their dynamics is still scarce (Cartes and Sorbe, 1999a,b; Cartes et al., 2002, Fanelli et al., 2011a,b), sostantially because suprabenthos was not properly sampled in previous studies on deep-sea trophic webs (Iken et al., 2001). In fact, suprabenthos is not

quantitatively sampled with box-corers (Cartes et al., 2011). However, these organisms are subject to gradients similar to those affecting benthos. Assemblage composition of deep-sea suprabenthos has mainly been related to depth (e.g. Western Mediterranean: Bellan-Santini, 1990; Cartes and Sorbe, 1993, 1997, 1999a; Cartes et al., 2003; Atlantic: Marques and Bellan-Santini, 1987; Brandt, 1995; Dauvin and Sorbe, 1995; Sorbe, 1999).

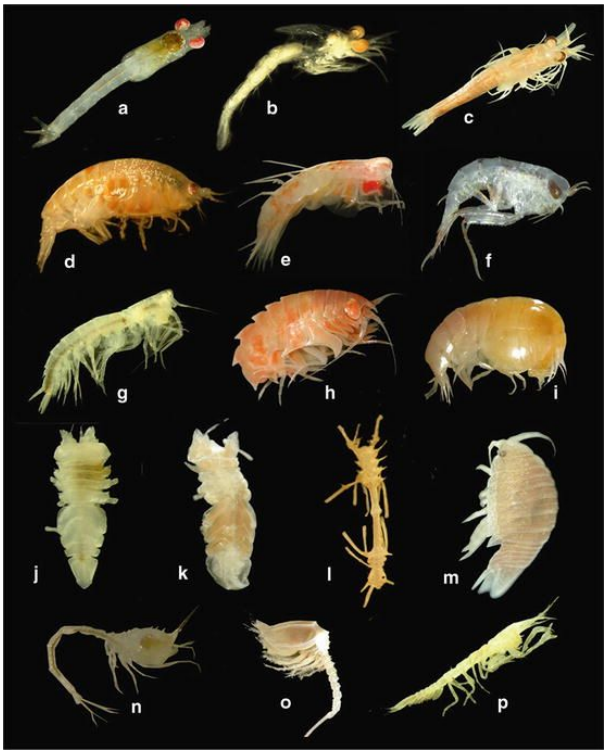

Fig. 1.2: Rapresentation of suprabenthos, an ecological assemblage composed by different taxa: mysids (a,b,c), hyperiid amphipods (d,e,f), gammariid anfipods (g,h,i), isopods (j,k,l,m) cumaceans (n,o), tanaids (p), (website: *link.springer.com*)

1.3 Suprabenthos and its role in the deep-sea food webs

Despite the lack of knowledge about suprabenthic communities, several studies have revealed that it constitutes the base of the diet of several littoral and bathyal animals, including demersal top predators (e.g. flatfish: Wildish et al, 1992, Fanelli et al., 2009; hake: Cartes et al., 2004c; the deep sea red shrimp *Aristeus antennatus*: Cartes, 1994a; Sardà and Cartes, 1997, *Merluccius merluccius*: Cartes et al., 2001; and other demersal fishes and epibenthic crustaceans: Madurell et al., 2008; Fanelli and Cartes, 2010), particularly for juveniles. Therefore suprabenthic species play a crucial role in food web dynamics.

In the Mediterranean, deep-sea fishes, especially those living below 1000 m (Carassòn and Cartes, 2002), were found to usually consume suprabenthos (mysids, cumaceans and amphipods; Cartes et al, 1994b, Sardà and Cartes, 1994; Bozzano et al., 1997). Still, juveniles of deep fishes and aldult decapods (Cartes et al., 2008a) consume merohyperbenthos-zooplankton (e.g. other decapods, small myctophids; Cartes et al., 2004c).

Suprabenthic communities are involved in the ecological process termed *bentho-pelagic coupling:* they connect the sea bottom with the water column, being preyed by bathyal benthic and pelagic predators, determinig the energy flow in deep waters (secondary productivity flux) (**Fig.1.3**).

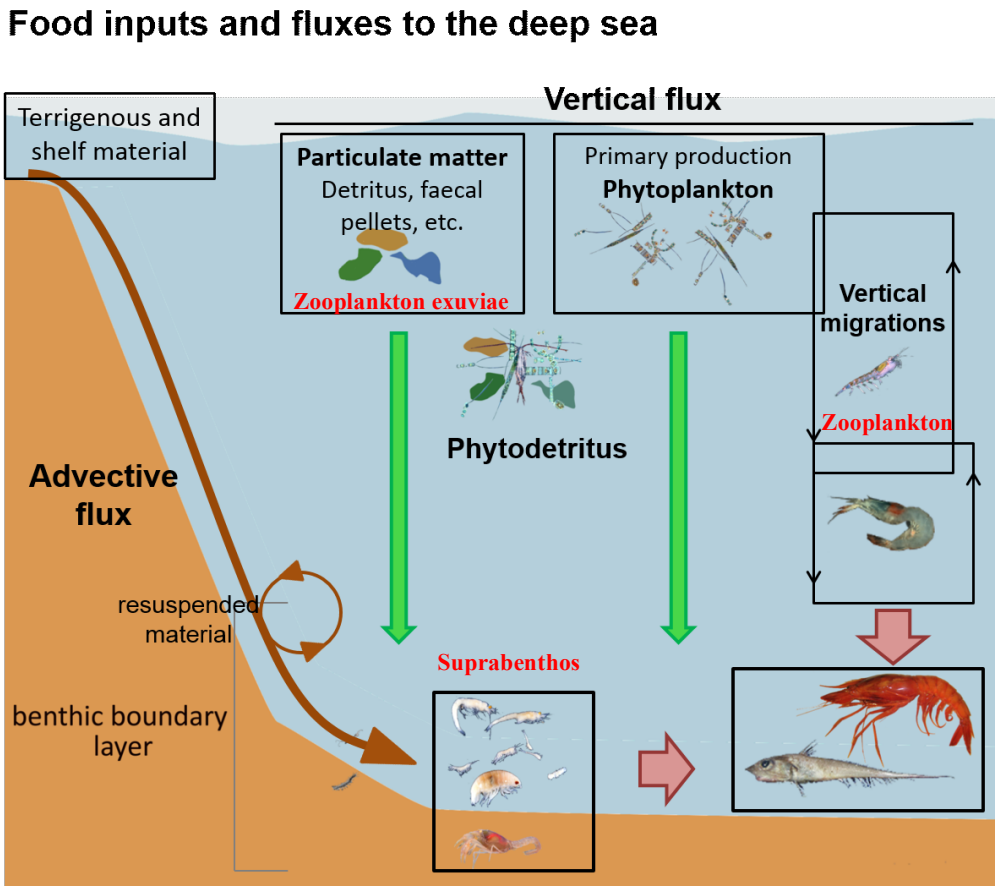

Fig. 1.3: Schematic rapresentation of deep-sea trophic web functioning (V. Papiol, PhD Thesis)

For these reasons, suprabenthic animals are considered key *taxa* in the near bottom ecosystems (Mees and Jones, 1997), and their knowladge acquires a particular importance in the study of trophic webs (Madurell et al., 2008). In addition, deep suprabenthos shows a higher P/B ratios compared to those of benthos (Fanelli, 2007). This is the reason why it is essential to take into account suprabenthos to understand trophodynamic processes in deep-sea ecosystems.

1.4 The deep-sea macro- and mesozooplankton

The zooplankton is a complex group of marine animals, characterized by organisms belonging to different size classes: microzooplankton (20-200 μm); mesozooplankton (0.2-2.0 cm); macrozooplankton (2.0-20 cm); megazooplancton (> 20 cm), (Danovaro, 2013).

In this study we focused on meso- and macrozooplankton collected using a WP2 net of 200 μm mesh size (see details in Material and methods section) (**Fig. 1.4**).

The mesozooplankton is composed by 90% of copepods (calanoids and cyclopoids), while the macrozooplakton by euphausiids, little mesopelagic fishes, chaetognaths etc. (Danovaro, 2013).

The information on some components of deep-sea zooplankton is still very scarce (Burd et al., 2002; Koppelmann et al., 2003; Tamelander et al., 2008), because they are more difficult to be collected compared to other components such as the deep-sea benthos (O'Dor et al., 2009).

This difficulty is largely due to the usage of different sampling gears, which do not allow to have comparable data, such as Bongos, IKMT, but also to differences in the mesh-size used. Still the different sampling design and variation in sampling design adopted can determine such difficulty of data comparison (Cartes et al., 2010). A common pattern observed in all studies, concerning deep-sea zooplankton, is the maximum biomass regularly reported

in spring (Sardou et al., 1996), sometimes along the continental shelf edge in association with hydrographic fronts (Sabatès et al., 1989) which can act as nursery areas for some zooplankton stages (Boucher et al., 1987).

Depending on their position in the water column, it is possible to classify the zooplankton in two different groups: the *near-bottom* zooplankton, which lives very close to the sea bed (Brunel et al., 1978), and the *middle-water* zooplankton, which occupy different positions within the water column (Genin, 2004; Simard et al., 1986; Vereshchaka, 1995).

The *near-bottom* zooplankton is composed by animals whose vertical or ontogenetic migrations have a more temporary relation with the water-sediment interface (e.g. euphausiids, natantian decapods: Cartes et al., 2010).

In this sense, *near-bottom* zooplankton belong to the Deep Scattering Layer (DSL), and it is also termed *non-permanent suprabenthos* (= *Eucarida*: Brunel et al., 1978; Fanelli et al., 2009).

The biological feature which distinguishes the permanent suprabenthos from the *near-bottom* zooplankton is their direct development of embryos in the marsupial sacs (oostegites) developed by adult females of peracarid crustaceans; while *middle-water* zooplankton have often free larvae that aggregate in the photic zone (illuminated surface waters) linked to phytoplankton production (Cartes et al., 2010).

Near the bottom, zooplankton aggregate around physical features such as shelf

breaks (Genin, 2004; Vereshchaka, 1995) and canyon heads (Macquart Moulin and Patriti, 1996), and the interaction of mesopelagic zooplankton layers with the bottom occurs typically around 200-700 m (Hargreaves, 1984; Omori and Otha, 1981; Reid et al., 1991).

The *middle-water* zooplankton is characterized by animals that can usually implement extensive vertical migrations along the water column, detaching from the seabed. Together with micronektonic communities (e.g. little pelagic fishes) tends to aggregate at different levels in midwater and at the seabed interface (Genin, 2004; Simard et al., 1986; Vereshchaka, 1995). They may also aggregate close to thermohaline fronts (boundaries between water masses with different T and S), which may constitute physical barriers for zooplankton migrations (Cartes et al., 2013). Despite this, at the time, it is not yet clear which are the environmental variables that control the distributions and abundance of zooplankton in intermediate and deep waters (Cartes et al., 2013). It is especially important to understand which environmental factors control the distribution of zooplankton in the deep Mediterranean basin, because changes in deep and intermediate water masses (the Mediterranean deep water: WMDW, and the Levantine intermediate water: LIW) have occurred since the 1950s (Rixen et al., 2005).

Fig. 1.4: Rapresentation of mesozooplankton, an ecological assemblage composed by numerous and highly diversified taxa. Here are rapresented euphausiids, mysids, copepods, decapod larvae and pteropods (website: *oceana.org*).

1.5 The role of deep-sea zooplankton in ecosystem functioning

Despite the lack of information about the deep zooplanckton, some studies have revealed that mesopelagic zooplankton and micronekton (small fishes, shrimps and squids) are distributed worldwide (Reid et al., 1991), and they support key biological processes in all bathyal and benthopelagic trophic webs (Cartes et al., 2008a). Their role in deep-sea food webs is of particular importance. In fact depicting the food web structure is fundamental to understand the exchange of matter among organisms within an ecosystem, including the energy flow from basal resources to top predators (Krumins et al., 2013).

The zooplankton is the most important component in the diets of slope fish

(Cartes and Carrassón, 2004; Pearcy and Ambler, 1974) and of some decapod crustaceans (Cartes, 1993a, 1994a,b, 2014). Aggregations of zooplankton may enhance fish biomass near the bottom (Cartes et al., 2013). Furthermore, small fish, shrimps and squids are energy-rich items in comparison with gelatinous zooplankton that are mostly composed of water (Lucas et al. 2011).

Zooplanktonic communities contribute, together with suprabenthos, to connect different "marine compartments". *Near-bottom* zooplankton supports the carbon flux from the seabed to the water column (*bentho-pelagic coupling*) and *mid-water* zooplankton connects different depths along the water column.

Vertical migrations of these organisms contribute to the "transport" of Particulate Organic Matter (POM) to higher trophic levels through both vertical migrations from the photic zone (including the contribution of their waste material, in the form of *faecal pellets*). They constitute the so-called *swimmer flux* (Miquel et al., 1994) (**Fig. 1.3**). Still zooplankton being prey of several megafaunal species, including demersal and benthopelagic organisms contribute to the *pelago-benthic coupling* (Fowler and Knauer, 1986).

1.6 The use of stable isotopes of carbon and nitrogen for the study of food webs

Both suprabenthos and zooplankton play an important role in the trophodynamics (= the energy and material fluxes), and their knowledge is essential to study the food web structure, both in the coastal marine environments and in the deep sea (Fanelli et al., 2009a,b,c).

Traditional approaches to the study of food web have been focalised on the analysis of gut contents, together with field and laboratory observations (Fanelli et al., 2011a,b). But this approach presents several important limitations, particularly for macrofauna: 1) gut contents provide only snapshots of the diet in a particular point of time and space (Fanelli and Cartes, 2008); 2) the duration of these snapshots is variable, bacause of an intensive turnover of gut contents (Jobling, 1993); 3) gut contents analyses do not consider certain types of dietary materials, like gelatinous plankton and detritus, which may be very important (Fanelli and Cartes, 2008); 4) live organisms for experimental studies are difficult to obtain (Fanelli et al., 2011); 5) gut content analyses are hampered by damage to specimens during sampling and from pressure effects (Fanelli et al., 2011a,b).

These limitations have paved the way for the stable isotope analysis approach, which tends to make up for the lacks of traditional approaches in the study of food web structure. This techique has been established in the last decades, as

an alternative approach to investigate the relative trophic position of organisms within the food web and their sources of carbon (e.g. Fry and Sherr, 1988).

From a chemical point of view, an isotope is an atom which differs from its congeneric, because of the presence of different atomic number, caused by a different number of neutrons (see **Fig. 1.6.a** as an example). Some isotopes are considered "stable" because they do not emit radioactivity (contrary to radioactive isotopes) and they are rapresented by C, N, S, O, H.

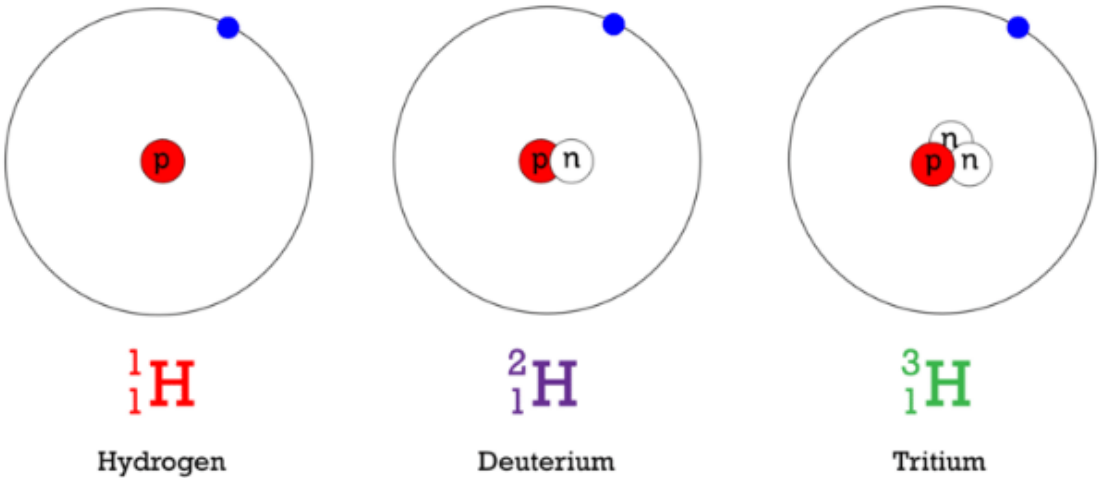

Fig. 1.6.a: Example of isotopes of hydrogen. The three forms present the same number of protons ($_1H$) and electrons, but deutherium has one neutron ($_2H$) and tritium two neutrons (^3H) more than the natural form (^1H), (website: *chem.libretexts.org*).

Even if this techique started some decades ago, it has become popular in acquatic studies in more recent years (Cabana and Rasmussen, 1996; Pinnegard and Polunin, 2000).

One of the most important benefit of using stable isotopes is that they provide

time-integrated informations about feeding relationships and energy flow through the food webs, and therefore they solve the problem of the non-ability of gut contents in providing informations about diet in a longer time (Peterson and Fry, 1987; Kling et al., 1992; Cabana and Rasmussen, 1994).

In the deep sea, some studies have been conducted using stable isotopes with success: the analysis of the trophic links in deep-sea corals (e.g. Kiriakoulakis et al 2005), in foraminifera (e.g. Corliss et al., 2002), and in polychaetes from hydrothermal vents (e.g. Levesque et al., 2003). Nevertheless in the study of macrofauna this approach has been rarely adopted, especially in deep-sea environments (Iken et al., 2001, 2005, Polunin et al., 2001); and the application of isotopic analysis on suprabenthos fauna at species level has been limited to the Antarctic Ocean (Nyssen et al., 2002, 2005) and recently, to the Western Mediterranean (Madurell et al., 2008; Fanelli et al., 2009a,b).

The stable isotopes chose to depict the structure and dynamics of ecological communities are carbon and nitrogen, respectively $\delta^{13}C$ ($^{13}C/^{12}C$) and $\delta^{15}N$ ($^{15}N/^{14}N$) (Kling et al., 1992; France, 1995; France et al., 1995; Vander Zanden et al., 1999).

$\delta^{13}C$ is used to determine the origin of the assimilated organic matter.

It is useful to discriminate between the pelagic vs. benthic origin of food (France, 1995) or between terrestrial vs. marine sources (Hobson, 1987).

The amount of ^{13}C is enriched or fractionated by ca. 0-1‰ per trophic level

(De Niro and Epstein, 1978; Fry and Sherr, 1984;Wada et al., 1991; Michener and Schell, 1994; McCutchan et al., 2003).

$\delta^{15}N$ is used to determine the trophic position of specie/taxon within the food web, displaying a stepwise enrichment of about 3-4‰ at each trophic level (Minagawa and Wada, 1984; Owens, 1987; Vander Zanden and Rasmussen, 2001; Post, 2002). In this way, carnivorous groups will show the higher values of $\delta^{15}N$, and the herbivorous the lowest (**Fig. 1.6.b**).

However, these stepwise enrichment factors were deduced from a large variety of both freshwater and marine studies, but a restrict number of studies have been conducted on stable isotope accumulation in tissues of deep-sea species (Fanelli et al., 2009b,c).

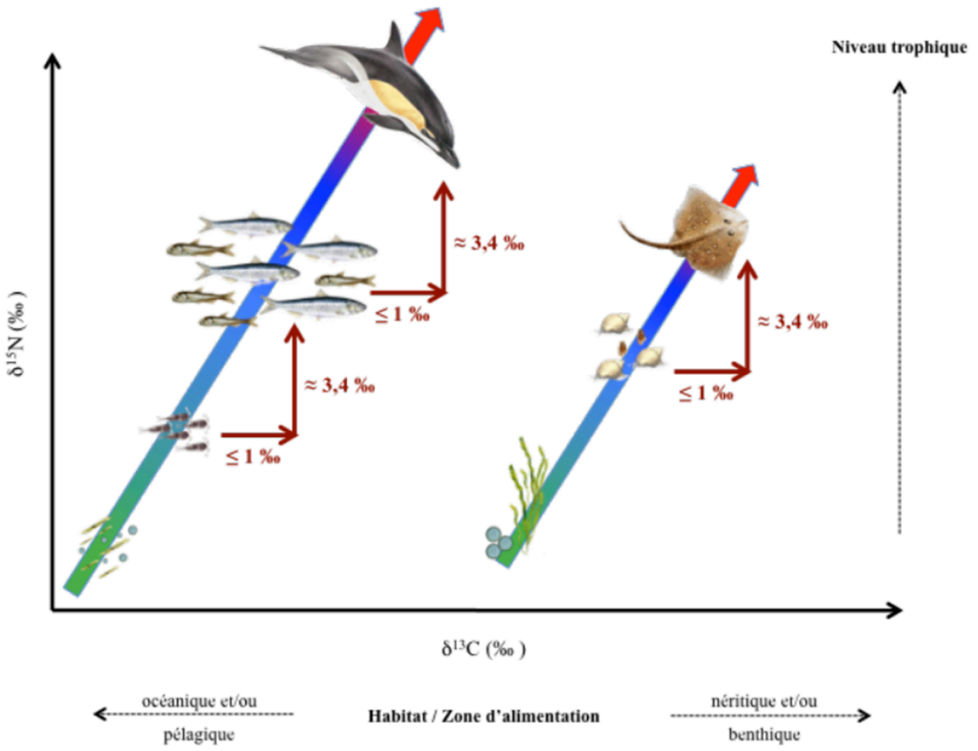

Fig. 1.6.b: Example of a $\delta^{13}C$-$\delta^{15}N$ biplot (websource: *researchgate.net*).

1.7 Aim of the thesis

The work of this thesis is the result of the activities conducted within the Italian founded project RITMARE (SP4 – maritime spatial planning: deep-sea environment), by analyzing samples collected during the oceanographic campaign Anomcity, carried out in June 2016.

The monitoring activities focused their attention both on the environmental characterization of different deep-sea areas and the possible anthropogenic impact, considering that most of these areas are canyons, very close to the

mainland and highly anthropised coasts, with potentially greater concentration of contaminants with adverse effects on marine biodiversity.

The aims of the thesis were:

1. To assess the overall biodiversity of BBL fauna of suprabenthos and zooplankton of submarine canyons of the Ionian Sea;
2. To highlight bathymetric trends in species composition, assemblage structure and food web in each canyon;
3. To analyse mesoscale variability in species composition, assemblage structure and food web between the two canyons;
4. To identify potential environmental drivers of such trends and differences.

To comply with these aims, multiple samples across a bathymetric transect were collected in each canyon. Samples of suprabenthos from three different dephts within the canyon axis (close to the head, at ca. 400 m, in the middle, at ca. 800 m and in the depocenter, at ca. 1500 m) were collected and analysed. For zooplankton, samples were collected at the Deep Scattering Layer, at ca. 500 m, in proximity of the three depths described above.

Chapter two

MATERIALS AND METHODS

2.1 Study area

The investegated areas by the Anomcity oceanographic campaign included two submarine canyons of southern Italy, central Mediterranean.

Submarine canyons are submarine incisions of the continental shelf, where their head is usually positioned, reaching with deep bottoms up to over 3000 m such as the Nazarè canyon off Portugal, thus conditioning the integrity of the deep sea.

During the Anomcity oceanographic compaign the following areas, off the southern Italian coasts, were explored: 1) the Gulf of Naples; 2) The Gulf of Augusta; 3) the Gulf of Taranto; 4) the Gulf of Squillace (**Fig. 2.1**).

These areas are strongly affected by human activities, due to the presence of industries, urban centers, port activities, etc. (e.g. Gulf of Naples: Adamo et al., 2005; Sprovieri et al., 2006; Sprovieri et al., 2007. Gulf of Augusta: ICRAM, 2005, 2008; Sprovieri et al., 2011; Bellucci et al., 2012; Bonsignore et al., 2013, 2015; Salvagio Manta et al., 2016).

As canyons act as corridors for the transport of organic matter, they also funneled potentially polluted sediments, conditioning the health and the integrity of deep biological communities (Fernandez-Arcaya et al., 2019).

In these work, we analysed samples from two canyons surveyed during Anomcity, these are the Amendolara canyon, in the Gulf of Taranto, and the Squillace canyon, in the omonymous gulf (Anomcity, 2016).

Fig 2.1: Satellite maps of the investigated areas during the Anomcity oceanographic compaign, respectively: a) The Gulf of Naples (Dohrn Canyon); b) The Gulf of Augusta (Augusta canyon); c) The Gulf of Taranto (Amendolara canyon); d) The Gulf of Squillace (Squillace canyon). The red dots indicate the sampling sites (Anomcity, 2016).

2.1.1 The Amendolara canyon

The Gulf of Taranto is located in the northern Ionian Sea, Central Mediterranean, and it expands to approx 16.000 km^2 .

The Amendolara ridge is extended over 80 km in NE direction in the Gulf of Taranto, and it is characterized by the precence of three banks of about 10-20 km: Amendolara, Rossano and Cariati (**Fig. 2.1.1.a**); they grow up above dead-end ramps, forming a segmenteted system (Ferranti et al., 2012).

Based on two ROV dives carried out in the Amendolara ridge at 307-450 m and 321-346 m (**Fig. 2.1.1.b**), the area appears to be characterized by highly bioturbated muddy bottoms, with extensive thanatocoenosis of *Dendrophyllia cornigera* (Cnidaria, Anthozoa). Only one live colony of this coral was observed at 363 m (**Fig. 2.1.1.c**).

At about 363 m, an accumulation of rocks of landslide derivation colonized by hydroids, sponges, serpulid polychates occurs.

Here, the Mediterraean endemic species *Nidalia studeiri* was found [**Fig. 2.1.1.d (a**)]. This Alcyonacea was reported only from two sites of the North-western Mediterranean, in the Gulf of Naples (Kock, 1891) and the Menorca Channel (Lòpez-Gonzàles et al., 2012).

Finally, the decapod species *Paramola cuvieri* was observed near the accumulated landslide-rocks [**Fig. 2.1.1.d (b**)] (Anomcity, 2016).

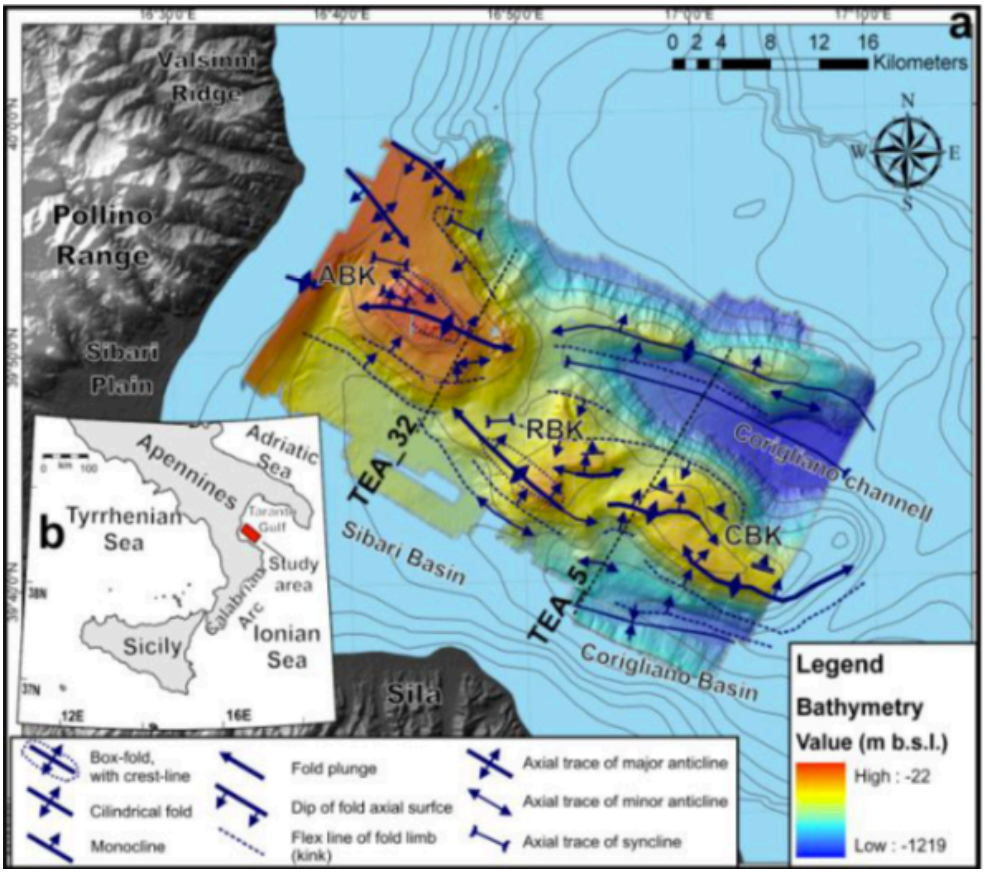

Fig. 2.1.1.a: Morphobathymetrical and structural map of Amendolara ridge. ABK = Amendolara Bank; RBK = Rossano Bank; CBK = Cariati Bank (Ferranti et al., 2012; Atomcity, 2016).

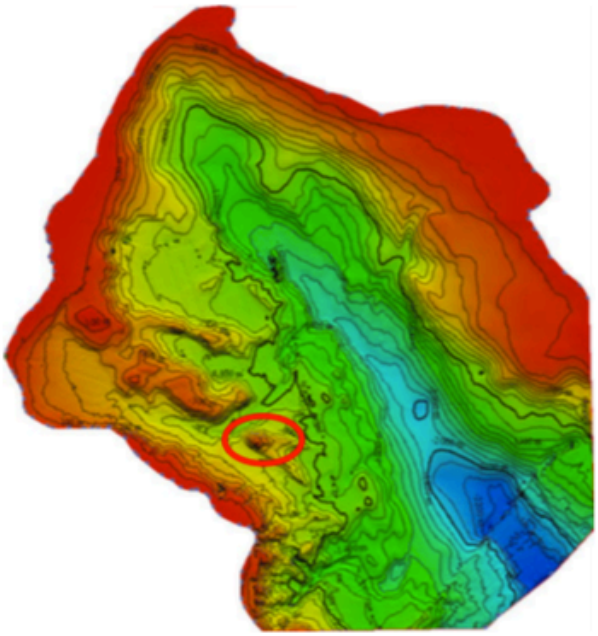

Fig. 2.1.1.b: The Multibeam reconstruction of the bathymetry canyon of Amendolara. The red circle indicates the location inspected area by the ROV (Anomcity, 2016).

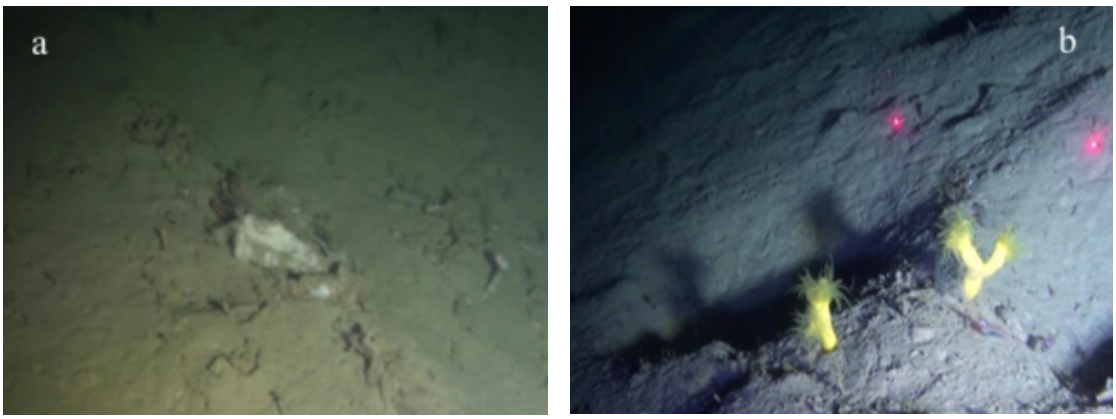

Fig. 2.1.1.c: a) Thatocoenosis of *Dendrophyllia cornigera*; b) live colonies of *D. cornigera* (Anomcity, 2016).

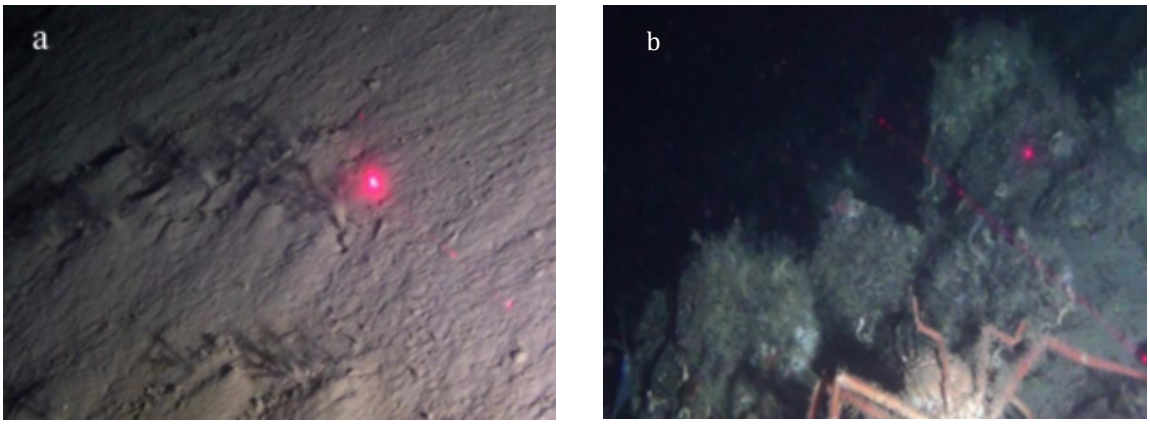

Fig. 2.1.1.d: a) Ground built by *Nidalia studeri*; b) the decapod specie *Paramola cuvieri* above a rocky accumulation (Anomcity, 2016).

2.1.2 The Squillace canyon

The Gulf of Squillace is a sedimentatry basin located in an highly active geodynamic zone in the cental Mediterranean Sea, which connects the southern Appenines and the Maghrebide Sicilian mountain range (Patacca and Scandone, 2004).

The Gulf of Squillace is located in the Avanarco area, and it is a part of the sedimentary system of the Crotone-Spargivento basin, between Punta Stilo and the southern margin of the *on-shore* zone of Crotone basin.

The morphology of the sea bottom is the result of an intesive tectonic activity, *mud diapirism* and by erosion-depositional precesses.

These characteristics determined unstable slopes, influenced by gravidic processes (Capozzi et al., 2012).

The submarine canyon of Squillace connects the continental shelf with the deeper part of the sedimentary basin of Crotone-Sprargivento (**Fig. 2.1.2.a**).

A ROV exploration was conduced in a small area in the South-West of the Gulf of Squillace (**Fig. 2.1.2.b**).

According to ROV data, the area is characterized by muddy bottoms, with high densities of ceriantharians.

Different fish species were here observed, i.e. *Chlorophtalmus agassizii*, *Helicolenus dactylopterus* including commercial species, i.e. *Lophius piscatorius*, *Chelidonichthys lucerna* and the decapod crustacean *Nephrops norvegicus* (**Fig. 2.1.2.c**).

In the last section of the transect, abandoned fishing nets occured (Anomcity, 2016).

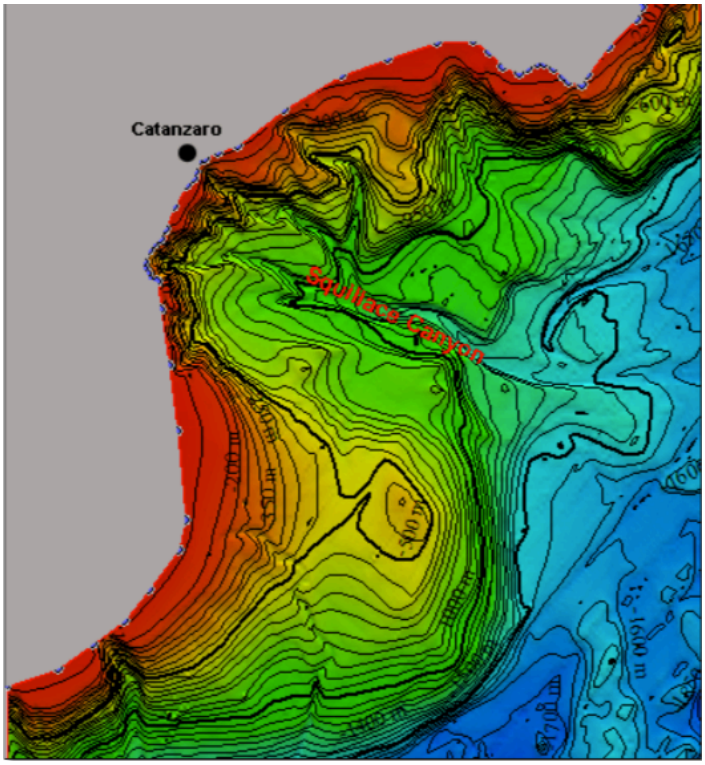

Fig. 2.1.2.a: Morphobathymetric map of the Canyon of Squillace (Anomcity, 2016).

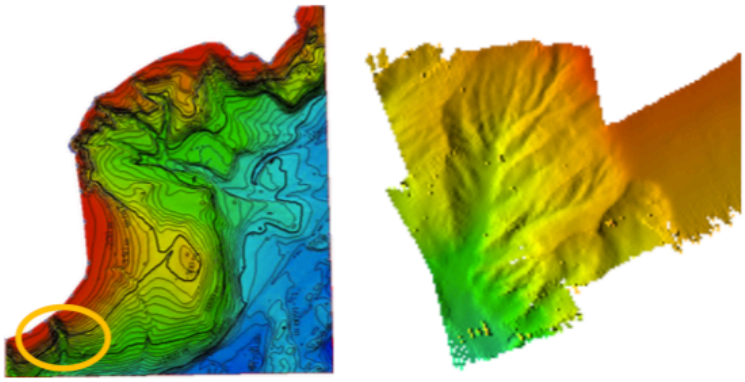

Fig. 2.1.2.b: The Multibeam reconstruction of the bathymetry canyon of Squillace. The yellow circle indicates the location inspected area by the ROV (Anomcity, 2016).

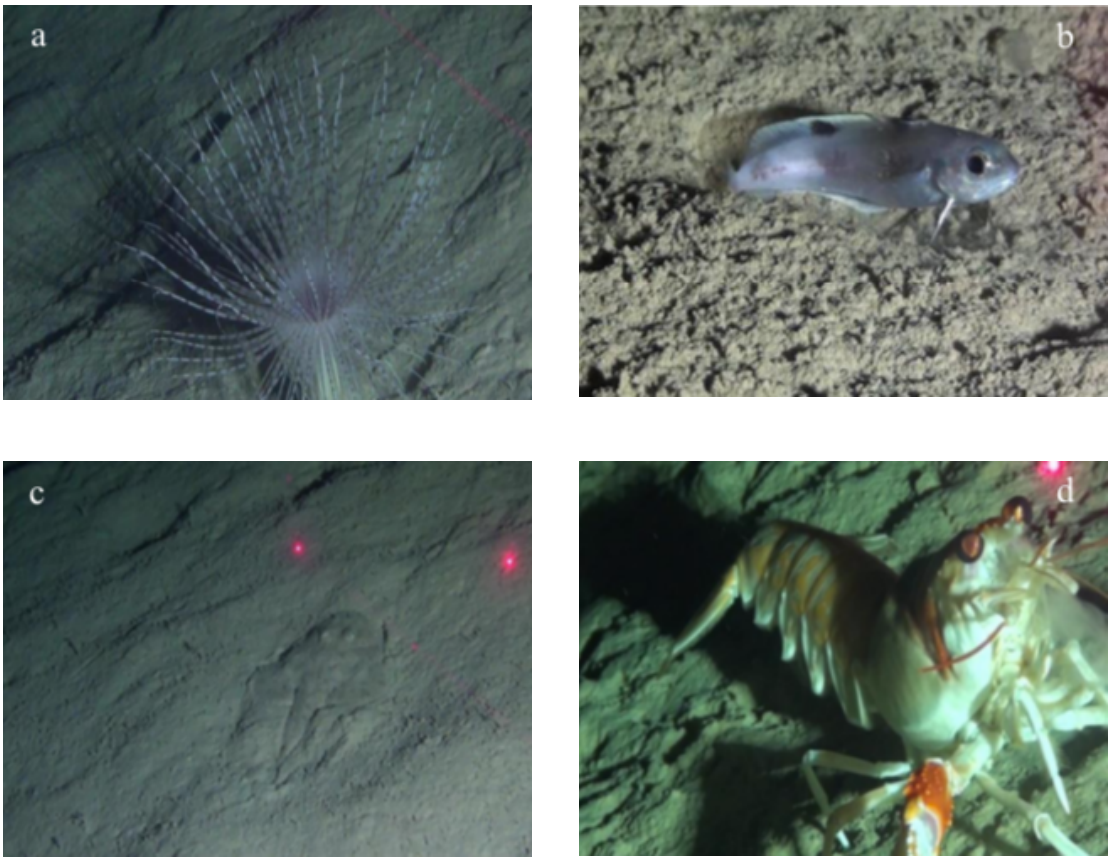

Fig. 2.1.2.c: Some speciments of megafauna inhabiting Ionian a) *Pachycerianthus* sp.; b) *Phycis blennoides*; c) *Lophius piscatorius*; d) *Nephrops norvegicus* (Anomcity, 2016).

2.2 Samples collection

The sampling consisted in the collection of six samples for suprabenthos and six for zooplankton. Each sample corresponds to a bathymetry along the canyon in the case of suprabenthos, and to a vertical net in the case of zooplankton. Suprabenthic samples were taken using the Macer-Giroq sledge, zooplanktonic samples were taken using a Nansen net.

The sediments intended for the analysis of organic matter were collected thanks to a Box-Corer (Anomcity, 2016).

2.2.1 Macer-Giroq sledge for suprabenthos

The Macer-Giroq sledge (Dauvin and Lorgère, 1989) was specifically designed to sample the bentho-pelagic fauna or suprabenthos (Benthic Boudary Layer: BBL). One haul was taken at each station (depth) because previous studies using sledges had shown that one haul was enough to characterize the community of suprabenthos for a particular area/time (Brattegard and Fossa, 1991).

These sledge used in this study has a single rectangular "mouth" of 40-80 cm, equipped with an opening-closing system (**Fig. 2.2.1**) in order to minimize sample contamination during the descent and the ascent (Fanelli et al., 2009b, 2011a).

Macer-Giroq sledge was equipped with a 500 μm net, and thawed at a speed of about 1.5 knot for 10-15 minutes per haul. In this way, the sledge is able to sample a part of the water coulmn at 0.1-0.5 m above the sea bottom (Cartes et al., 1994b). A flowmeter is installed at the center of the sledge to estimate the volume of filtered water.

The Macer-Giroq sledge took samples at three different bathymetries: in the the canyon depocenter (1300-1500 m), hereafter indicated as DC, in the middle part of the canyon, at ca. 600-750 m, hereafter called MC and at the head of the canyon (HC) at ca. 430-550 m.

All collected samples were frozen at -20°C for subsequent analyses in the laboratory (Anomcity, 2016).

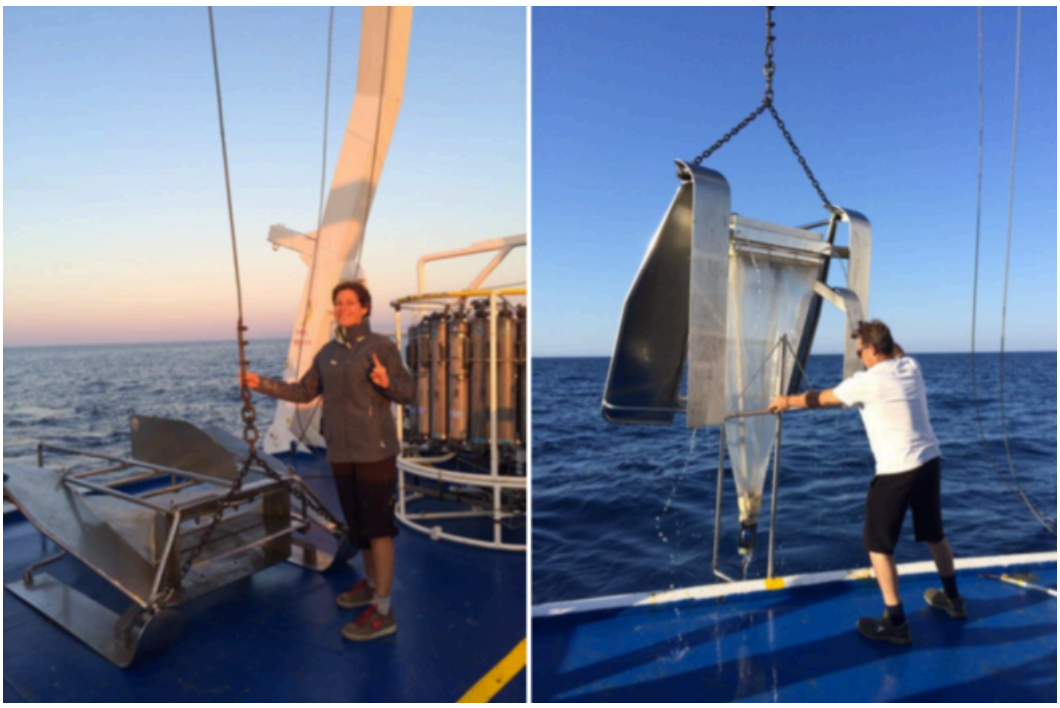

Fig. 2.2.1: The Macer-Giroq sledge used to collect samples of suprabenthic fauna (Anomcity, 2016)

2.2.2 Nansen net for zooplankton collection

The Nansen net, also called WP2, is used to sample mesozooplankton (**Fig 2.2.2**). It has a mouth with ca. 113 cm diameter, and equipped with a net of 200 μm mesh. The net is equipped with a release mechanism inserted on the winch cable. This system allows the messenger to close the net at the desired depth, and to collect several layers of the water column, in order to determine the vertical distribution of the community. A flowmeter is installed at the center of the net mouth to estimate the volume of filtered water.

The Nansen net was used during the survey to analyse different depth ranges: at 50-0, 100-50, 200-100, 300-200, 500-300, 1000-500 m. However in this study we focused on the Deep Scattering Layer (DDL = the layer inhabited by dense aggregations of planktonic and nektonic organisms, detectible by sonar, which exibite daily vertical migrations along the water column: Boden, 1950), thus we approximately sampled at 300-500 m according to the indication of the echosounder onboard, on the different depths detailed above, thus on the depocenter, the middle canyon and the canyon head.

Also for zooplankton, all collected samples were frozen at -20°C for subsequent analyses in the laboratory (Anomcity, 2016).

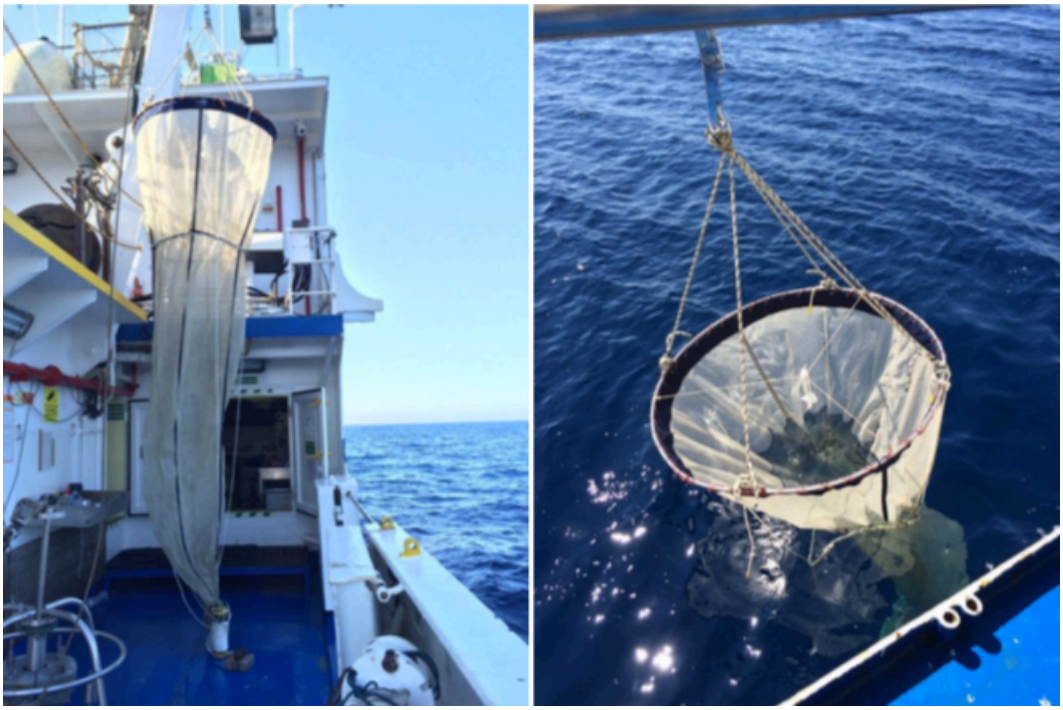

Fig. 2.2.2: The Nansen ned used to collect mesozooplankton samples (Anomicity, 2016).

2.3 Taxonomic determination of suprabenthos and zooplankton

The collected samples were analysed in the laboratory, suprabenthos were analysed first.

The first step consisted in filering the sample with 500 μm sieve and sorting the organisms for large taxonomic groups under a stereomicroscope (**Fig. 2.3**).

The sorted animals were kept on Petri dishes, and these were located on ice, in order to maintain tissues' integrity.

All the animals were first sorted to highest level (i.e. Order, Class and Phylum), then fozen again to be classified to the lowest taxonomic level, as possible.

Fig. 2.3: The stereomicroscope used for sorting activity and for animal identification. The ice was used to keep cold sorted animals.

2.3.1 Suprabenthos

Suprabenthos samples contained sediments and small amounts of water. After a partial thawing, samples were sieved on a 500 μm mesh-size. A little amount of sample was analysed each time, until the sample was completely sorted.

All the samples contained high amount of vegetable remains, both of marine origin, such as remains of *Posidonia oceanica* and marine algae, and

terrestrial plants (leaves, piece of woods, canes etc.). High abundances of foraminifera, particularly *Globigerina* sp. were annotated.

For each sample, animals were sorted out from the sediment and the vegetable detritus, and divided in large taxonomic groups, then frozen again at -20°C, while vegetable detritus was preserved in ethanol 70%.

Freezing was preferred as preservation method, because sample would have been analysed for stable isotopes later and both ethanol and formaldeyde may alter the $\delta^{13}C$ signatures (Fanelli et al., 2010b). This is particularly true for formaldeyde, the preservative that mostly changes the chemical integrity of cells and tissues (Fanelli et al., 2010b).

All samples were identified to the lowest taxonomical level as possible **(i.e. Fig. 2.3.1.a, 2.3.1.b).**

For the identification several dichotomous keys were used:

- Ruffo S., 1982. The Amphipoda of the Mediterranean, part 1: Gammaridea: Acanthonotozomatidae to Gammaridae. Memoires dell'Institute Oceanographique, Fondation Albert I^{er} , Prince de Monaco. Pp. 392.
- Ruffo S., 1982. The Amphipoda of the Mediterranean, part 2: Gammaridea: Hustoriidae to Lysianassidae. Memoires dell'Institute Oceanographique, Fondation Albert I^{er}, Prince de Monaco. Pp. 228.

- Ruffo S., 1982. The Amphipoda of the Mediterranean, part 3: Gammaridea: Melphidippidae to Talitridae, Ingolfiellidea, Caprellidea. Memoires dell'Institute Oceanographique, Fondation Albert I^{er} , Prince de Monaco. Pp.252.
- Ruffo S., 1982. The Amphipoda of the Mediterranean, part 4: Localities and Maps, Addenda to Parts 1-3, Key to Families, Ecology, Faunistic and Zoogeography, Bibliography, Index. Memoires dell'Institute Oceanographique, Fondation Albert I^{er} , Prince de Monaco. Pp.84.
- Holdich D.M., Jones J.A., 1983. Tanaids. Keys and Notes for the Identification, n°27. Cambridge University Press, Cambridge. London. New York, Malbourne, Sydney. Pp. 98.
- Naylor E., 1972. British Marine Isopods. Key and Notes for the Identification. Synopes of the British Fauna n°3. Accademic Press, London and New York. Pp. 80.
- Tattersall W.M., Tattersall S. Tattersal, 1951. The British Mysidacea. London, 1951.Pp. 267.
- Chevreux Èd., Louis Fage. Faune De France. Amphipodes. Fèdèration Française de Sociètes de Sciences Naturelles. Office Central de Faunistique. Paris, pp. 486.
- Fage L., 1951. Cumacès, Faune de France. Fèdèration Française des Sociètès de Sciences Naturelles. Office Central de Faunistique. Pp. 136.

Once identified, all individuals of a specific taxonomic group (species, genus, family, etc.) were counted to estimate the abundance and weighed with the analytical balance, in order to obtain the biomass estimation.

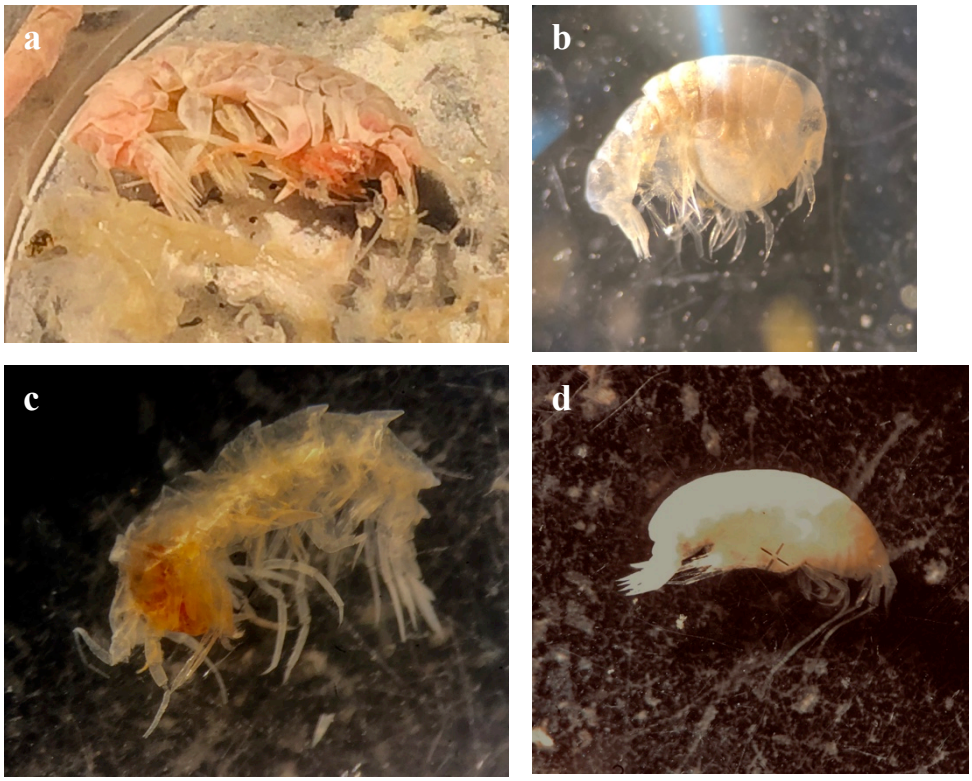

Fig. 2.3.1.a: Some Amphipoda Gammaridea sorted from the sample at the stereomicroscope: a) *Epimeria parasitica* (picture not taken at the stereomicroscope) b) *Stegocephaloides christianensis;* c) *Iphimedia jugoslavica*; d) *Paracentromedon crenulatum*.

Fig. 2.3.1.b: Other sorted animals from the samples at the stereomicroscope (a,b,c = isopods; d = gammariid amphipod: a) *Munnopsurus atlanticus*; b) *Natatolana borealis*; c) *Gnathia maxillaris* (female); d) *Leucothoe lilljeborgi*.

2.3.2 Zooplankton

The sorting and the identification of zooplankton samples were similar to that carried out for suprabenthos. First small amounts of samples were defrozen each time, main taxa separated and then frozen again at -20°C. Filtration of zooplankton samples was done by using a 200 µm mesh size. Once a sample was completely sorted, the taxonomical identification to the lowest level, as possible, was carried out (**i.e. Fig 2.3.2.)**

For the indentification of zooplankton the following dichotomous keys were used:

- Rose M., 1993. Faune De France. Copèpodes Pèlagiques. Federation Française de Sociètes de Sciences Naturelles. Office Central de Faunistique. Paris, pp. 374.
- ICRAM, 2006. Guida al riconoscimento del plancton neritico dei mari italiani, Volume II - Zooplancton Neritico - Tavole . Pp. 196.
- Mauchline J., 1984. Euphausiid, Stomatopod and Leptostracan Crustaceans. Key and notes for the identification of species. London, Leiden, Koln,

As in the case of suprabenthos, each individual of a taxonomic group was counted, for the estimation of abundance, and weighed for the estimation of biomass (in terms of wet weight). Subsequently the animals were oven-dried at 60°C for 24 hours minimum, to be later analysed for stable isotopes.

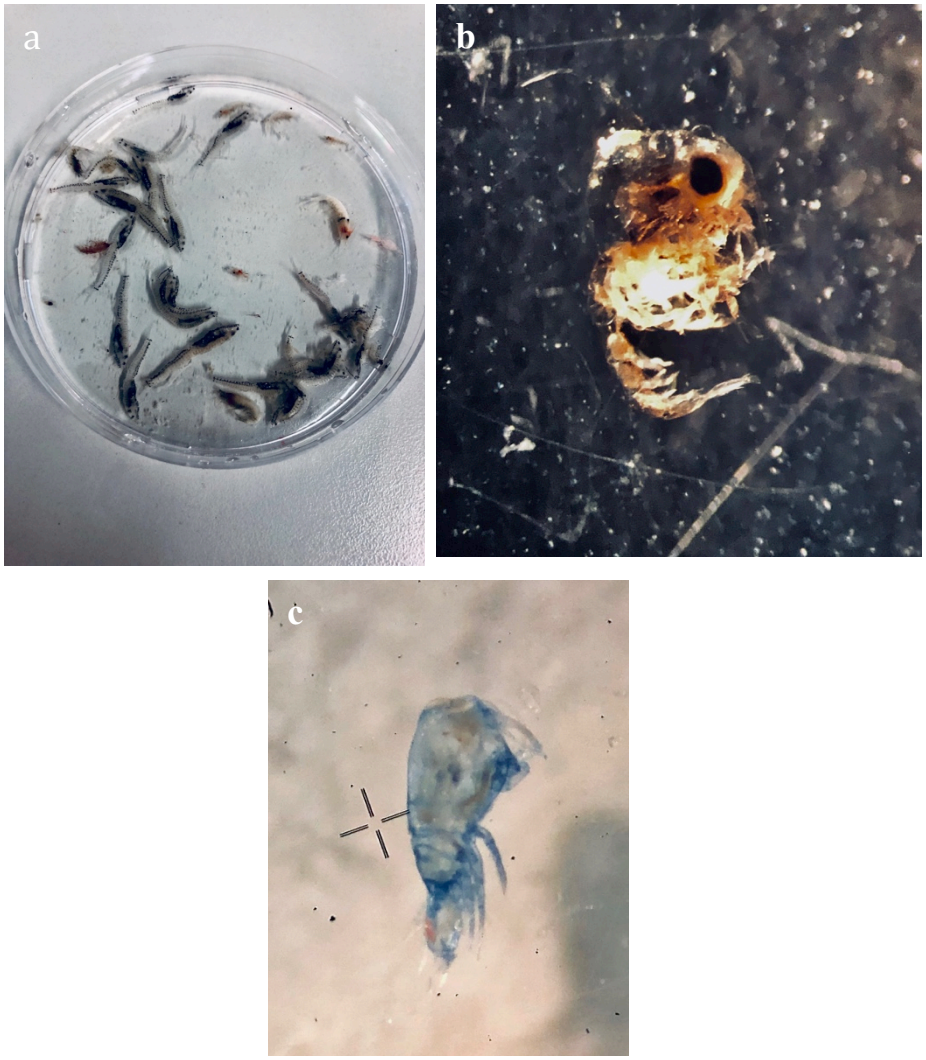

Fig. 2.3.2: Examples of zooplanktonic animals sorted: a) Fish (*Cyclothone braueri*), euphausiids (*Meganyctiphanes norvegica*, picure not taken at the stereomicroscope); (c) Zoea (a decapod larva); d) *Corycaeus* sp.

2.3.3 Sample preparation for isotope analysis

Selected taxa, i.e. the most abundant observed in the samples, or species never analysed before, according to the few literature existing on this topic, were oven-dried for 24 hours at 60°C. Afterthat dried samples were converted to a fine powder with a mortar and pestle and ca. 1 mg of dry weight were weighed and placed into tin capsules for the subsequent analysis. For those organisms characterized by an exoskeleton, such as *Epimeria parasitica*, in order to remove the inorganic carbon, which can influence the $\delta^{13}C$ signal, a subsample were acidified with HCl 1M, by adding it drop by drop to the sample until bubble cessation. Samples for the analysis of N were not acidified, as several studies demonstrated that the acidification procedure can alter the N signal (Kolasinski et al., 2008). All instruments used to powder samples (i.e. mortar, pestle and tweezers) were cleaned after each sample, with deionized water, in order to avoid contaminations.

Afterthat samples were oven-dried again for 24 hours at 60°C.

A minimum, when possible, of three replicates per taxonomic group were weighed, by using an analytical balance (five decimals) and from 0.3 to 1.3 mg of dry weight were put into tin capsules. All capsules were sorted in a numbered rack, that allowed to easy identify the corresponding position of a particular taxonomic group (**Fig. 2.3.3.a**).

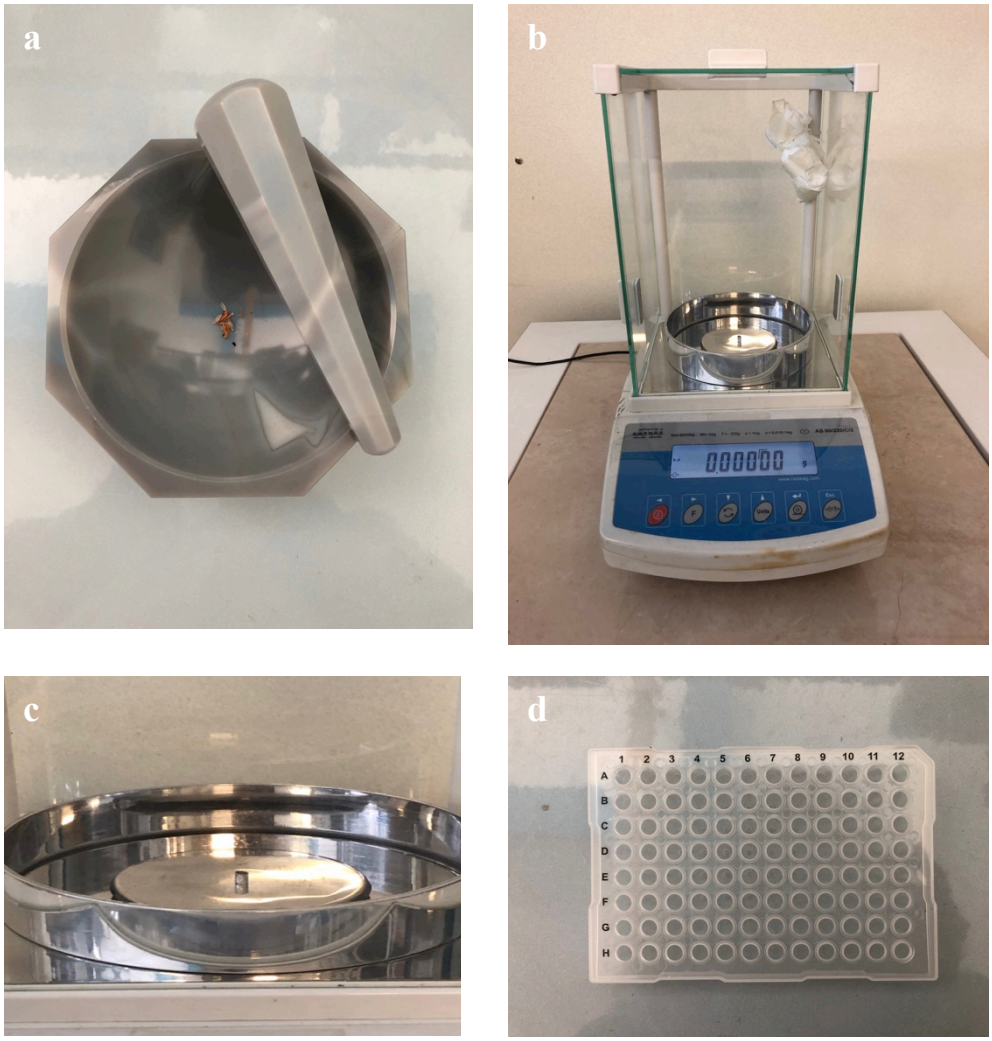

Fig. 2.3.3.a: Sample preparation for the following stable isotope analysis: a) dry animals in a mortar; b) five-decimals analytical balance used to weigh animal powder in the tin capsule; c) a tin capsule on the plate of the balance; d) the numbered rack used to store the closed tin capsules containing the dry material.

The isotope analysis was conducted at the ENEA center in Bologna. The instrument used for this analysis was an Isotope Ratio Mass Spectrometer (**Fig. 2.3.3.b**), coupled with an Elemental Analyser (EA-IRMS).

The Elemental Analyser provides %TOC and %TN, while the IRMS gives the values of $\delta^{13}C$ and $\delta^{15}N$.

Generally, before the analyses, a tuning procedure was carried out, which consists in the instrument calibration in order to work at the best instrumental conditions. This procedure must be done every day.

The ENEA operator proceeds doing a batch of analyses, preparing sample sequences to be analysed as follows: 1) *dummy*, which corresponds to an empty capsule; 2) *blank*, which corresponds to "white" sample; 3) *reference*, which corresponds to a reference sample; 4) *standard*, generally caffeine is used; 4) *sample sequences* to be analyzed.

Samples inserted in the instrument are burnt at 850°C with production of O_2, CO_2 and NO_x, the latter is then converted into N_2. Subsequently, a ionizer implements a separation for different masses (**Fig. 2.3.3.c**). A specific *software* connected to the instrument provides a graph, whose curves allowes the operator to understand if there are some problems in the instrument. Finally, it provides the related values of $\delta^{13}C$, $\delta^{15}N$, %TOC, %TN.

$\delta^{13}C$ and $\delta^{15}N$ were obtained in parts per thousand (‰) relative to Vienna Pee Dee Belemnite (vPDB) and atmospheric N_2 standards, respectively, according to the following formula:

$\delta^{13}C$ or $\delta^{15}N$: $[(R_{sample}/R_{standard})-1)]10^3$, where R = $^{13}C/^{12}C$ or $^{15}N/^{14}N$

Fig. 2.3.3.b: The isotope Ratio Spectrometer (IRMS) at the ENEA center of Bologna.

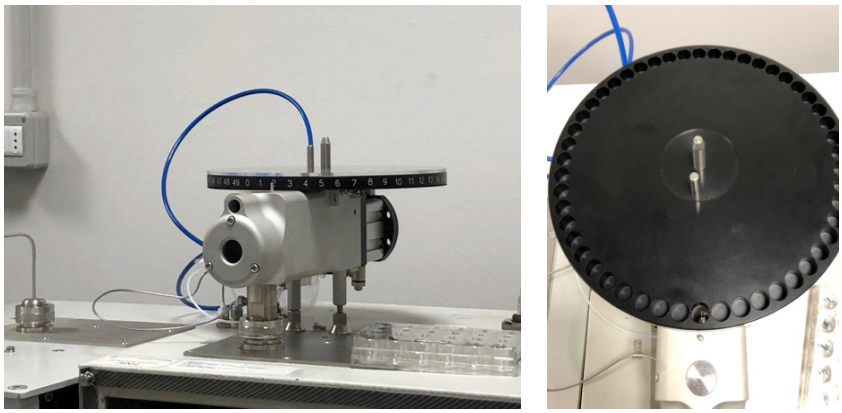

Fig. 2.3.3.c: The Elemental Analyser grid where the tin capsules to be analysed were positioned

2.4 Data analyses

First of all data were standardized to a costant value.

To do so, in the case of suprabenthos, knowing the volume of filtered water by the sledge during each haul (obtainded by the difference between the lecture of the flowmeter at the end and at the begining of the haul), the area of the mouth and multiplying per a costant value, it is possible to obtain the swept area and then standardizing each mesure (abundance and biomass) to a costant value of 100 m^2.

In the case of zooplankton, the procedure is similar, but the volume of the net mouth, the constant adopted (both are provided by the flowmeter manufacturer), and the constant value with which abundance and biomass mesures were standardized (1000 m^3), and different and specific for the Nansen net and its different shape.

2.4.1 Analysis of abundance and biomass data

The suprabenthic abundance data were expressed as number of individuals per 100 m^2 (N/100 m^2), and the biomass data were expressed as grams of wet weight per 100 m^2 (g WW/100 m^2). The zooplanktonic abundance data were expressed as number of individuals per 1000 m^3 (N/1000 m^3), and biomass data were expressed as grams of wet weight per 1000 m^3 (g WW/1000 m^3).

Both for the suprabenthic and and zooplanktonic samples, the total abundances and biomasses per bathymetry along each canyon transect were determined. Finally, the calculation of the percentages of the suprabenthic and zooplanktonic taxa per each canyon, in terms of abundance and biomass, was carried out.

2.4.2 Multivariate analysis

Multivariate analyses were run on the abundance data both for suprabenthos and zooplankton. Firstly, the abundance data were square root transformed and fourth root transformed, respectively for suprabenthos and zooplankton, and the resemblance matrix was obtained by using the Bray-Curtis distance.

On the resemblance matrix, a nMDS (non metric Multidimensional Scaling) was carried out, followed by a PERMANOVA (Permutational Multivariate Analysis of Variance; Anderson, 2001), which allowed to test for differences

between the two sites and the three depths considered. In this analysis 9999 permutations were used.

Then, SIMPER analysis, which provides the % contribution of the different taxa to the average similarity/dissimilarity was calculated. SIMPER was calculated per site (Amendolara group and Squillace group), and per depth (HC, MC, DC). The SIMPER analysis was conducted basing on Bray-Curtis similarity (with a cut-off at 50%). Finnaly, the Shannon-Wiener diversity index was calculated.

All multivariate analyses were run by using the software *PRIMER6+* (Anderson et al., 2008; Clarke et al., 2008).

2.4.3 Environmental data analyses

In order to better understand the relashionships between biodiversity assemblage along the canyons and the environmental variables, biotic data were correlated to environmental data.

Environmental data here considered are temperature, salinity and fluorescence, obtained during Anomcity oceanographic campaign, and chlorophyll a concentration (Chl*a*, expressed as mg/m^3) and the Particulate Organic Carbon (POC, expressed as mg/m^3), derived by satellite data downloaded at http://giovanni.gsfc.nasa.gov/giovanni/ website. Data

considered in this case were Chl*a* and POC recorded simultaneously to sampling and from 3 to 1 month before sampling (March, April, May).

2.4.4 Stable isototope analyses

The most abundant species found were used to depict the trophic web structure, both for the suprabenthos and zooplankton.

The definition of trophic-web structure was obtained for both the suprabenthic and zooplanktonic assemblages, by performing Hierarchical cluster analysis (Euclidean distance, average grouping methods) on the bivariate matrix of $\delta^{13}C$ and $\delta^{15}N$ untranformed data. The groups obtained were compared with postulated trophic groups - TG (i.e. filter-feeders/grazers, suspension-feeders, deposit-feeders, omnivores, carnivores), based on the analysis of literature.

Afterthat, TG were compared by means of a one-way PERMANOVA (Permutational Multivariate Analysis of Variance; Anderson, 2001; 9999 permutations used), carried out on the matrix detailed before. Pairwise comparison were also performed to define which trophic groups differed among each other.

Than, $\delta^{15}N$ values were converted to trophic level (TL) based on the assumption of about 2.54‰ fractionation per trophic level (Vanderklift and Posnsard, 2003). The base material (filter-feeders or deposit-feeders) had a trophic level of 2:

$$TL_i = (\delta^{15}N_i - \delta^{15}N_{PC}/2.54)+2$$

where TL_i is the trophic level of species *i*, $\delta^{15}N_i$ is the mean $\delta^{15}N$ of the species *i* and $\delta^{15}N_{PC}$ is the $\delta^{15}N$ of a primary consumer, used a baseline. The % of C and N were used to calculate the C/N ratio that, related with the $\delta^{13}C$, allowed to estimate the lipidic content of tissues (i.e. samples containing more lipids have higher C/N ratio; Tieszen et al., 1983). C/N ratios were measured simultaneously during stable isotope analysis from the elemental percentages of C and N, and $\delta^{13}C$ were normalized for lipidic concentration according to the equation of Post et al. (2007): $\delta^{13}C$ of untreated samples (not defatted) were converted to $\delta^{13}C_{normalized} = \delta^{13}C_{untreated} - 3.32 + 0.99\ C/N_{sample}$.

Chapter three

RESULTS

3.1 Faunal composition

3.1.1 Suprabenthos

The analysis of suprabenthos sample has revealed a highly diversified faunal composition and a complex assemblage structure.

At Amendolara canyon, a total of 1650 individuals (6.22 individuals/100 m^2) were totally collected (**Annex 1**), Amphipoda was the most abundant taxon (833 individuals collected, 3.16 individuals/100 m^2), with the genus *Rhachotropis* being by far the most abundant among amphipods, with the species *Rhachotropis integricauda* [**Fig. 3.1.1.a (a)**], *Rhachotropis rostrata* [**Fig 3.1.1.a (b)**] and *Rhachotropis grimaldii* [**Fig. 3.1.1.a (c)**].

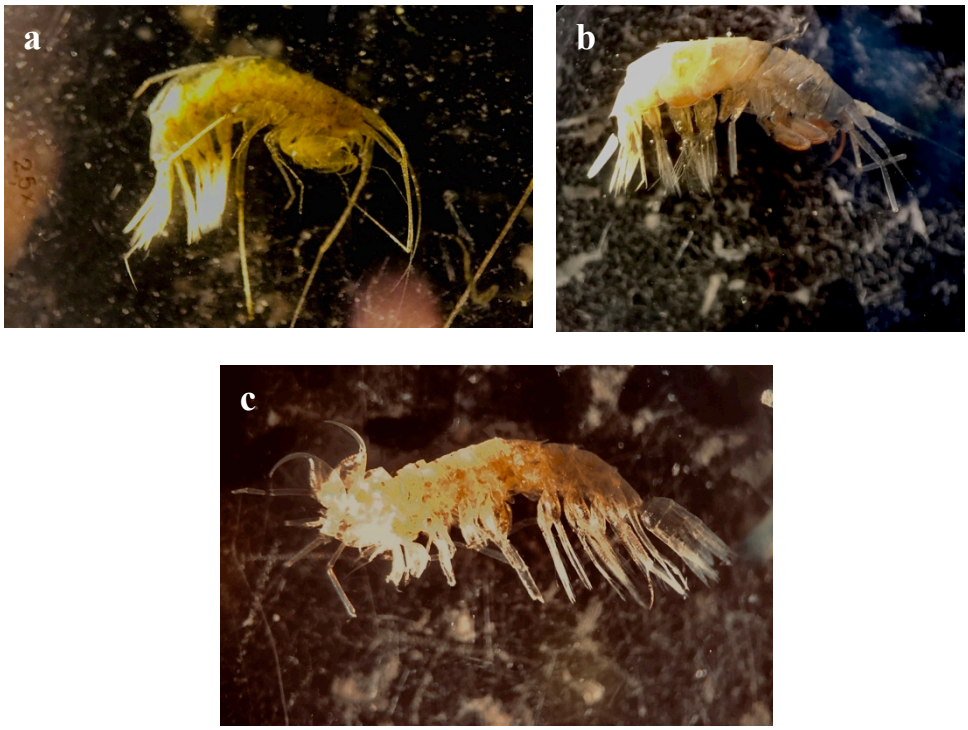

Fig. 3.1.1.a: a) *Rhachotropis integricauda*; b) *Rhachotropis rostrata*; c) *Rhachotropis grimaldii*.

Cumacea was the second most abundant taxon (206 individuals collected, 0.71 individuals/100 m^2), mostly rapresented by *Campylaspis glabra* (with the predominance of female individuals), *Procampylaspis bonnieri* [**Fig. 3.1.1.b (a)**], *Leucon* spp. (mainly *Leucon longirostris* and *Leucon macrorhinus* [**Fig. 3.1.1.b (b)]**), *Platysympus typicus* [**Fig 3.1.1.b (c)**] and *Makrocylindrus* spp.

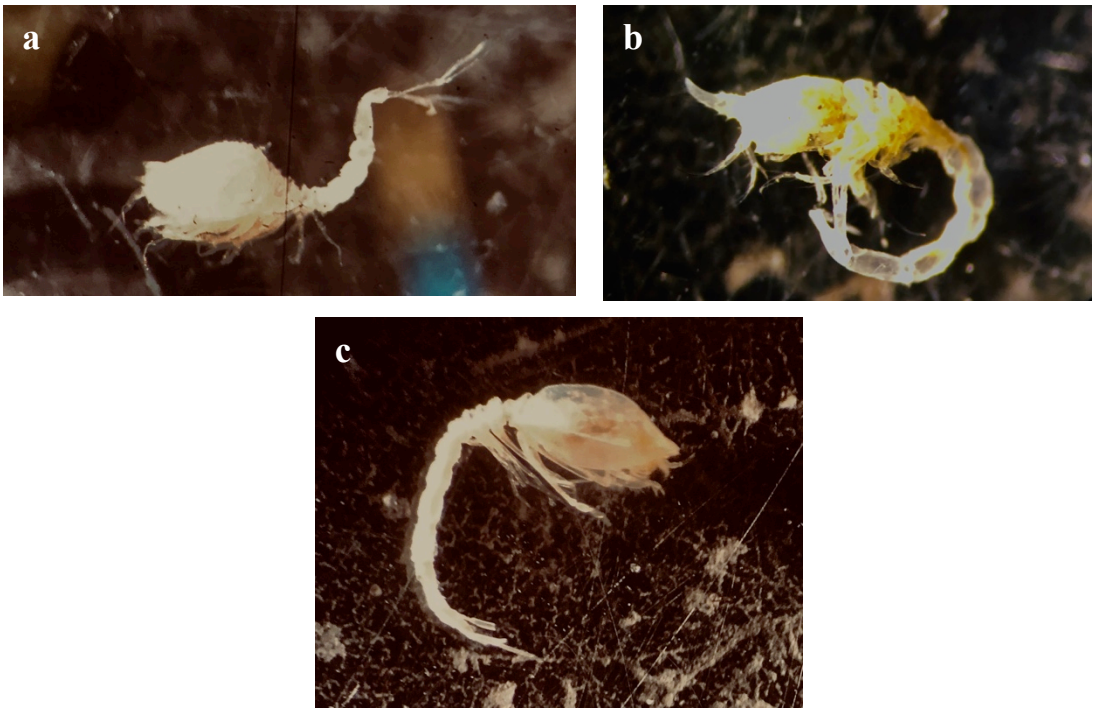

Fig 3.1.1.b: a) *Procampylaspis bonnieri*; b) *Leucon macrorhinus*; c) *Platysympus typicus*.

Isopoda was the third most abundant taxon (130 individuals collected, 0.48 individuals/100 m^2), with *Munnopsurus atlanticus* [**Fig. 3.1.1.c (a)**], *Eurycope* sp. and *Natatolana borealis* [**Fig 3.1.1.c (b)**] as the most abundant species found.

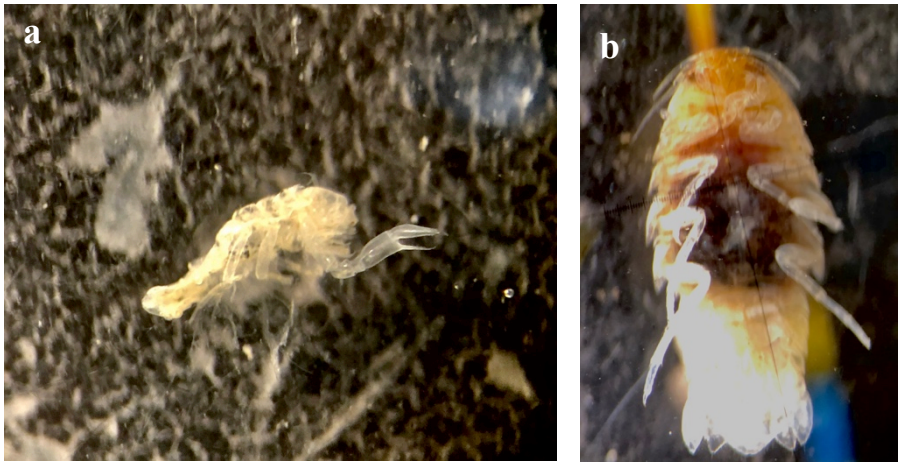

Fig. 3.1.1.c: a) *Munnopsurus atlanticus;* b) *Natatolana borealis*.

Other suprabenthic taxa found were Mollusca (107 individuals collected, 0.37 individuals/100 m^2), Anellida Polychaeta (46 individuals collected, 0.17 individuals/100 m^2), and Mysida (39 individuals collected, 0.16 individuals/10 m^2).

Concernig Polychaeta, this taxon is not considered a member of suprabenthos, because polychaetes live within the sediment. During the Macer-Giroq sampling, the shallow layer of the sediment was mixed, bringing the polychaetes with it. For this reason, this taxa was included in the suprabenthic assemblage. At the deepest site of the canyon (DC), the presence of numerous members of the family Aphroditidae was noticed [**Fig. 3.1.1.d (a)**].

As far as concerns mysids, *Boreomysis arctica* was the most abundant species (**Fig. 3.1.1.e**).

Other minor taxa summed up for 55 individuals (0.25 individuals/100 m^2; i.e. Ostracoda, Euphausiacea, Decapoda, Tanaidacea, etc.).

Fig. 3.1.1.d (a): Aphroditidae (Anellida Polychaeta)

Moreover, numerous calanoid and cyclopoid copepods (0.98 individuals/100 m^2) occured in the samples, which are not considered suprabenthos members (i.e. *Calanus* spp., *Euchaeta* spp., etc. among calanoid; *Corycaeus* sp., *Shappirina* spp., etc. among cyclopoid). This is because some species, during their vertical migrations approached the sea bed, and thus they were sampled by the Macer-Giroq sledge. Aetideidae family was the most rapresentative

family among calanoid copepods in this canyon, particularly at its deepest site (DC = 1000-1500 m), [**Fig 3.1.1.d (b)**].

(see **Annex 1** and **2** for more details).

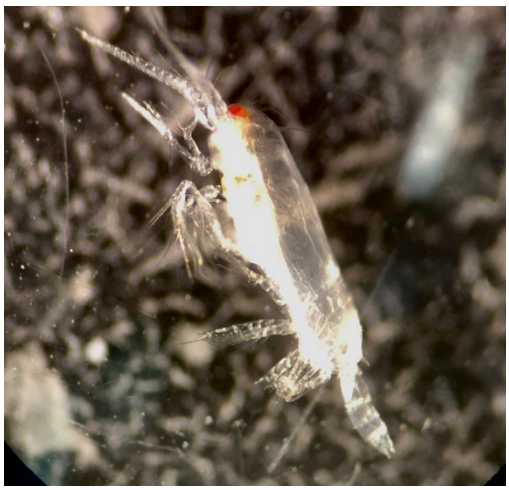

Fig 3.1.1.d (b): A member of the Aetideidae family (Copepoda Calanoida)

At Squillace canyon a total of 910 individuals (7.88 individuals/100 m^2) were totally collected (**Annex 1**). Amphipoda was the most abundant taxon (144 individuals collected, 0.97 individuals/100 m^2), with *Rhachotropis* sp. being by far the most abundant species among amphipods.

Isopoda was the second most abundant taxon (39 individuals collected, 0.26 individuals/100 m^2).

Mysida was the third most abundat taxon (35 individuals collected, 0.30 individuals/100 m^2), with *Boreomysis arctica* being by far the most abundant species among mysids (**Fig. 3.1.1.e**).

Numerous copepods occured in the samples (5.23 individuals/100 m^2) and also polychaetes (0.50 individuals/100 m^2), molluscs (0.36 individuals/100 m^2) and cumaceans (0.09 individuals/100 m^2).

Fig. 3.1.1.e: *Boreomysis arctica* (male).

Other minor taxa summed up for 47 individuals (0.25 individuals/100 m^2) (i.e. Ostracoda, Euphausiacea, Decapoda, Tanaidacea, etc.).

(see **Annex 1** and **2** for more details).

3.1.2 Zooplankton

The analysis of zooplanktonic samples has revealed a highly diversified zooplanktonic community and a complex assemblage structure:

At Amendolara canyon, a total of 2770 individuals (0.108 individuals/1000 m^3) were totally collected (**Annex 3**). Copepoda was the most abundant taxon (2582 individuals collected, 0.10 individuals/1000 m^3). *Calanus helgolandicus*, *Pleuromamma gracilis* [**Fig. 3.1.2.a (a)**], *Euchaeta* spp. [**Fig. 3.1.2.a (b)**], *Heterorabdus papilliger*, *Candacia longimana* [**Fig. 3.1.2.a (c)**], *Centropages* spp. [**Fig. 3.1.2.a (e)**] were the most abundant species collected among copepods. Calanoida was the most common order collected among the Copepoda taxon, but also some Cyclopoida-order-members occured (i.e. *Corycaeus* sp. [**Fig. 3.1.2.a (d)**]).

Numerous small-sized copepods, both adults and copepodites, were collected in the samples, and were included in the "Copepoda unidentified group" due to the impossibility of carrying out a lower taxonomic identification.

Oncaea sp. was the only abundant small-sized copepod identified [**Fig 3.1.2.a (f)**].

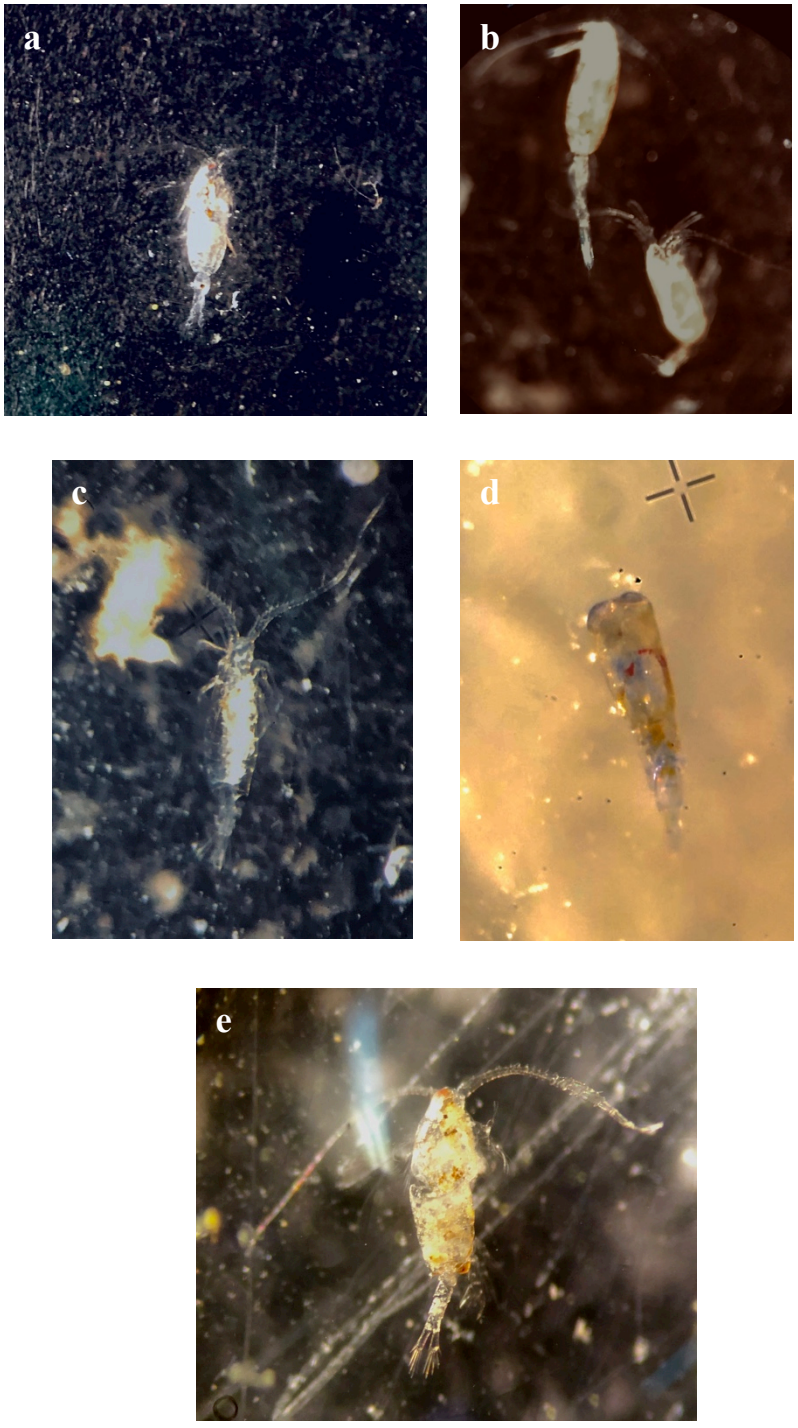

Fig. 3.1.2.a: a) *Pleuromamma gracilis*; b) *Euchaeta* spp.; c) *Candacia longimana* (male); d) *Corycaeus* sp.; e) *Centropages typicus* (male).

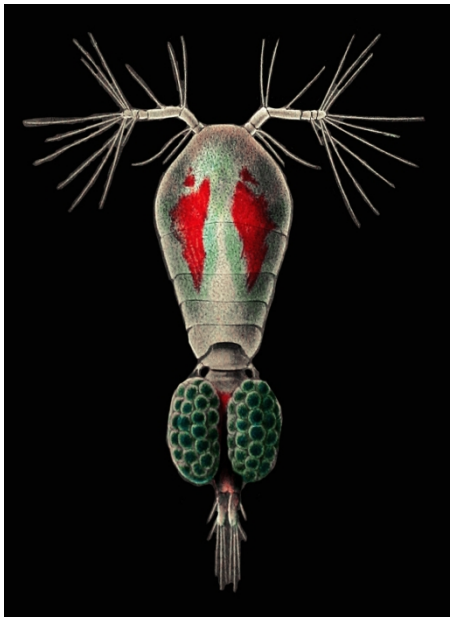

Fig. 3.1.2.a (f): Schematic rapresentation of *Oncaea* sp. (Website: *marinespecies.org*).

Cladocera was the second most abundant taxon (78 individuals collected, 0.0029 individuals/1000 m^3) (**Fig. 3.1.2.b**).

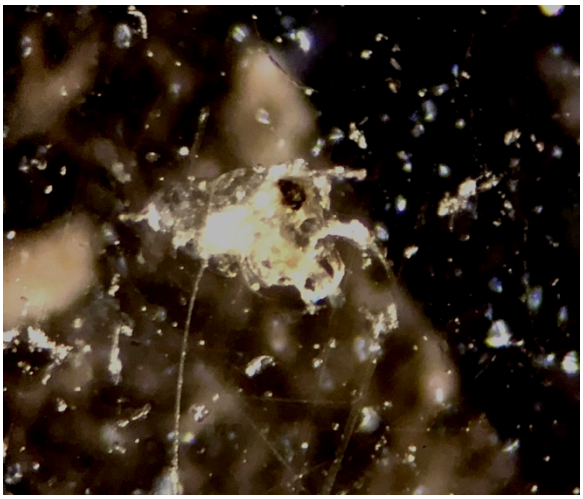

Fig. 3.1.2.b: *Evadne* sp. (cladocera).

Ostracoda was the third most abundant taxon (71 individuals collected, 0.00172 individuals/1000 m^3).

Hyperiid amphipods were also collected in the samples (8 individuals collected, 0.0017 individuals/1000 m^3), with *Vibilia jeangerardi* [**Fig. 3.1.2.c (a)**]), *Phronima sedentaria* [**Fig. 3.1.2.c (b)**] *Primno macropa* [**Fig 3.1.2.c (d)**], *Hyperia* spp. as the most common species. Also the very rare *Streetsia challengeri* [**Fig. 3.1.2.c (c)**], was found.

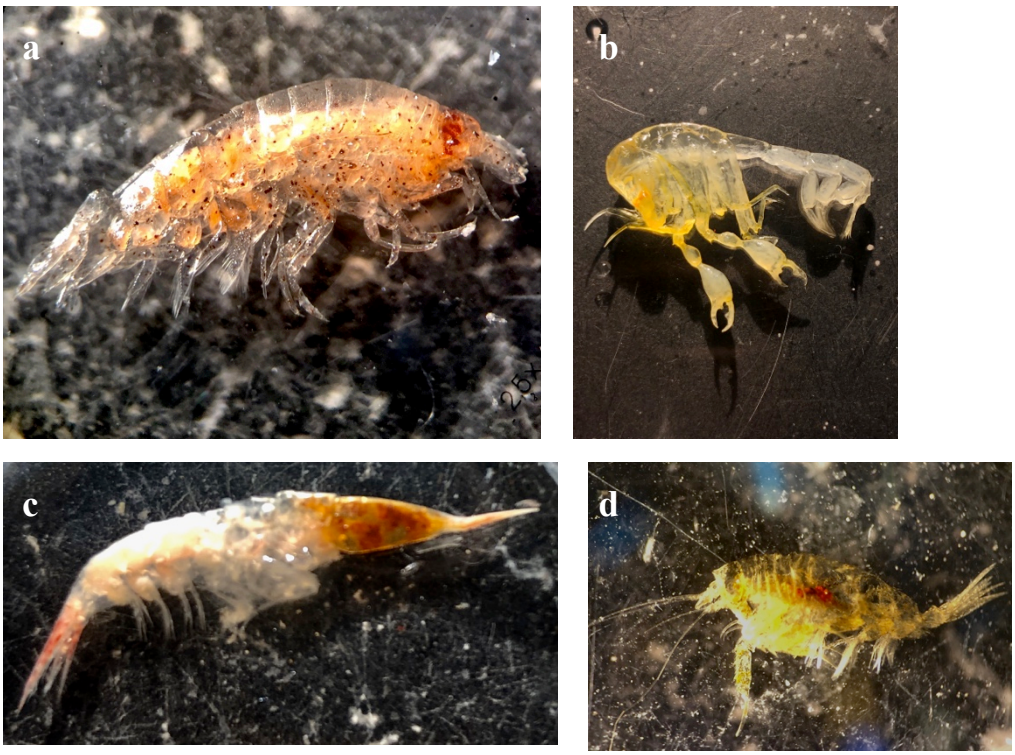

Fig. 3.1.2.c: a) *Vibilia jeangerardi*; b) *Phronima sedentaria* (picture not taken at the stereomicroscope); c) *Streetsia challengeri*; d) *Primno macropa*.

Euphausiacea (13 individuals collected, 0.00035 individuals/1000 m^3) was another taxon collected in the samples, with *Meganyctiphanes norvegica* (**Fig 3.1.2.d**) and *Nematoscelis megalops* as the most abundant species.

Fig. 3.1.2.d: *Meganyctiphanes norvegica.*

Concerning vertebrates, some fish individuals were collected (9 individuals collected, 0.00023 individuals/1000 m^3), with *Cyclothone braueri* as the only species found (**Fig. 3.1.2.e**).

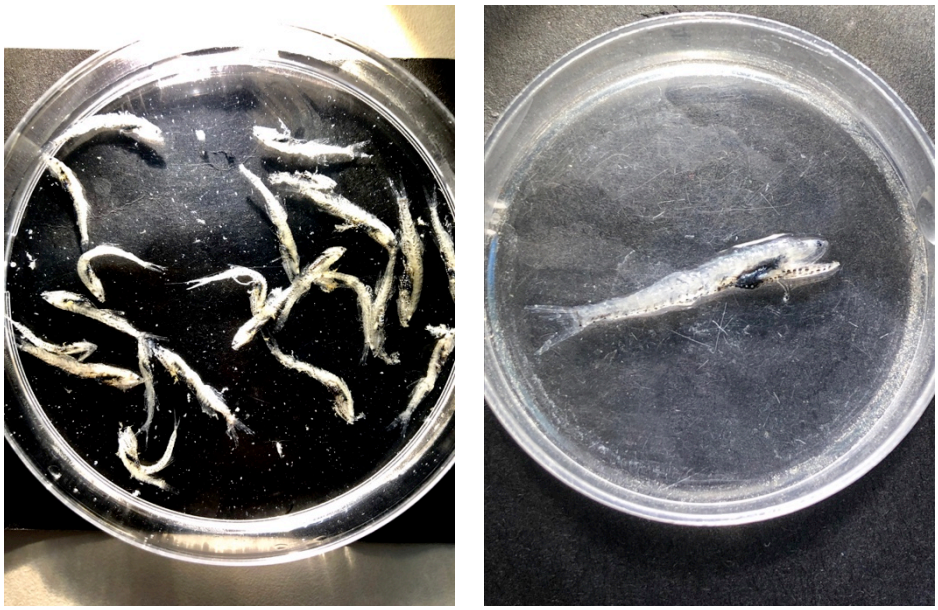

Fig. 3.1.2.e: *Cyclothone baueri* (pictures not taken at the stereomicroscope).

Other minor taxa summed up for 9 individuals (0.00027 individuals/1000 m^3 (i.e. Siphonophora, Decapoda and Urochordata, with *Pyrosoma atlanticum* as the only species found among Urochordata (**Fig. 3.1.2.f**)).

(See **Annex 3** and **4** for more details).

Fig. 3.1.2.f: *Pyrosoma atlanticum*.

At Squillace canyon a total of 1978 individuals (0.045 individuals/1000 m^3) were totally collected (**Annex 3**). Copepoda was the most abundant taxon (1895 individuals collected, 0.04 individuals/1000 m^3), with a species composition similar to that of Amendolara canyon.

Concerning fish, *Cyclothone braueri* was the only species found in the samples (33 individuals collected, 0.00085 individuals/1000 m^3).

Other zooplanktonic taxa collected were Ostracoda (23 individuals collected, 0.00052 individuals/1000 m^3), Euphausiacea (14 individuals collected, 0.00034 individuals/1000 m^3), with *Meganyctiphanes norvegica* and *Nematoscelis megalops* as the only two species found among the euphausiids,

Amphipoda Hyperidea (11 individuals collected, 0.00027 individuals/1000 m^3), with a species composition similar to that of Amendolara canyon (See **Annex 3** and **4** for more details).

3.2 Trends in abundance and biomass

3.2.1 Suprabenthos

A difference between the inspected canyons, in terms of total abundances per canyon depth was noticed (**Fig. 3.2.1.a**). The Amendolara canyon showed a moderate increasing of the total abundance moving progressively from the HC to DC site, while the Squillace canyon showed the highest values of the total abundance at the HC site (considerably higher than at the HC of Amendolara). Abundance values dropped sharply moving toward the MC and the DC, where they tended to be quite similar.

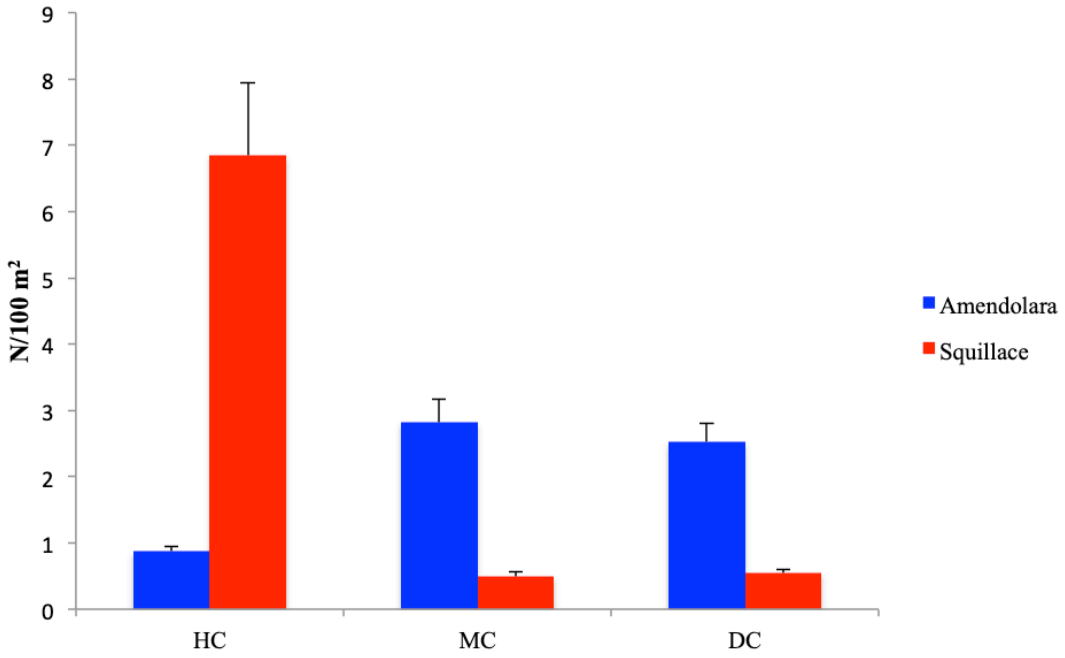

Fig. 3.2.1.a: Suprabenthic trends in abundances along the Amendolara and Squillace canyon.

The trend of the total abundance was consistent with that of biomass one, except for DC, where Squillace canyon showed a moderate higher total biomass value compared to the Amendolara one (**Fig 3.2.1.b**).

In general, a higher total biomass value at HC in the Squillace canyon was found, with a sharply decline moving to MC, and a moderate increase at DC. In the case of Amendolara, the total biomass values was low at HC, with a moderate increase moving towards the DC.

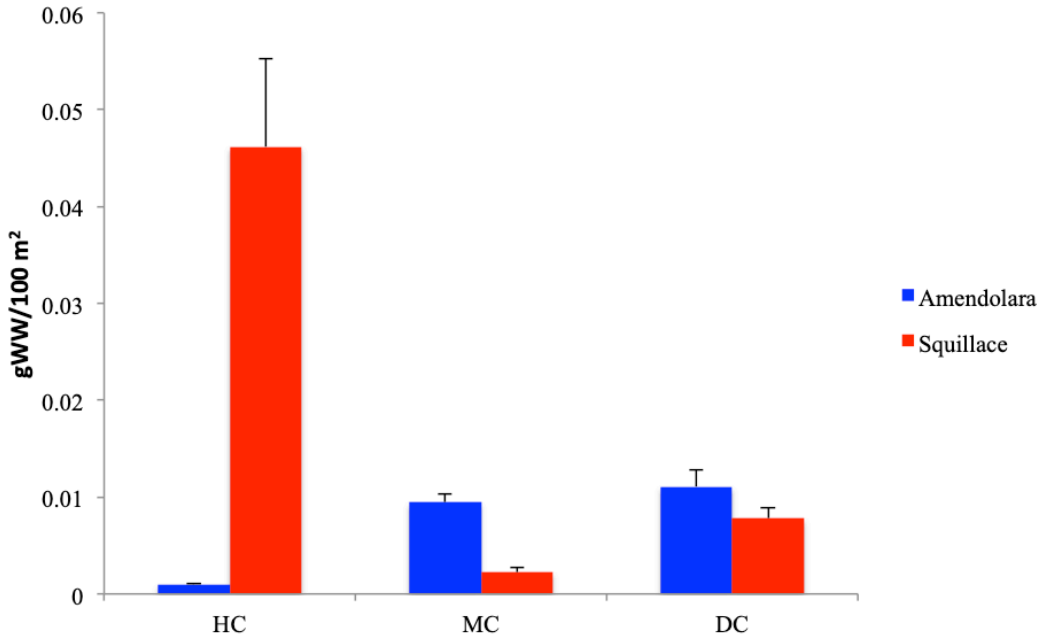

Fig. 3.2.1.b: Suprabenthic trends in biomass along the Amendolara and Squillace canyon.

In terms of taxa composition, at Amendolara canyon, the most abundant taxon was Amphipoda, mostly Gammaridea (**Fig. 3.2.1.c**), with occasional finding of some Amphipoda Hyperidea. This taxon is generally part of the zooplanktonic assemblage, but some species often occur near the sea bottom. Other taxa summed up for the other 50%, each with low percentage, these were Copepoda (16%), Cumacea (11%), Isopoda (8%), Mollusca (6%). Other taxa, such as polychaetes and mysids occured with very low abundances.

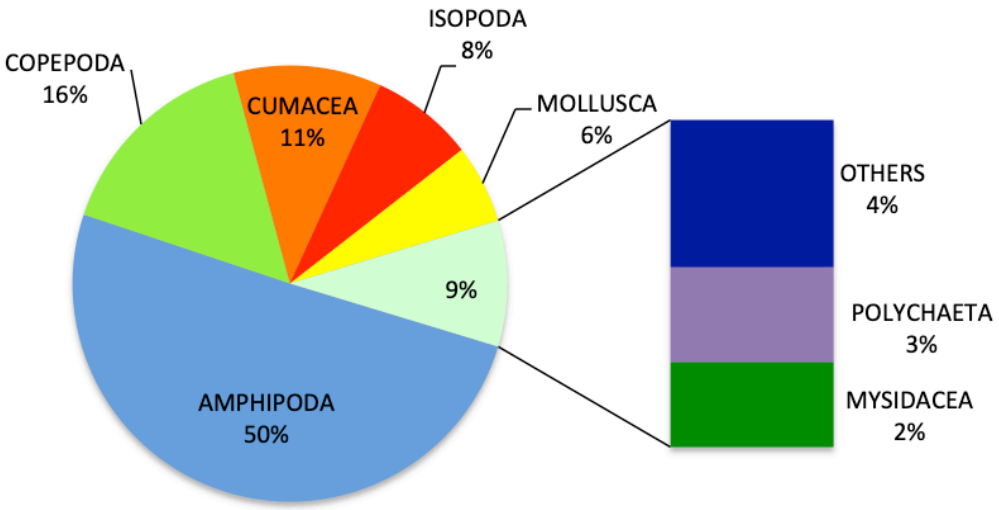

Fig. 3.2.1.c: Percentage contribution (in terms of abundance) of the different suprabentic taxa in the Amendolara canyon.

In terms of taxa composition, at Squillace canyon the suprabenthic community seemed to show a different abundance pattern. Copepoda were the most abundant taxon (70%) (**Fig. 3.2.1.d**), while Amphipoda were less rapresentented compared to the Amendolara canyon (7%). In the Squillace canyon some additional taxa occured, such as Decapoda (2%). Cumacea were less abundant and Mysidacea more abundant (4%) compared to Amendolara canyon (1%).

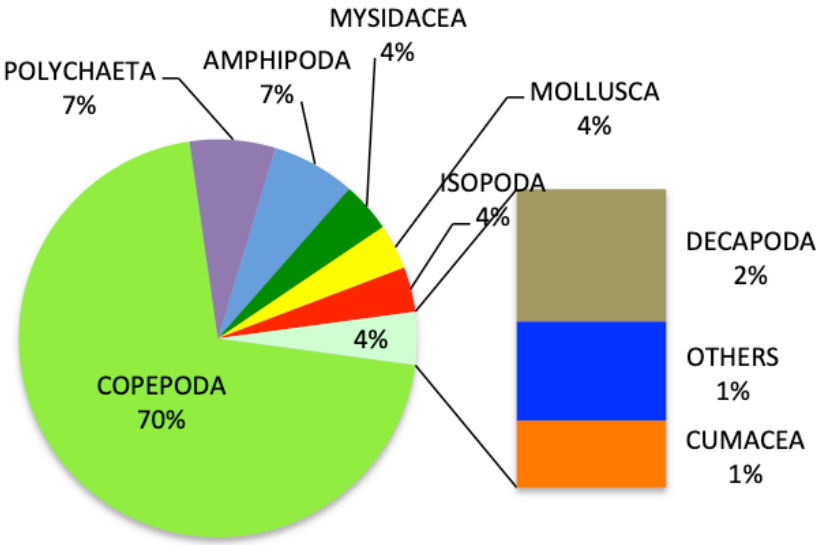

Fig. 3.2.1.d: Percentage contibution (in terms of abundance) of the different suprabenthic taxa in the Squillace canyon.

In terms of biomass, Mollusca was the taxon which mostly affected the total wet weight in the Amendolara canyon (52%), due to their heavy shells (**Fig. 3.2.1.e**). Amphipoda were the second taxon which more affected the total biomass (28%), showing consistency with the abundance data.

Copepoda did not contribute largely to the total biomass (3%), due to their small size.

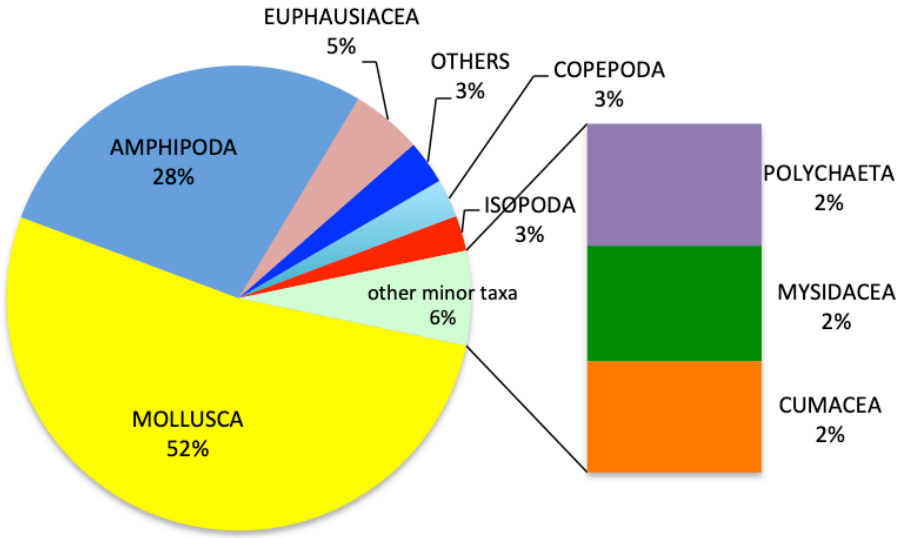

Fig. 3.2.1.e: Percentage contibution (in terms of biomass) of different suprabenthic taxa in the Amendolara canyon.

Amphipoda and Polychaeta taxa mostly contributed to the total wet weight at Squillace canyon (repectively 60% and 29%) (**Fig. 3.2.1.f**). In both cases such dominance in terms of biomass, was caused by the occurrence of very large animals, such as *Epimeria parasitica*, in the case of amphipods (**Annex 2**).

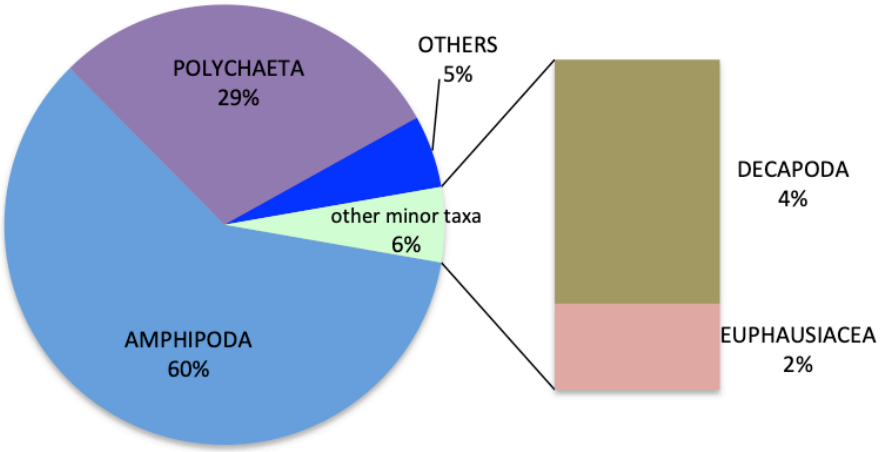

Fig. 3.2.1.f: Percentage contribution (in terms of biomass) of different suprabenthic taxa in the Squillace canyon.

3.2.2 Zooplankton

A general decline of abundance moving from HC the DC was observed (**Fig 3.2.2.a)**.

In the Amendolara canyon, a higher abundance at the HC site compared to the Squillace canyon occured, followed by a decline towards the MC and DC sites. At the DC site the abundance was considerably low both at Amendolara and Squillace canyon, but in the case of Squillace canyon the abundance trend was quite different. Here, a low number of individuals/100 m^2 was found at the HC site, with abundances increasing from the HC to the MC site, and then declining again at the DC site.

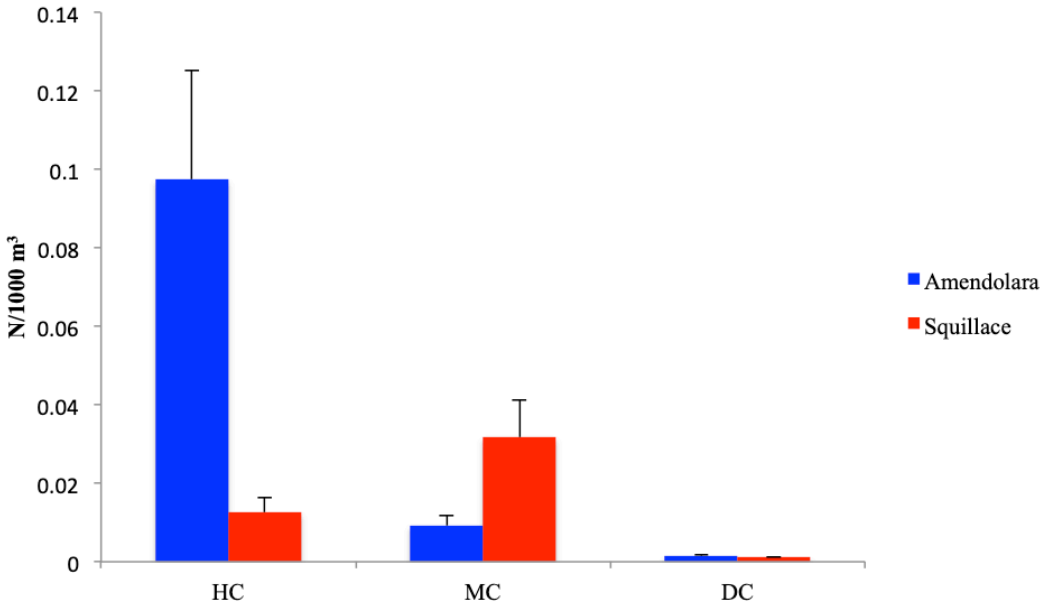

Fig. 3.2.2.a: Zooplanktonic trends in abundances along the Amendolara and Squillace canyons.

Biomass trends were consistent with those of abundance, at the HC and MC sites (**Fig. 3.2.2.b**), with a higher increase of biomass from the HC to the MC. However a different trend at the DC site was observed, with a higher biomass value in the Squillace canyon, due to the presence of a low number of animals having greater wet weight, particularly the fish species *Cyclothone braueri*.

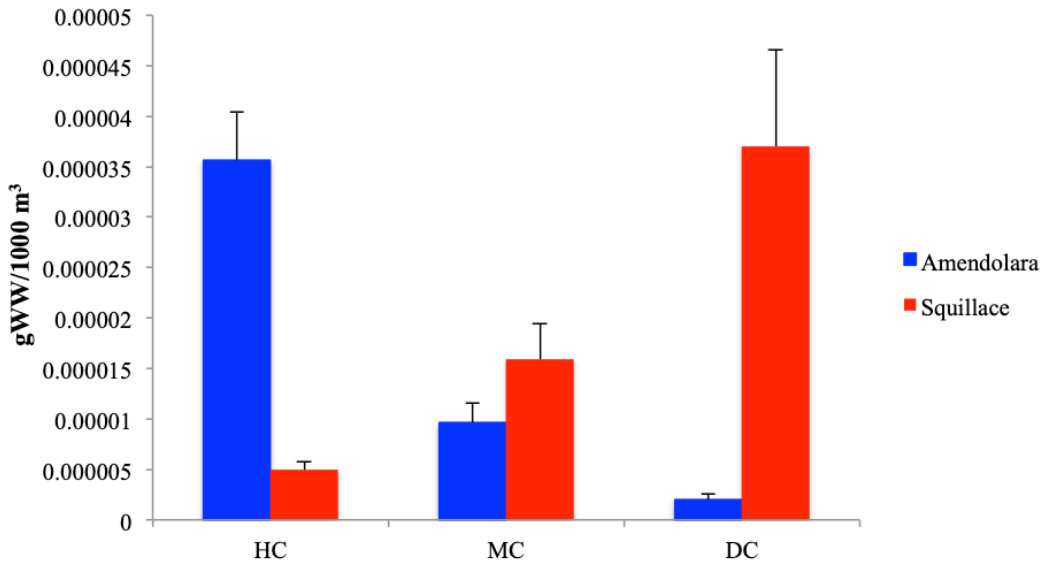

Fig. 3.2.2.b: Zooplanktonic trends of biomasses along the Amendolara and Squillace canyons.

In terms of taxa composition, at Amendolara canyon a dominance of Copepoda (95%) was observed (**Fig. 3.2.2.c**), both Calanoida and Cyclopoida orders, which raprensented almost all zooplanktonic animals. Cladocera and Ostracoda were less abundant (respectively 3% and 1%).

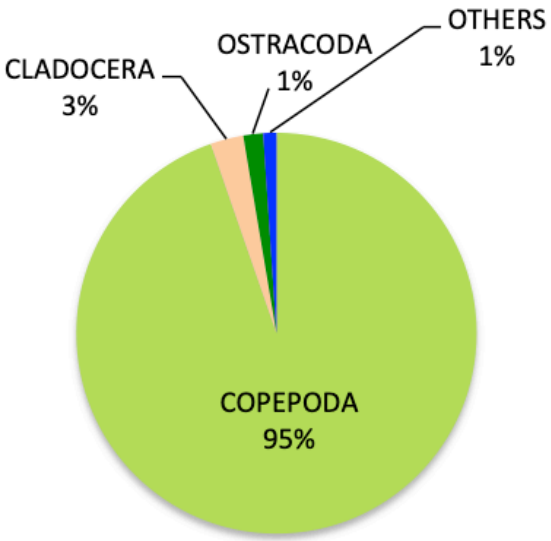

Fig. 3.2.2.c: Percentage contribution (in terms of abundance) of different zooplanktonic taxa in the Amendolara canyon.

Also in the case of Squillace, Copepoda is the most abundant taxon found (96%), (**Fig. 3.2.2.d**). Pisces occured with the only species *Cyclothone braueri* (2%).

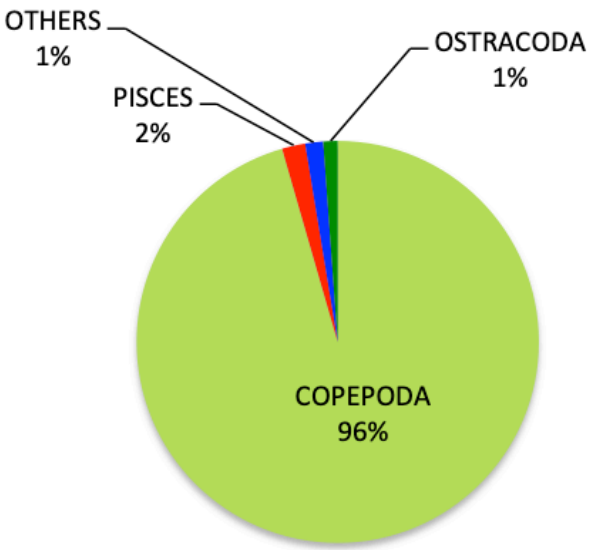

Fig. 3.2.2.d: Percentage contribution (in terms of abundance) of different zooplanktonic taxa in the Squillace canyon.

The numeorus copepods found in the Amendolara canyon had a low biomass (such as *Oncaea* sp., copepodites, and numeorous small-sized unidentified individuals), and contributed 38% to the total wet weight (**Fig 3.2.2.e**).

Amphipoda Hyperidea and Euphausiacea contributed 17% to the total biomass. The hyperriid *Phronima sedentaria* and the euphausiid *Meganyctiphanes norvegica*, in the case of euphausiids, were the species which mostly constributed to the total biomass (**Annex 4**). Thaliacea (*Phylum* Urochordata), only rapresented by the species *Pyrosoma atlanticum*, contributed 14% to the total biomass (**Annex 4**).

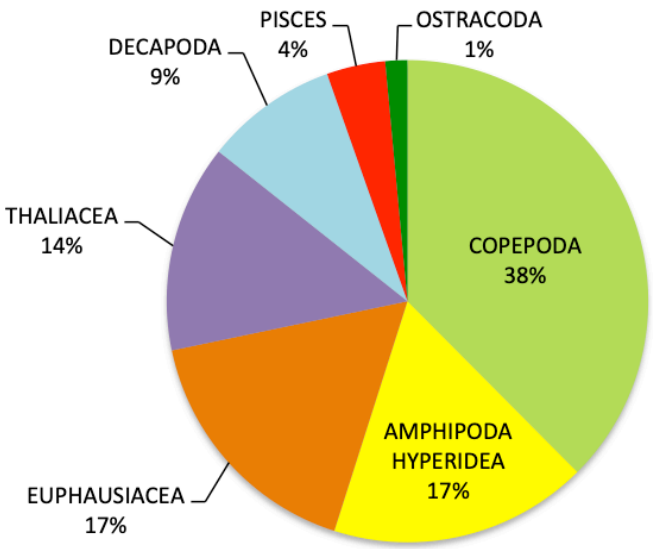

Fig 3.2.2.e: Percentage contribution (in terms on biomass) of different zooplanktonic taxa in the Amendolara canyon.

Pisces was the taxon which mostly contributed to the total biomass in the Squillace canyon (59%) (**Fig 3.2.2.f** and **Annex 4)**. Amphipoda Hyperidea taxon was the second dominant taxon in terms of biomass. Copepoda, both Calanoida and Cyclopoida order, had a less contribution to the total biomass compared to the Amenodolara canyon (10%).

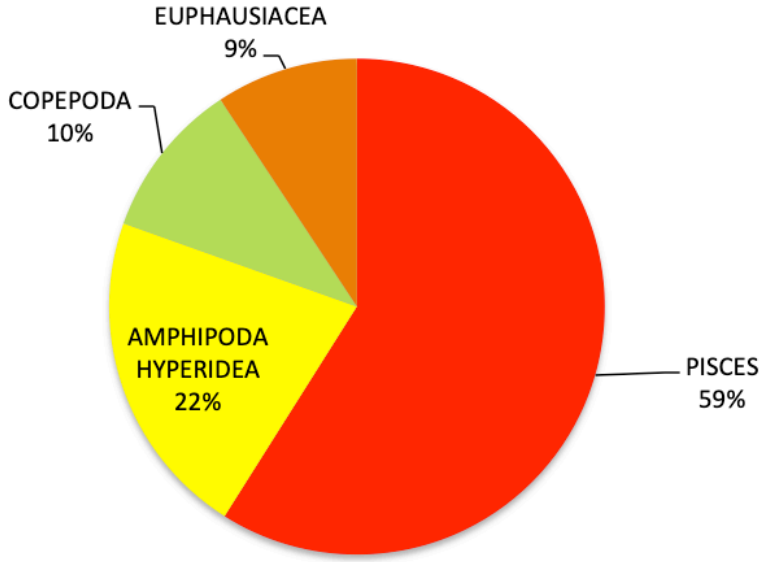

Fig. 3.2.2.f: Percentage contribution (in terms of biomass) of different zooplanktonic at Squillace canyon.

3.3 Species assemblages

3.3.1 Suprabenthos

The cluster analysis showed a clear separation between the suprabenthic assemblages of the two canyons (**Fig. 3.3.1.a**).

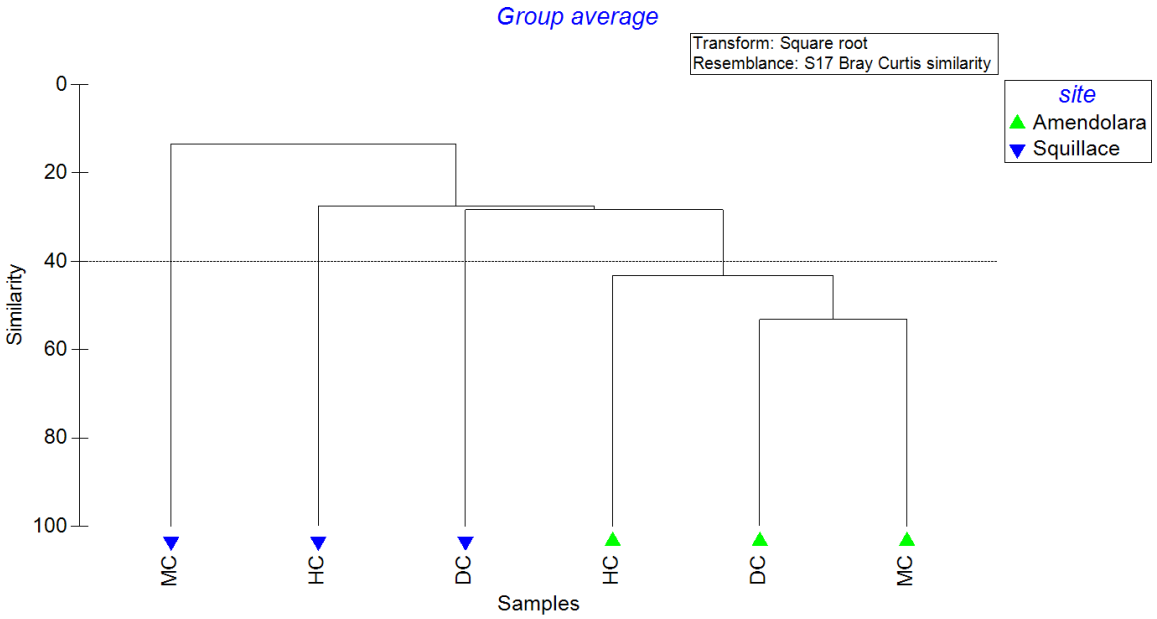

Fig. 3.3.1.a: Cluster performed on suprabenthic abundance.

At 40% of similarity samples of the Amendolara canyon were clearly separated from those of Squillace and clustered together, with samples from the medium and the deepst parts of the canyon (MC and DC) separated from that at the canyon head (HC). Samples from Squillace differed among each other, although the HC and DC were closer in the cluster, being more similar to each other (**Fig. 3.1.1.a**).

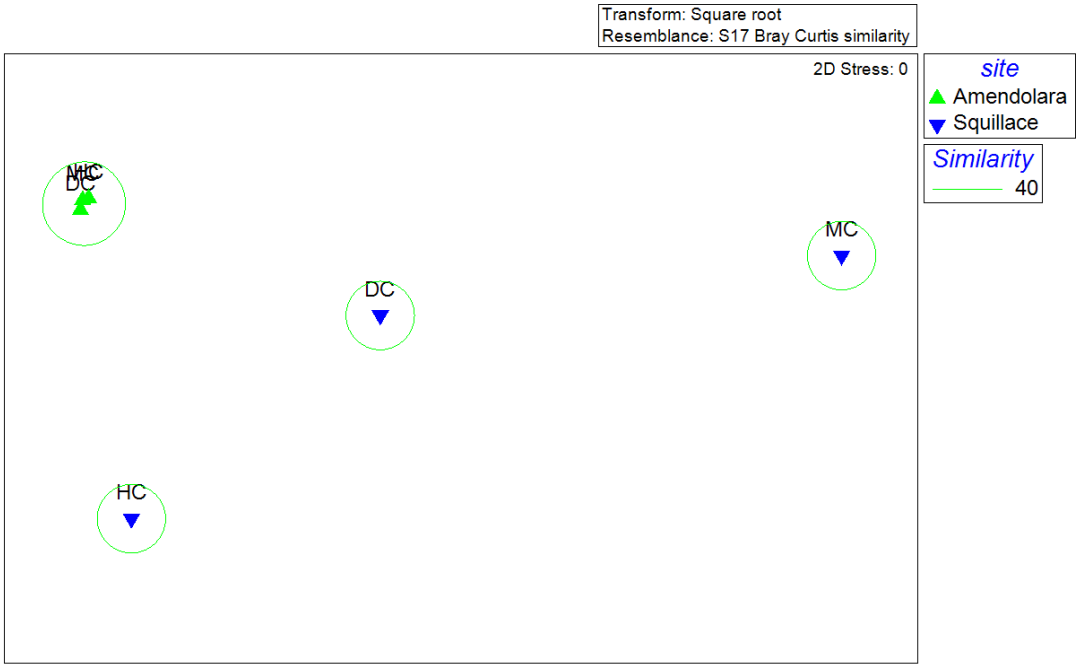

Fig 3.3.1.b: nMDS performed on suprabenthic abundance. The green circles indicates the 40% of similarity.

The nMDS, with overlaid cluster at 40% of similarity, showed a similar representation, with samples from Amendolara grouping together (**Fig 3.3.1.b**). In agreement with results provided by the cluster analysis, in the nMDS samples from the Amedolara grouped together at 40% of similarity. Samples from the Squillace canyon were all separated, with the HC and the DC closer to Amendolara samples, and the MC farther, being the assemblage at this site very dissimilar to those at the other depth ranges.

However, such differences were not significant (PERMANOVA test, $p > 0.05$ for all terms).

According to SIMPER results, at Amendolara canyon, the amphipod *Rhachotropis* sp. was the genus which mostly contributed to the total similarity (9.86%), (**Table 3.3.1.a**) with *Rhachotropis integricauda* (6.28%) as the most abundant spieces. The cumacean *Campylaspis glabra* contributed 8.01% to the total similarity, followed by the isopod and *Munnopsurus atlanticus* (6.96%) and the copepod family Aetideidae contributed 6.59% to the total similarity, being dominant at the DC site.

At the Squillace canyon, Polychaeta was the taxon which mostly contributed to the total similarity (17.2%), followed by Copepoda (14.13%) and Amphipoda Gammaridea as a whole (13.63%) (**Table 3.3.1.a**).

Table 3.3.1.a: Results of SIMPER per site based on Bray-Curtis similarity (cut-off at 50%)

Group Amendolara	Average similarity: 46.55			
Taxa	Av.Abund	Av.Sim	Contrib%	Cum.%
Rhachotropis sp.	0.49	4.59	9.86	9.86
Campylaspis glabra	0.31	3.73	8.01	17.87
Munnopsurus atlanticus	0.33	3.24	6.96	24.84
Aetideidae	0.3	3.07	6.59	31.43
Mollusca bivalvia unid.	0.24	3	6.45	37.88
Rhachotropis integricauda	0.45	2.92	6.28	44.16
Mollusca gastropoda unid.	0.22	2.47	5.3	49.46
Oedicerotidae	0.23	2.36	5.07	54.53
Group Squillace	Average similarity: 19.55			
Taxa	Av.Abund	Av.Sim	Contrib%	Cum.%
Polychaeta unid.	0.29	3.36	17.2	17.2
Copepoda unid.	0.89	2.76	14.13	31.33
Gammaridea unid.	0.2	2.66	13.63	44.95
Rhachotropis sp.	0.22	2.46	12.58	57.54

At HC, Amphipoda Gammaridea mostly contributed the total similarity (21.77%) (**Table 3.3.1.b**). Mollusca Bilvalvia was the second most abundant taxon (15.4%), followed by *Rhachotropis* sp. (14.36%).

At MC *Rhachotropis grimaldii* was the species with the highest contribution (22.34%), followed by unidentified Polychaeta (19.51%).

At DC unidentified Copepoda had the highest contribution (25.45%) followed by *Rhachotropis integricauda* (11.65%), the mysid *Boreomysis arctica* (9.62%) and the amphipod *Stegocephaloides christianensis* (7.02%).

Table 3.3.1.b: Results of SIMPER per depth based on Bray-Curtist similarity (cut-off at 50%).

Group HC	Average similarity: 27.61			
Taxa	Av.Abund	Av.Sim	Contrib%	Cum.%
Gammaridea unid.	0.39	6.01	21.77	21.77
Mollusca bivalvia unid.	0.36	4.25	15.4	37.17
Rhachotropis sp.	0.36	3.96	14.36	51.53
Group MC	Average similarity: 11.17			
Taxa	Av.Abund	Av.Sim	Contrib%	Cum.%
Rhachotropis grimaldii	0.19	2.5	22.34	22.34
Polychaeta unid.	0.35	2.18	19.51	41.84
Gammaridea unid.	0.44	1.76	15.8	57.64
Group DC	Average similarity: 31.71			
Taxa	Av.Abund	Av.Sim	Contrib%	Cum.%
Copepoda unid.	0.53	8.07	25.45	25.45
Rhachotropis integricauda	0.48	3.69	11.65	37.1
Boreomysis arctica	0.24	3.05	9.62	46.72
Stegocephaloides christianensis	0.16	2.23	7.02	53.74

Biodiversity trend, expressed in terms of Shannon-Wiener index, was greater at Amendolara than at Squillace (**Fig. 3.3.1.c**). At Amendolara, biodiversity increased from HC to MC and decreased at the DC site. At Squillace an opposite trend was observed, with higher values at HC and DC and lower at MC (**Fig. 3.3.1.c**).

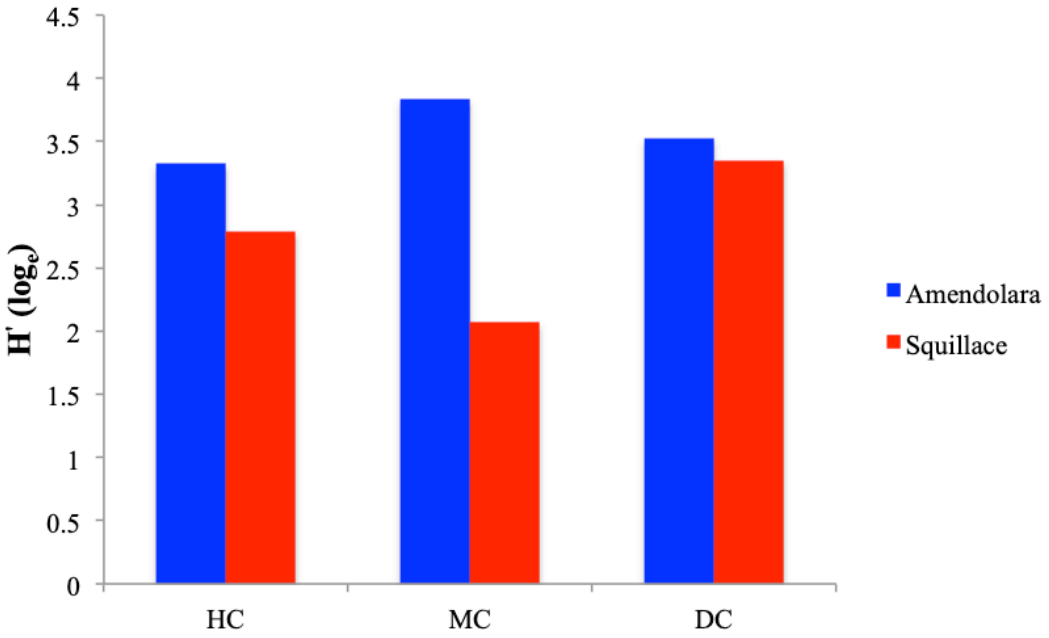

Fig. 3.3.1.c: Suprabenthic biodiversity trend expressed as Shannon-Wiener diversity index (H', $\log_e$), performed on suprabenthos abundance along Amendolara and Squillace canyon.

Merging all samples at each canyon, at Amendolara suprabenthic biodiversity was significantly greater compared to Squillace. (**Fig. 3.3.1.d, F=, p=**).

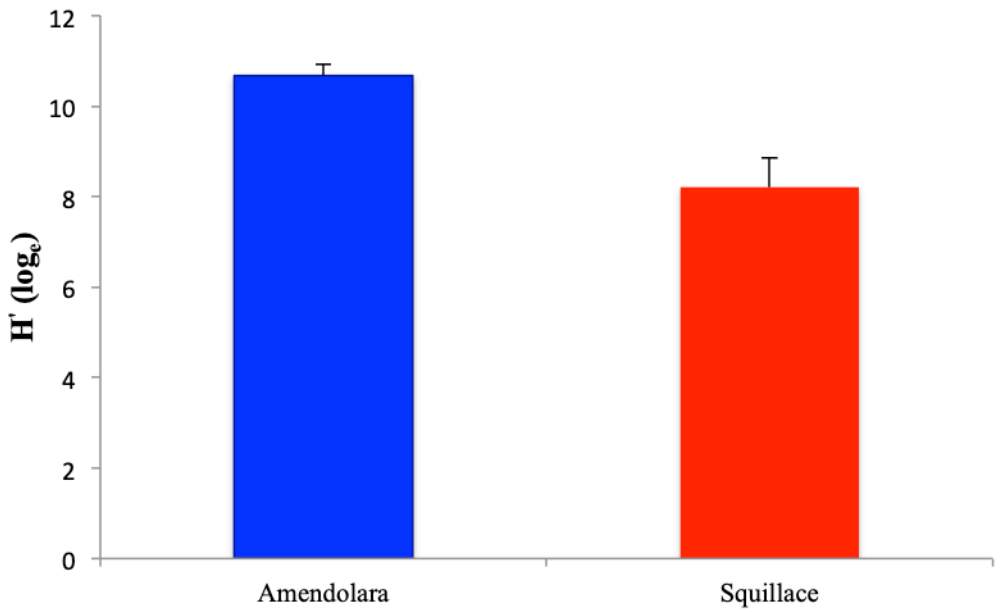

Fig. 3.3.1.d: Suprabenthic biodiversity trend, expressed as Shannon-Wiener diversity index (H', $\log_e$), obtained merging all samples at each canyon.

Merging the similar depths together of the two canyons, biodiversity trend was similar between the HC and MC, and tended to increase from the MC to the DC. (**Fig.3.3.1.e**).

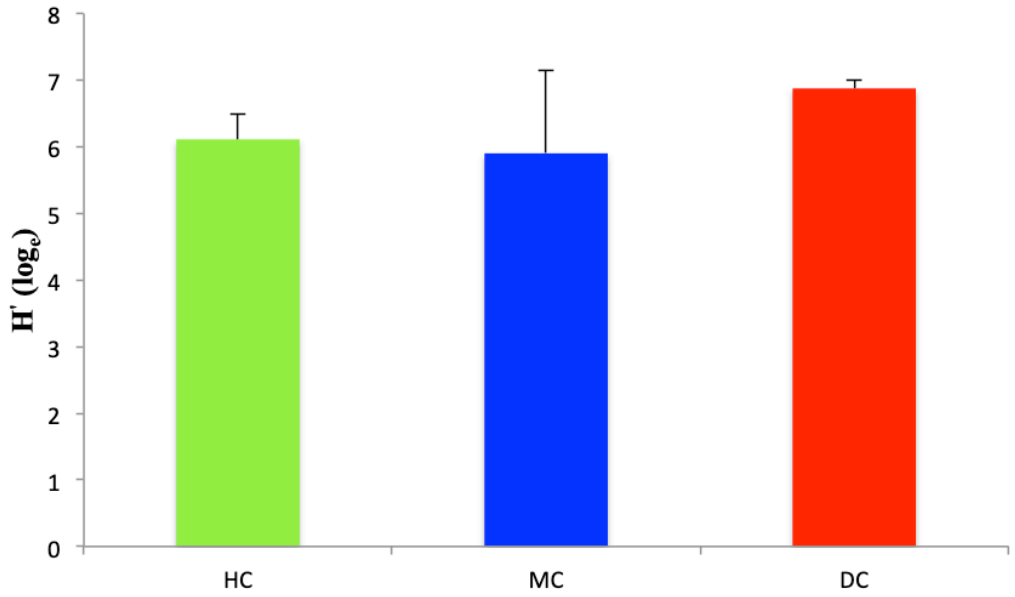

Fig. 3.3.1.e: Suprabenthic biodiversity trend, expressed as Shannon-Wiener diversity index (H', $\log_e$), obtained merging the similar depths together of the two canyons.

3.3.2 Zooplankton

The cluster analysis did not show a clear separation between the two canyons but, merging Amedolara and Squillace data, the HC and MC sites of each canyon showed to be more similar within each other than compared to the DC sites. The DC samples of both canyons grouped together (**Fig. 3.3.2.a**). At 40% of similarity, samples of the HC and MC were clearly separated from those of DC and clustered together, with the highest similarity between the MC of Amendolara and the MC of Squillace. The DC sites of each canyon tended

to be more similar within each other compared to the other canyon sites, and clustered together.

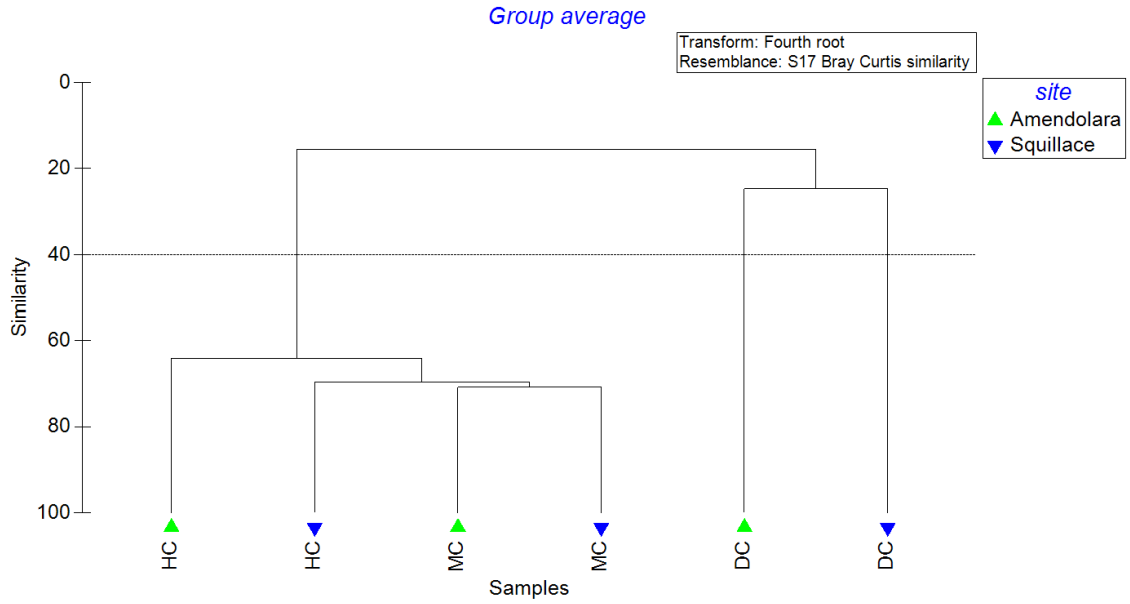

Fig. 3.3.2.a: Cluster performed on zooplaktonic abundance.

The nMDS, with overlaid cluster at 40% of similarity, showed a similar representation, with the HC and MC sites of each canyon grouping together (**Fig. 3.3.2.b**) In agreement with results provided by the cluster analysis, in the nMDS samples from HC and DC of the Amendolara and Squillace canyon showed more similarity to each other. The DC sites are separated from the other canyon depths.

However, such differences were not significant (PERMANOVA test, $p > 0.05$ for all terms).

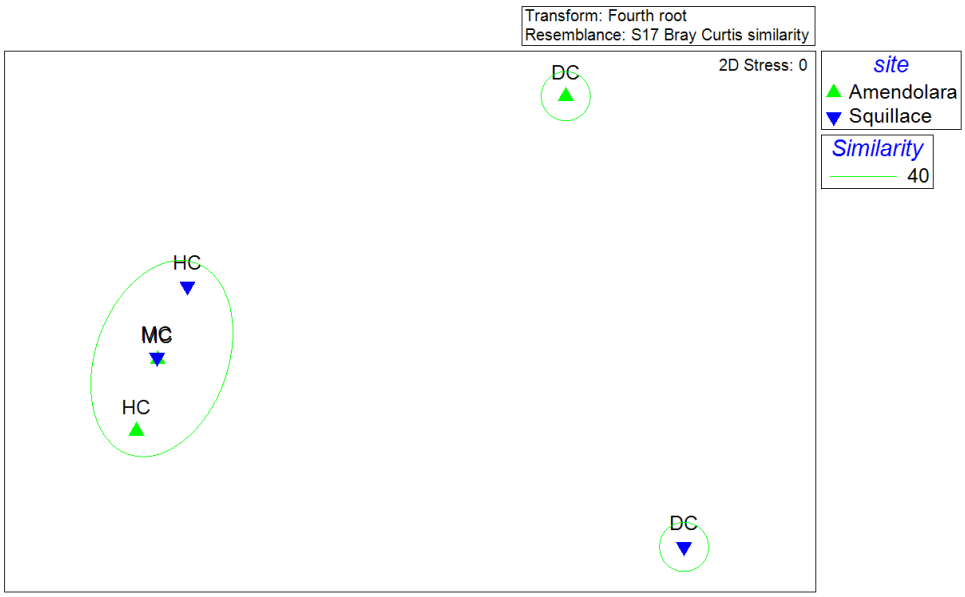

Fig. 3.3.2.b: nMDS performed on zooplanktonic abundance.

SIMPER analysis revealed at Amendolara, unidentified Copepoda, mostly contributed to the total similarity (25.76%) (**Table 3.3.2.a**). Unidentified Ostracoda was the second most contributing taxa (14.85%).

At Squillace, as at Amendolara, unidentified Copepoda mostly contributed to the total similarity (16.27%). The small copepod *Oncaea* sp. contributed 9.5% to the total similarity, followed by the small mesopelagic fish *Cyclothone braueri* (8.79%).

Table 3.3.2.a: Results of SIMPER per site based on bray-Curtist similarity (cut-off at 50%).

Group Amendolara	Average similarity: 34.90			
Taxa	Av.Abund	Av.Sim	Contrib%	Cum.%
Copepoda unid.	0.3	8.99	25.76	25.76
Ostracoda unid.	0.14	5.18	14.85	40.61
Oncaea sp.	0.2	2.03	5.8	46.42
Calanus helgolandicus	0.16	1.54	4.43	50.84
Group Squillace	Average similarity: 27.56			
Taxa	Av.Abund	Av.Sim	Contrib%	Cum.%
Copepoda unid.	0.23	4.48	16.27	16.27
Oncaea sp.	0.15	2.71	9.85	26.12
Cyclothone braueri	0.08	2.42	8.79	34.91
Meganycthiphanes norvegica	0.07	2.31	8.38	43.28
Calanus helgolandicus	0.12	2.25	8.16	51.44

At HC, unidentified Copepoda mostly contributed to the total similarity (14.87%), followed by the copepods *Calanus helgolandicu*s (10.03%) and *Oncaea* sp. (9.01%) (**Table 3.3.2.b**).

At MC, unidentified Copepoda mostly contributed to the total similarity (14.25%), with *Oncaea* sp. (12.34%) and *Calanus helgolandicus* (8.48%), as the most typifying genus/species. At DC, *Cyclothone braueri* contributed 100% to the total similarity.

Table 3.3.2.b: Results of SIMPER per depth based on Bray-Curtist similarity (cut-off at 50%)

Group HC	Average similarity: 60.60			
Taxa	Av.Abund	Av.Sim	Contrib%	Cum.%
Copepoda unid.	0.38	9.01	14.87	14.87
Calanus helgolandicus	0.26	6.08	10.03	24.9
Oncaea sp.	0.29	5.46	9.01	33.91
Heterorhabdidae	0.18	4.37	7.21	41.12
Corycaeus sp.	0.16	4.22	6.97	48.09
Euchaeta spinosa	0.16	3.88	6.41	54.5
Group MC	Average similarity: 70.86			
Taxa	Av.Abund	Av.Sim	Contrib%	Cum.%
Copepoda unid.	0.32	10.09	14.25	14.25
Oncaea sp.	0.24	8.74	12.34	26.58
Calanus helgolandicus	0.16	6.01	8.48	35.06
Ostracoda unid.	0.14	5.65	7.98	43.04
Acartia spp.	0.14	5.05	7.12	50.16
Group DC	Average similarity: 24.67			
Taxa	Av.Abund	Av.Sim	Contrib%	Cum.%
Cyclothone braueri	0.13	24.67	100	100

Biodiversity trend, expressed in terms of Shannon-Wiener diversity index, showed a decrease both in the Amendolara and Squillace canyon moving from HC to DC. At Amendolara, a higher biodiversity than at Squillace was noticed to then became almost the same at DC (**Fig. 3.3.2.c**).

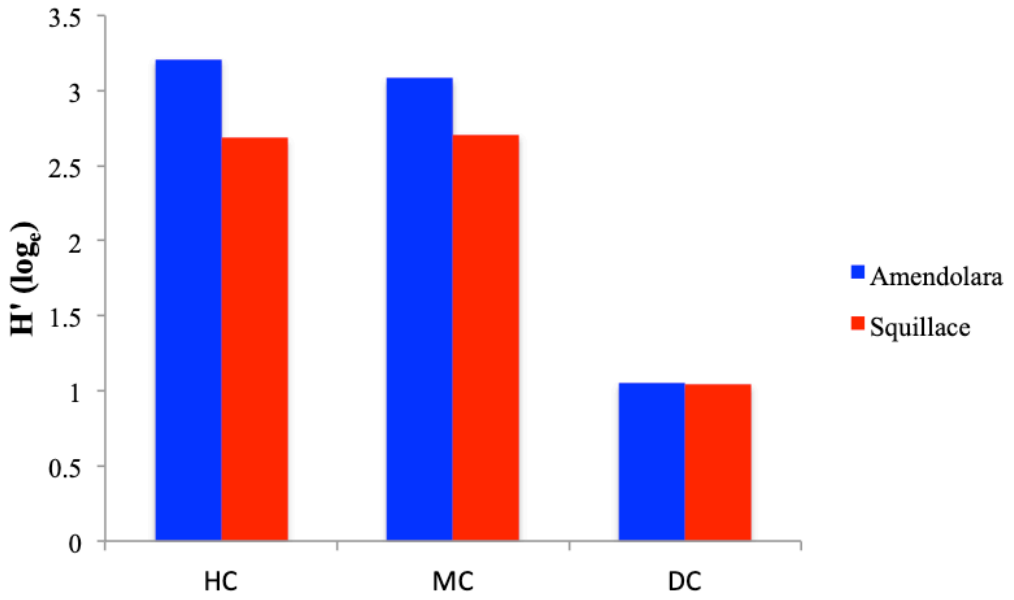

Fig. 3.3.2.c: Zooplanktonic biodiversity trend expressed as Shannon-Wiener diversity index (H', $\log_e$), performed on zooplankton abundance along the Amendolara and Squillace canyon.

Merging all samples at each canyon, at Amendolara biodiversity was greater compared to Squillace, although such differences were not statistically significant ($p > 0.05$; **Fig. 3.3.2.d**).

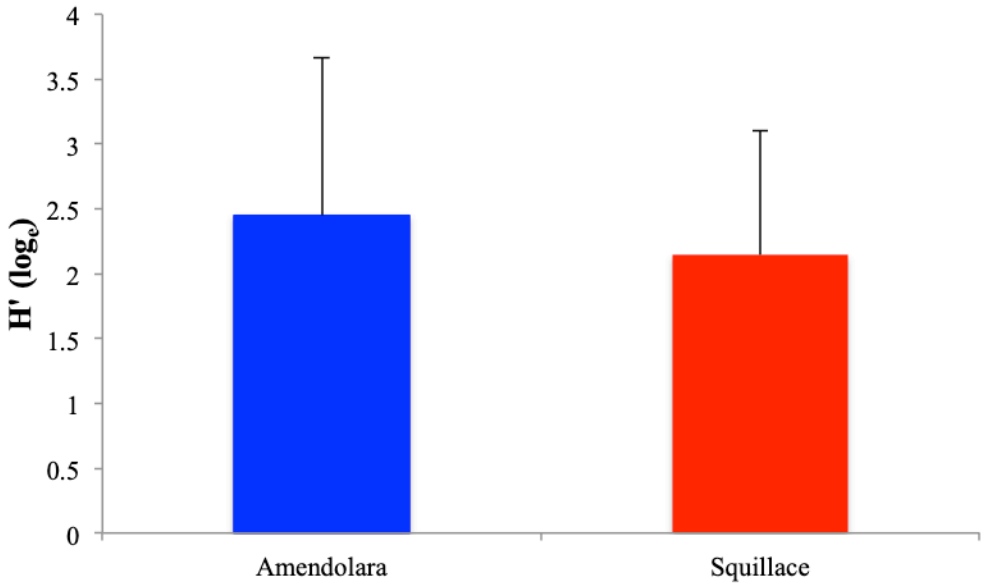

Fig. 3.3.2.d: Zooplaktonic biodiversity trend, expressed as Shannon-Wiener diversity index (H',$\log_e$) obtained merging all samples at each canyon.

Merging the similar depths of the two canyons, biodiversity trend showed a decrease moving from the HC to DC, although such differences were, again, not significant ($p > 0.05$; **Fig. 3.3.2.e**).

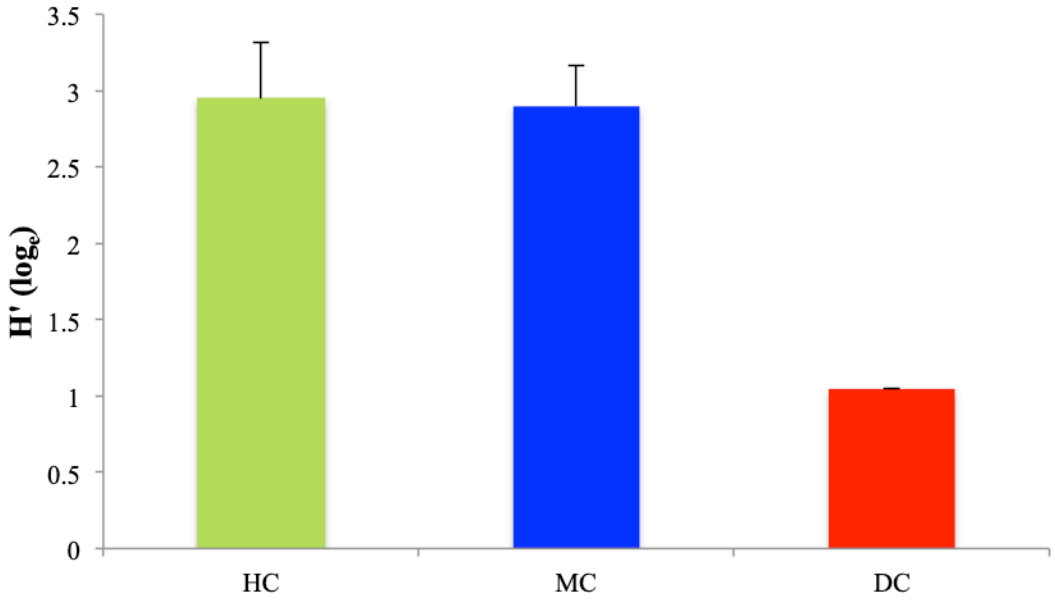

Fig. 3.3.2.e: Zooplanktonic biodiversity trend, expressed a Shannon-Wiener diversity index (H', $\log_e$) obtained merging the similar depths of the two canyons.

3.4 Environmental variables

A decrease in temperature was observed at Amendolara canyon from HC to DC (from approx.. 15°C to 13.9°C). Salinity followed the same trend (from approx. 38.8 to 38.79 p.s.u). Fluorescence values were not recorded at the depth ranges analysed (being close to 0) (**Fig 3.4.a**).

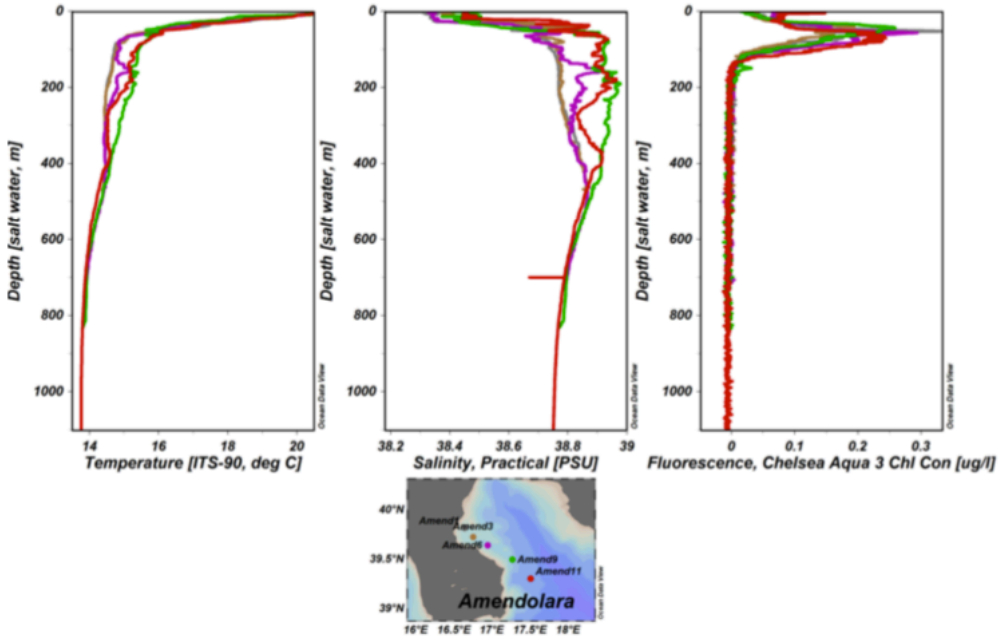

Fig 3.4.a: Tempterature, salinity and fluorescence profiles obtained by in situ measurements through CTD probe, at Amendolara canyon (source: Anomcity report, 2016).

A decrease in temperature was noticed also at Squillace canyon from the HC to the DC level (from approx. 14.6 °C to 14 °C). Salinity followed the same trend (from approx. 38.85 to 38.76 p.s.u.). Fluorescence values were not recorded at the depth ranges analysed (being close to 0) (**Fig. 3.4.b**).

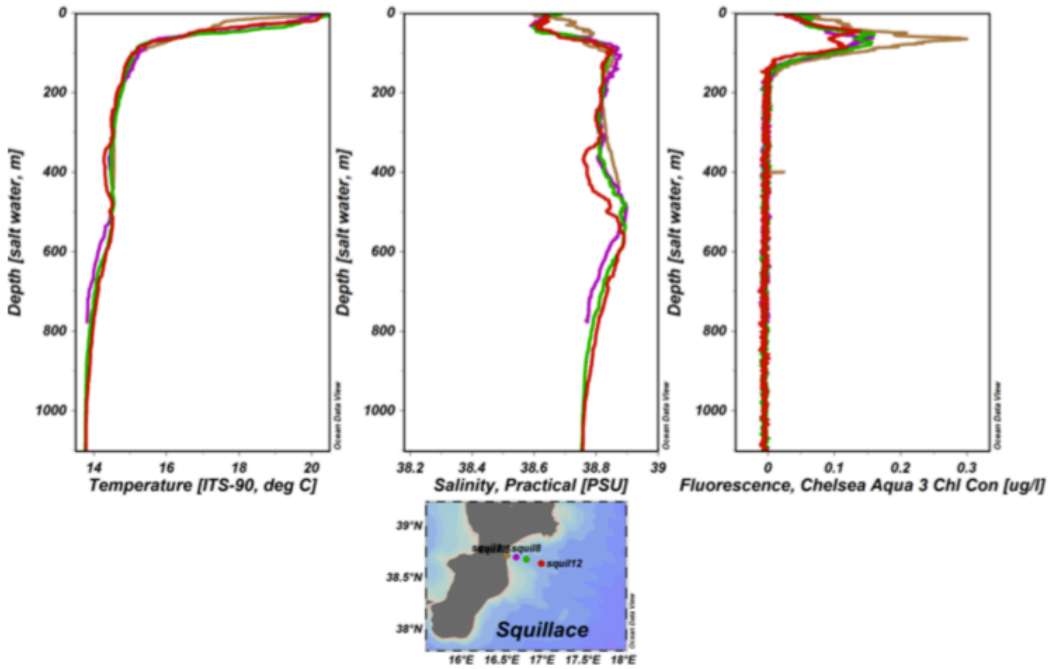

Fig. 3.4.b: Temperature, salinity and fluorescence profiles obtained by in situ mesurements through CTD probe, at Squillace canyon (source: Anomcity, 2016).

The Chl*a* concentration (mg/m^3), at surface, at Amenodolara canyon, showed a first peak in April at the three depths, with another lower second peak in May at MC and DC then values declined from May to June 2016. In proximity of the HC site the highest value of surface Chl*a* concentration was observed, followed by MC and DC. In proximity of the DC site, the Chl*a* concentration sharply declined from April to June (**Fig. 3.4.c**).

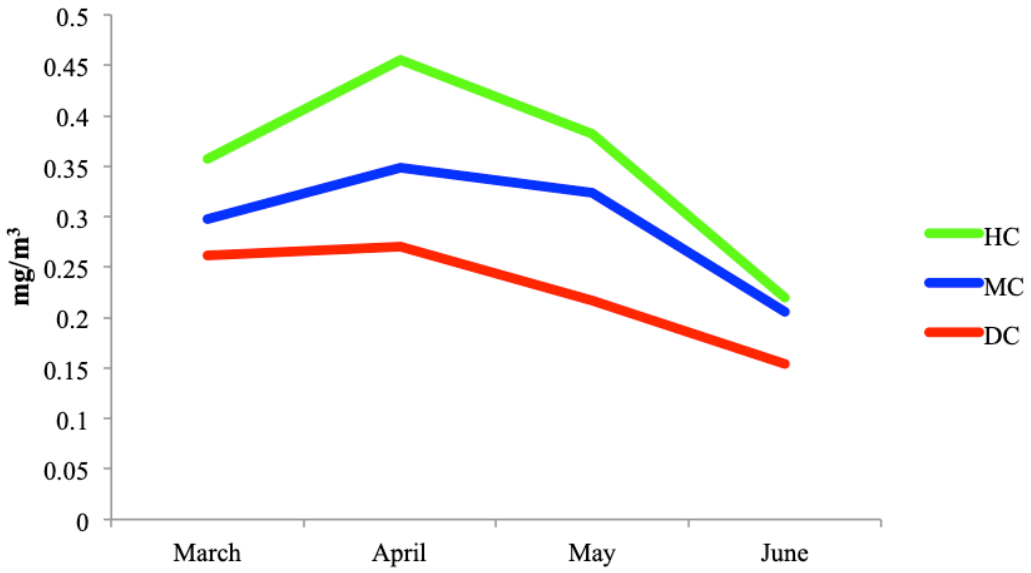

Fig. 3.4.c: Chl*a* concentration (mg/m^3) from March to June 2016, recorded at surface along the Amendolara canyon (satellite data obtained from *gsfc.nasa.gov/giovanni/* web site).

The Chl*a* (mg/m^3), at surface, at Squillace canyon, showed two higher peaks of concentration: the first was observed in March and the second in May 2016, then values declined from May to June 2016. From March to April a decrease of Chl*a* concentration was observed, and an increase from April to May. Chl*a* concentration value was higher at the surface corresponding to HC followed by the MC and then the DC one. Because of the low Chl*a* concentration at each bathymetry, the Squillace canyon showed overall a lower Chl*a* concentration compared to the Amendolara one (**Fig. 3.4.b**).

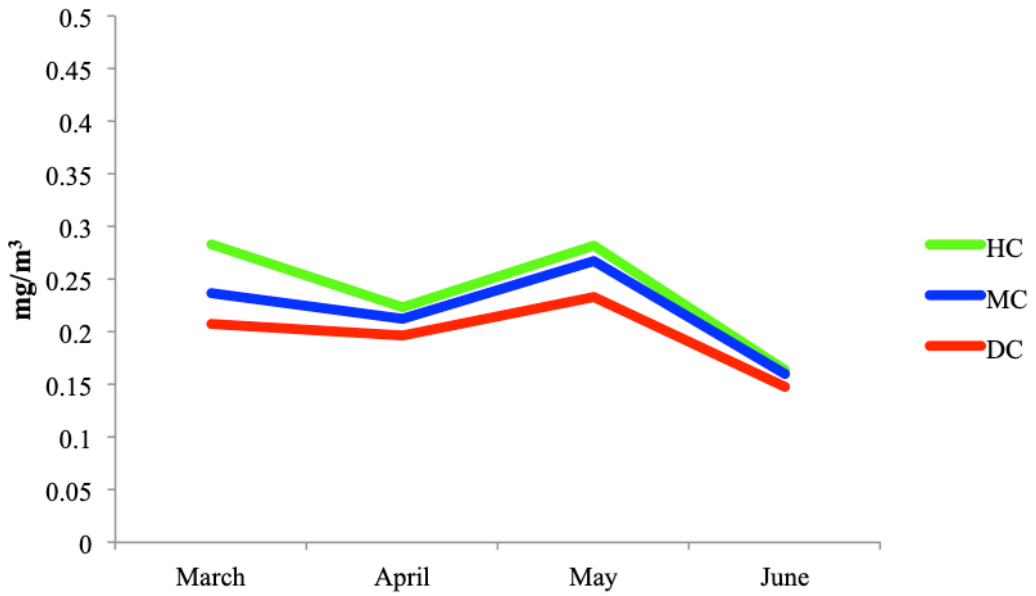

Fig. 3.4.b: Chl*a* concentration (mg/m^3) from March to June, recorded at surface along the Squillace canyon (satellite data obtained from *giovanni.gsfc.nasa.gov/giovanni/* website).

The Particulate Organic Carbon (POC) trend were similar to Chl*a* one along the Amendolara canyon. One higher POC concentration peak occurred in April at all three bathymetries, considerably higher at the HC than at MC and DC.

A second POC concentration peak was not observed at the DC level, which showed the lowest POC concentration values (**Fig 3.4.c**).

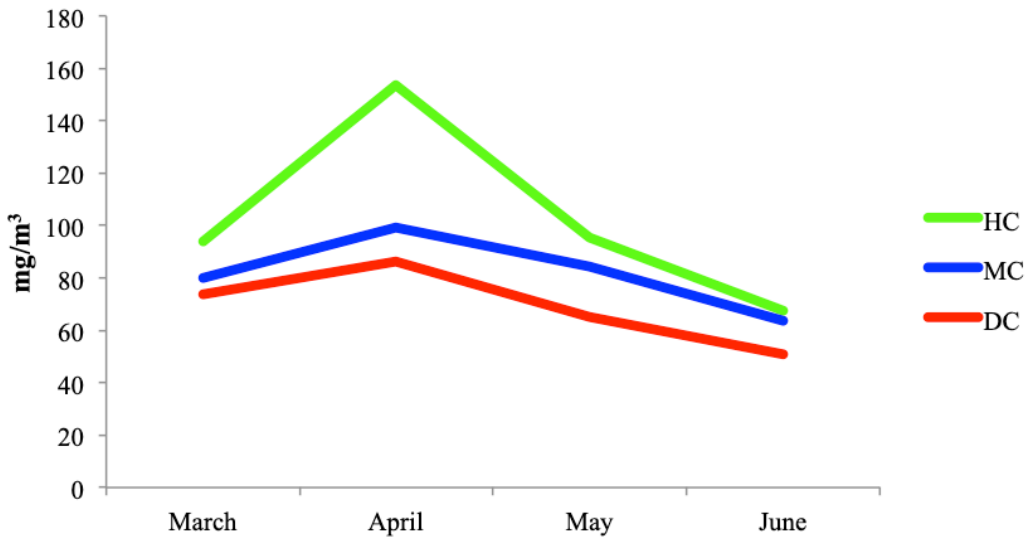

Fig. 3.4.c: POC concentration (mg/m^3) from March to June, recorded at surface along Amendolara canyon (satellite data obtained from giovanni.gsfc.nasa.gov/giovanni/ website.

At Squillace canyon, the POC concentration (mg/m^3) showed a overall lower value compared to Amendolara canyon, following the same trend of Chl*a* concentration (**Fig 3.4.d**).

From March to June, the POC concentration value was similar, with the presence of two low concentration peaks in March and in May, and a decline from May to June.

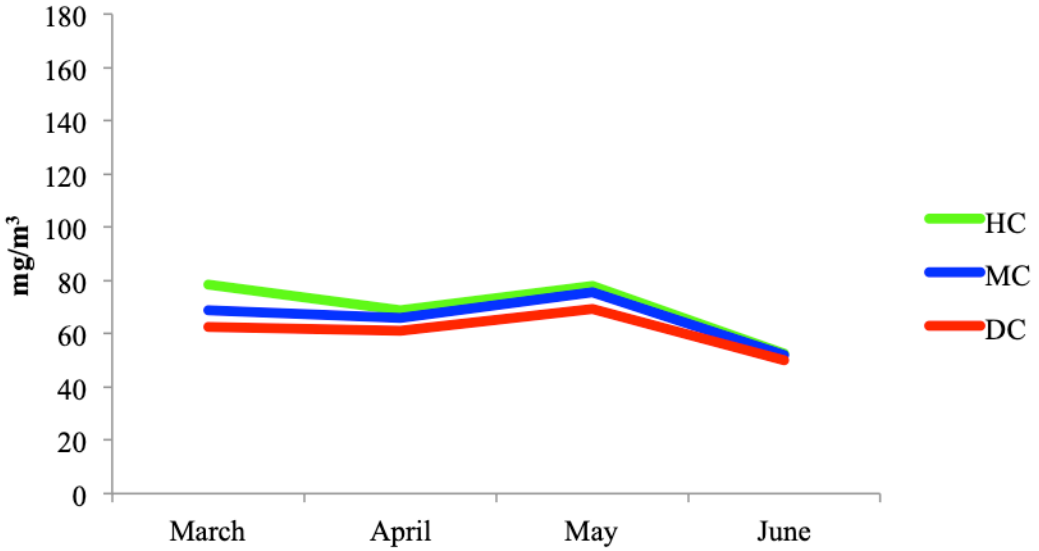

Fig. 3.4.d: POC concentration (mg/m^3) from March to June, recorded at surface along Squillace canyon (satellite data obtained from *giovanni.gsfc.nasa.gov/giovanni/* website.

3.5 Results of stable isotope analyses

3.5.1 Suprabenthos

Thirty taxa collected at Amendolara and Squillace canyon (13 amphipods, 6 cumaceans, 4 copepods, 3 isopods, 2 decapods, 1 ostracod and 1 mysid), were analysed (**Table 3.5.1**). The isotopic analyses revealed a considerable range of $\delta^{13}C$ and $\delta^{15}N$ values for suprabenthic taxa: $\delta^{13}C‰$ ranged from -18.57‰ (*Richardina fredericii*) to -13.12‰ (*Bathymedon monoculodiformis*); $\delta^{15}N‰$ ranged from 11.76‰ (*Richardina fredericii*) to 2.93‰ (Pseudocalanidae).

The cluster analysis based on $\delta^{15}N$ and $\delta^{13}C$ (**Fig. 3.5.1.a**) showed a very complex food web structure, in terms of feeding modes. Assuming a trophic enrichment factor of 2.54‰, the overall of $\delta^{15}N$ values implied three trophic levels, with filter feeders/deposit feeders and carnivores on large zooplankton positioned at the two estremes of the food web. Filter feeders and deposit feeders ranged from TL = 2 (i.e. the filter feeder *Vibilia cutripes*) to TL = 3 (i.e. the filter feeder *Boreomysis arctica* and the deposit feeder *Munnopsurus atlanticus*). Carnivores and omnivores ranged from TL = 4 (C = Carnivores on small zooplankton or meiobenthos, such as *Rhachotropis* spp.) to TL = 5 (CZ = Carnivores on large zooplankton, such as *Richardina fredericii* and *Aristaeus antennatus*). The omnivore *Bruzelia typica* showed a low TL (= 2), while the omnivore *Stegocephaloides christianensis* showed a higher TL (= 3). Parasites

assumed the same TL of the parasitized animal, and ranged from TL = 2 (*Epimeria parasitica*) to TL = 4 (*Aega* sp.) (**Fig. 3.5.1.a, 3.5.1.b)**.

Table 3.5.1: $\delta^{15}N$ and $\delta^{13}C$ values of suprabenthic species collected at Amendolara and Squillace canyon Feeding modes of species, according to literature and the related reference are also reported.

Group	Acronym	Taxa	$\delta^{15}N$ (‰)	$\delta^{13}C$ (‰)	Feeding mode	References
AMP	Bmono	*Bathymedon monoculodiformis*	4.41 ± 0.4	-13.12 ± 1.3	Unk	-
AMP	Btyp	*Bruzelia typica*	3.62 ± 0.5	-15.25 ± 0.0	O	Fanelli et al., 2009
AMP	Epar	*Epimeria parasitica*	3.26	-15.66	P	Coleman, 1983
AMP	Ijugo	*Iphimedia jugoslavica*	7.22	-13.94	Unk	-
AMP	Matl	*Munnopsurus atlanticus*	4.08 ± 2.6	-12.95 ± 2.8	DF	Cartes et al., 2000
AMP	Mpack	*Monoculodes packardi*	5.91	-13.69	Unk	-
AMP	Pcren	*Paracentromedon crenulatum*	5.13 ± 0.2	-16.02 ± 0.7	Unk	-
AMP	Rgla	*Rhachotropis glabra*	6.78 ± 1.2	-15.98 ± 0.4	C	Cartes et al, 2002
AMP	Rgrim	*Rhachotropis grimaldii*	7.98 ± 0.7	-15.92	C	Cartes et al., 2001
AMP	Rhacho	*Rhachotropis* sp.	6.49 ± 0.2	-15.32 ± 0.2	C	Cartes et al., 2001
AMP	Rint	*Rhachotropis integricauda*	7.01 ± 1.6	-17.35 ± 0.4	C	Cartes et al., 2001
AMP	Rros	*Rhachotropis rostrata*	5.22 ± 2.4	-14.52 ± 0.6	C	Cartes et al., 2001
AMP	Schri	*Stegocephaloides christianensis*	6.43 ± 0.4	-16.03 ± 1.1	O	Fanelli et al., 2001
AMP	Vcut	*Vibilia cutripes*	3.19 ± 1.8	-18.23 ± 0.6	FF	Fanelli et al., 2001
COP	Aetidsp1	Aetideidae sp.1	7.90	-18.09	Unk	-
COP	Cop	Copepoda	6.22 ± 0.5	-17.47 ± 0.9	Unk	-
COP	Pseudocal	Pseudocalanidae	2.94 ± 1.6	-14.66 ± 0.1	Unk	-
COP	Pygm	*Paracalanus pygmaeus*	4.44	-17.05	Unk	-
CUM	Cgla	*Campylaspis glabra*	3.69	-13.85	Unk	-
CUM	Ptyp	*Platysympus typicus*	3.88	-13.85	DF	Fanelli et al., 2009
CUM	Makroc	*Makrocylindrus* sp.	9.24	-16.05	Unk	-
CUM	Llong	*Leucon longirostris*	3.48	-12.73	DF	Fanelli et al., 2009
CUM	Cvit	*Campylaspis vitrea*	5.72	-11.91	Unk	-
CUM	Chorr	*Campylaspis horridoides*	2.95 ± 3.4	-13.29 ± 0.9	Unk	-
DEC	Aant	*Aristaeus antennatus*	9.84 ± 0.7	-18.36 ± 0.1	CZ	Cartes et al., 2008
DEC	Rfred	*Richardina fredericii*	11.76 ± 0.2	-18.57 ± 0.3	CZ	Cartes et al., 1994
ISO	Aega	*Aega* sp.	8.65 ± 2.0	-13.47 ± 0.7	P	Bakhrebah, 2006*
ISO	Nbor	*Natatolana borealis*	4.65	-14.11	P	Fanelli et al., 2009
MYS	Barc	*Boreomysis arctica*	6.01	-18.53	DF	Cartes and Sorbe, 1998
OSTR	Ostra	Ostracoda	5.32	-18.18	Unk	-
*reference on *Aega psora*						

AMP = Amphipoda, COP = Copepoda, CUM = Cumacea, DEC = Decapoda, ISO = Isopoda, MYS =Mysidacea, OSTR = Ostracoda. Feeding modes are also indicated: CZ = carnivore on large zooplakton, C = carnivore on small zooplankton or meiobenthos, DF = deposit feeders, FF = filter feeders; O = omnivore, P = parasite, Unk = unknown.

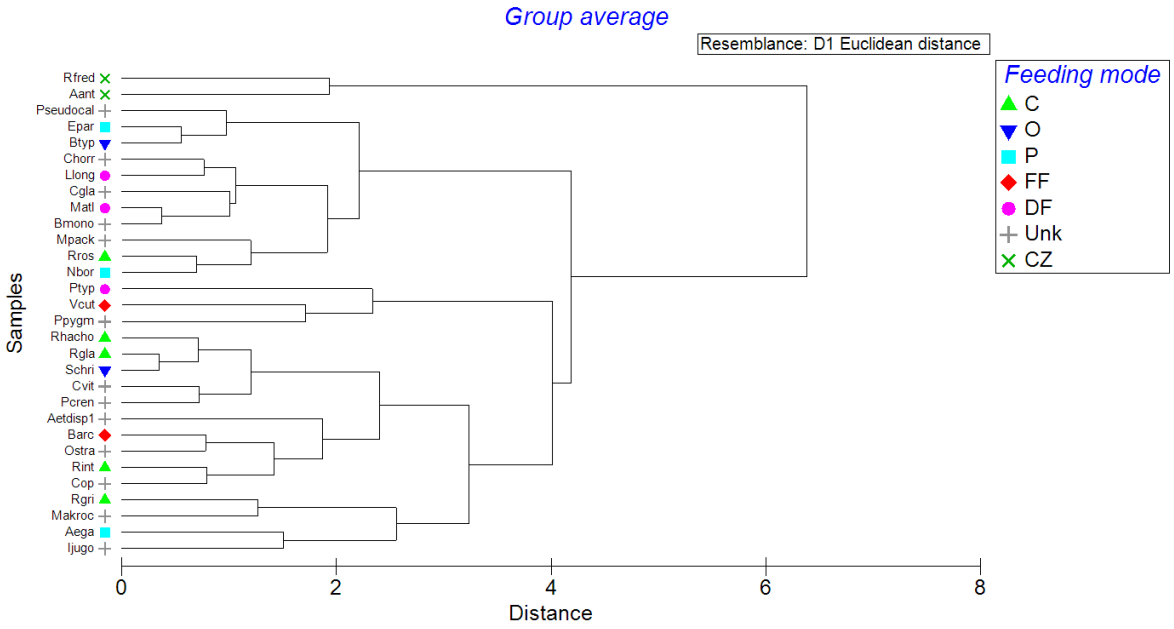

Fig. 3.5.1.a: Hierarchical clustering (Euclidean distance of untransformed data subjected to averaged grouping) of $\delta^{13}C$ and $\delta^{15}N$ for 30 suprabenthic taxa (CZ = carnivore on large zooplakton, C = carnivore on small zooplankton or meiobenthos, DF = deposit feeders, FF = filter feeders; O = omnivore, P = parasite, Unk = unknown).

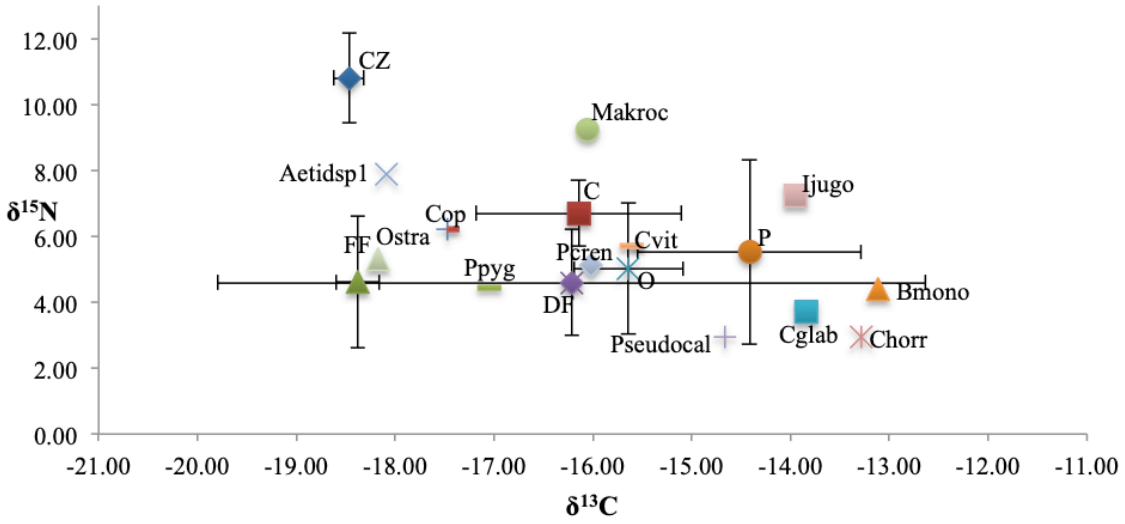

Fig. 3.5.1.b: Scatterplot of mean of $\delta^{13}C$ (‰) vs.$\delta^{15}N$ (‰) values of each major thopic gropus, as obtained by cluster analysis, for suprabenthos. The average $\delta^{13}C$ and $\delta^{15}N$ values of all the species that could not be attributed to a particular trophic group from data in literature are also shown. Vertical and horizontal bars are standard deviations (CZ = carnivore on large zooplakton, C = carnivore on small zooplankton or meiobenthos, DF = deposit feeders, FF = filter feeders; O = omnivore, P = parasite, Unk = unknown Abbreviation of species as in the **Table 3.5.1)**.

The nMDS of $\delta^{15}N$ and $\delta^{13}C$ performed on the common species collected in the Amendolara and Squillace canyon, showed a clear separation of sample as function of the canyon (**Fig 3.5.1.c**). Observed differences were significant (PERMANOVA test, pseudo-$F_{1,92} = 55.31$, $p < 0.05$).

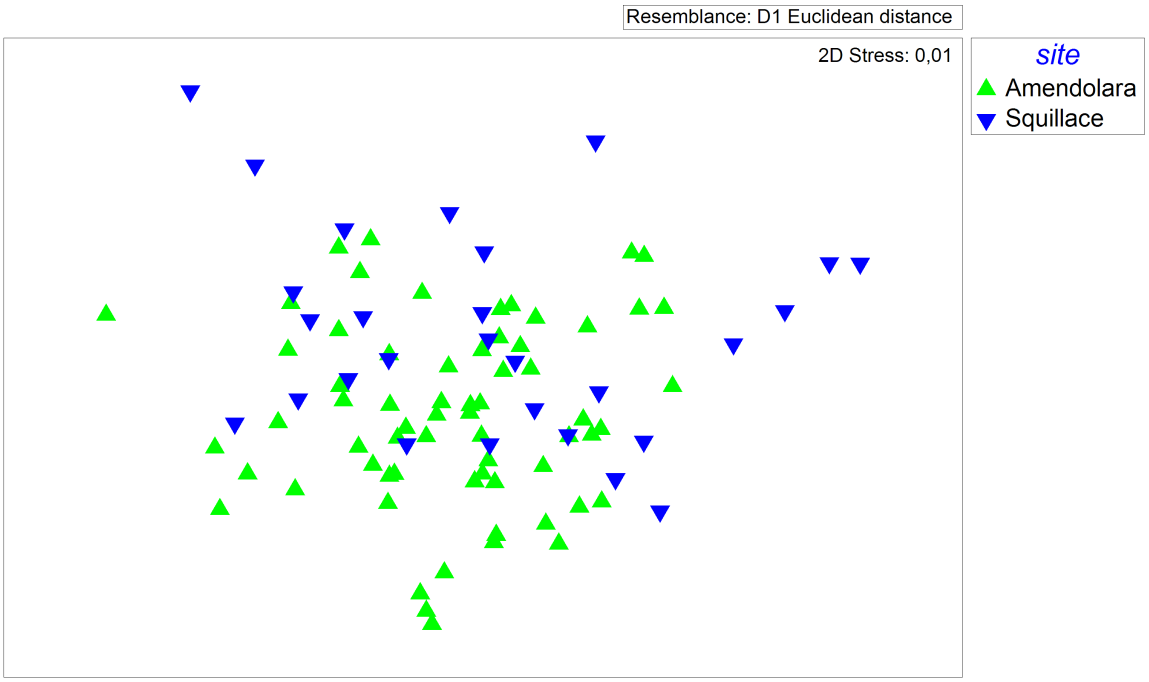

Fig. 3.5.1.c: nMDS plot of $\delta^{13}C$ and $\delta^{15}N$ for the common suprabenthic species collected in the Amendolara and Squillace canyon (Euclidean distance).

3.5.2 Zooplankton

Seventeen taxa collected at Amendolara and Squillace canyon (7 copepods, 3 hyperiid amphipods, 3 euphausiids, 1 fish, 1 ostracod, 1 decapod and 1 thaliacean) were analysed (**Table 3.5.2**). δ^{13}C‰ values ranged from -23.27‰ (unidentified Ostracoda) to -18.86‰ (*Phronima sedentaria*). δ^{15}N‰ ranged from 3.11‰ (unidentified Ostracoda) to 8.04‰ (*Streetsia challengeri*).

Table 3.5.2: δ^{15}N and δ^{13}C values of suprabenthic species collected at Amendolara and Squillace canyon Feeding modes of species, according to literature and the related reference are also reported.

Group	Acronym	Taxa	δ^{15}N (‰)	δ^{13}C (‰)	Feeding mode	References
AMP	Pmac	*Primno macropa*	7.74	-18.71	Unk	-
AMP	Psed	*Phronima sedentaria*	7.10	-16.86	C	Fanelli et al., 2009
AMP	Schall	*Streetsia challengeri*	8.04 ± 1.9	-17.91 ± 0.3	Unk	-
COP	Acar	*Acartia* sp.	7.66	-19.40	Unk	-
COP	Chelg	*Calanus helgolandicus*	5.19	-17.59	FF	Schnack, 1979
COP	Clongim	*Candacia longimana*	7.37	-18.50	Unk	-
COP	Emar	*Euchaeta marina*	8.27	-17.88	C	Øresland, 1991*
COP	Espin	*Euchaeta spinosa*	7.08	-18.49	C	Øresland, 1991*
COP	Hpap	*Heterorhabdus papilliger*	6.16	-19.34	C	-
COP	Pgrac	*Pleuromamma gracilis*	5.60	-19.49	Unk	-
DEC	Gele	*Gennadas elegans*	7.77 ± 1.6	-18.70 ± 0.2	C	
EUPH	Mnor	*Meganyctiphanes norvegica*	6.43 ± 1.6	-18.77 ± 0.5	O	Fanelli et al., 2009
EUPH	Nmeg	*Nematoscelis megalops*	7.49 ± 0.3	-19.10 ± 0.0	C	Fanelli et al., 2009
EUPH	Stylo	*Stylocheiron* sp.	7.56 ± 0.7	-19.25 ± 0.1	C	Cartes, 2009
OSTR	Ostra	Ostracoda unid.	3.11	-23.37	Unk	-
PISC	Cbra	*Cyclothone braueri*	7.03	-19.90	C	Fanelli et al., 2009
THAL	Patl	*Pyrosoma atlanticum*	6.99 ± 0.9	-16.74 ± 0.5	FF	Drits and Arashkev, 1992
*reference on *Euchaeta antarctica*						

AMP = Amphipoda, COP = Copepoda, , DEC = Decapoda, EUPH = Euphausiacea, OSTR = Ostracoda, PISC = Pisces, THAL = Thaliacea. Feeding modes are also indicated: C = carnivores, FF = filter feeders; O = omnivores, Unk = unknown.

Assuming a trophic fractionation of 2.54‰, the overall $\delta^{15}N$ values implied two trophic levels (**Fig. 3.5.2.a**): filter feeders and carnivores positioned at the two extremes, with a predominance of carnivores. Filter feeders ranged from TL = 3 (*Calanus helgolandicus*) to TL = 4 (*Pyrosoma antanticum*). Carnivores and omnivores ranged from TL = 3 (the omnivore *Meganyctiphanes norvegica*) to TL = 4 (i.e. the carnivores *Streetsia challengeri*, *Gennadas elengans*, *Euchaeta* spp., etc.) (**Fig. 3.5.2.a, 3.5.2.b**).

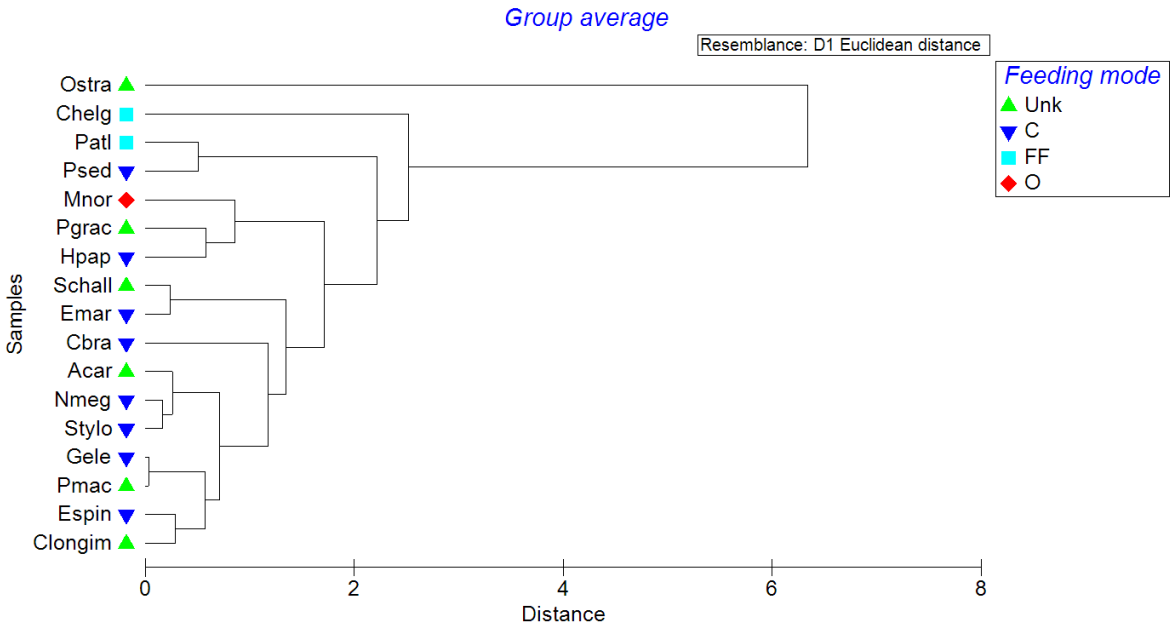

Fig. 3.5.2.a: Hierarchical clustering (Euclidean distance of untransformed data subjected to averaged grouping) of $\delta^{13}C$ and $\delta^{15}N$ for 17 zooplanktonic taxa (C = carnivores, FF = filter feeders, O = omnivores, Unk = unknown).

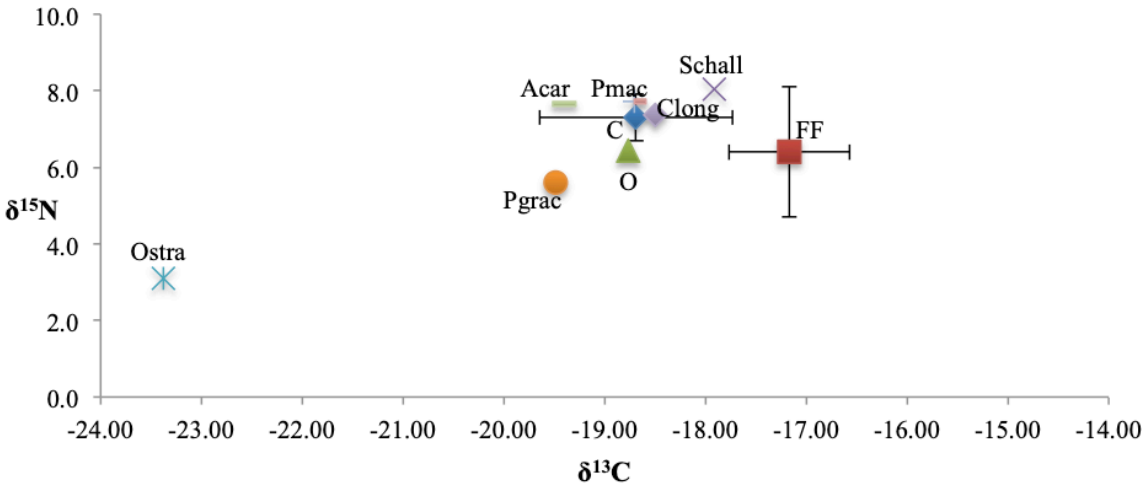

Fig. 3.5.2.b: Scatterplot of mean of $\delta^{13}C$ (‰) vs.$\delta^{15}N$ (‰) values of each major thopic gropus, as obtained by cluster analysis, for zooplankton. The average $\delta^{13}C$ and $\delta^{15}N$ values of all the species that could not be attributed to a particular trophic group from data in literature are also shown. Vertical and horizontal bars are standard deviations (C = carnivores, FF = filter feeders; O = omnivores, Unk = unknown, Abbreviation of species as in the **Table 3.5.2**).

The nMDS of $\delta^{15}N$ and $\delta^{13}C$ performed on the common species collected in the Amendolara and Squillace canyon, showed some separations (**Fig 3.5.2.c**). However, such differences were not significant (PERMANOVA test, pseudo-$F_{1.24} = 0.32$, $p > 0.05$).

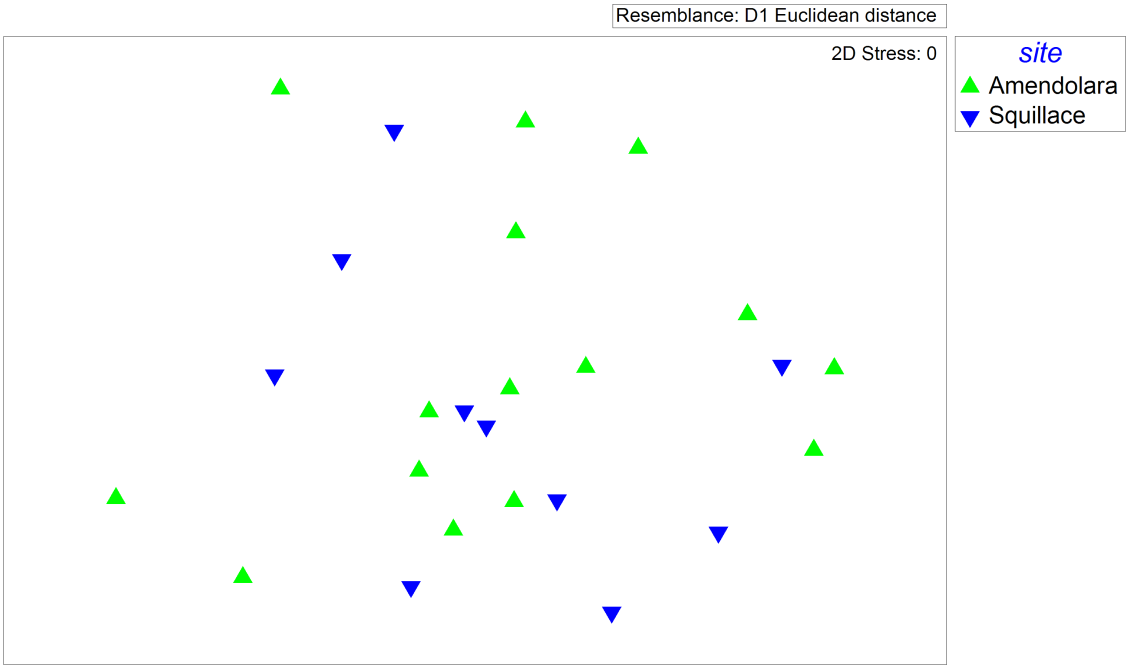

Fig. 3.5.2.c: nMDS plot of $\delta^{13}C$ and $\delta^{15}N$ for the common zooplanktonic species collected in the Amendolara and Squillace canyon (Euclidean distance).

Chapter four

DISCUSSION

4.1 Faunal composition and species assemblages

4.1.1 Suprabenthos

The suprabenthic assemblage seemed be very diverse. Amphipoda (Crustacea, Peracarida) were the most abundant taxon, with *Rhachotropis* sp. as the most representative species (i.e. *R. integricauda*, *R. grimaldii*, *R. rostrata*, *R. glabra*, *R. caeca*). *Rhachotropis* sp., a typical carnivorous genus being part of the Eusiridae family, appeared to be more numerous than previously observed in other Mediterranean areas (i.e. Balearic islands: Madurell et al, 2008; Fanelli et al, 2009a; Catalan Sea: Fanelli et al., 2011, Cartes et al., 2011). Within the amphipods, carnivory strategy showed to be the most common in these deep environments (see below).

Cumacea is an other representative taxon collected, composed primarily by Nannastacidae (i.e. *Campylaspis* spp.) and Leuconidae families (i.e. *Leucon* spp.). *Campylaspis glabra* was one of the most abundant species found, mainly females, which has been reported in a recent study conducted in the Levantine Shelf on the Mediterranean Sea (Corbera and Galil, 2016).

The rare cumacean species *Procampylaspis bonnieri* was also found (Nannastacidae), particularly at the MC depth of Amendolara. This species was previously reported in few studies from the Mediterranean (Ionian Sea and Egean Sea: Reys, 1972) and the Eastern Pacific (Petrescu, 2001).

The isopod *Munnopsurus atlanticus* and the mysid *Boreomysis arctica* were other common species collected along the Amendolara and Squillace canyon. These species were found to be abundant also in other areas of the Mediterranean, such as the Catalan Sea (Fanelli et al., 2011) and the Algerian basin (Fanelli et al., 2009).

Within the Copepoda Calanoida taxon, the highest abundance of family Aetideidae was observed. The taxonomonic composition of copepods collected in the suprabenthic samples showed to be considerably different compared to that observed in the zooplanktonic one. The meso-macrozooplankton biodiversity demonstrated, in a study conducted in the northwestern Mediterranean, to be significantly different between the BBL and the DDL (Cartes et al., 2010). Such differences can be reflected by the different environmental conditions of BBL and DDL (see below).

4.1.2 Zooplankton

The zooplanktonic community was formed for 96% of Copepoda (Arthropoda, Crustacea), and specifically by Calanoida and Cyclopoida orders. *Calanus helgolandicus* was the most abundant species found, both in the Amendolara and Squillace canyon. *Calanus helgolandicus* is a grazer (i.e. Schnack et al., 1979), living both in shallow waters and deep waters and being able to perform extensive vertical migrations (Figueroa et al., 2019). Such abundances of *Calanus helgolandicus* can be reflected by the high concentration values of Ch*a* recorded, by satellite data, at HC and DC sites. Other common species were *Pleuromamma gracilis*, *Euchaeta* spp. (i.e. *E. spinosa*, *E. marina*, *E. hebes*), *Candacia longimana*, *Centropages typicus*, *Corycaeus* sp. were other common copepod species found. The copepod species diversity seemed to be quiet similar to that observed in previous studies conducted on deep-sea zooplankon of the eastern Mediterranean Sea (Koppelmann and Weikert, 1999; Koppelmann et al, 2009). Concerning euphausids, *Meganyctiphanes norvegica* was the most abundant species at each canyon depth, and resulted to be widspred from the Mediterranean to the Subarctic Atlantic, and from shelf-break areas to deep-sea basins (Blanco-Bercial and Maas, 2018). The higher abundance of the mesopelagic fish *Cyclothone braueri* at the DC of Squillace was observed. This fish species was previously reported in other studies conducted in the Central Mediterranean Sea (the Strait of Messina: Battaglia et

al., 2016), on the deep waters of the Alegrian Basin (Fanelli et al., 2009) and in the Balaric basin (Fanelli et la., 2016).

Concerning hyperiid amphipods, the interesting precence of *Streetsia challengeri* was noticed. This hyperiid species was previously reported in some studies conducted, for example, off the Oregon coast (Van Ardale-Lorz and Pearcy, 1975), in the Tasman Sea (Young, 1989) and in a study conducted off the coast of west Africa (as one of the preys of the fish species *Katsuwonus pelamis* and *Thunnus albacarens* found in their stomachs: Dragovich and Potthoff, 1972). *Streetsia challengeri* was reported in very few studies conducted in the Mediterranean Sea, such as the study on the feeding habbits of *Tuna alalunga* from Central Mediterranean (Consoli et al., 2008).

4.2 Mesoscale variations in abundance, assemblage structure and biodiversity

4.2.1 Suprabenthos

A general increase of abundance, expressed as number of individuals/100 m^2, occured from the HC to the DC site, both in Amendolara and Squillace, but the Squillace canyon showed to have a substantial higher abundance than the Amendolara one at the HC site, probably due to the presence of accumulated organic matter at this level.

In fact, high amounts of terrestrial vegetable detritus were found in the collected samples, with the occasional finding of remains of land animals (e.i. insects), suggesting an intensive activity of the inspected canyons.

The sub-marine canyons are involved in the transportation and burial of organic carbon, and they are corridors for materials transported from the land to the deep sea (Puig et al., 2003) enhancing, in this way, the heterogeneity of continental slopes (Puig et al., 2000) and ensure that fauna living there has a greater abundance and biomass than at similar depths in the surrounding habitat, being 2- or 15-fold higher (Vetter and Dayton, 1998). Due to the precence of numerous rivers flowing at the Gulf of Squillace (i.e. Tacina, Scilotraco, Simeri, etc.: www.cfd.calabria.it/index.php/bacini-idrografici), a higher intake of terriestral-origin organic matter can be suggested; explaining, in this way, such higher abundances at the HC site of Squillace.

With the expetion of HC, the Amendolara canyon showed to be a litte richer in individuals than the Squillace one at the MC and DC.

A higher biodiversity, expressed as Shannon-Wiener diversity index, was determined at the Amendolara canyon compared to Squillace. However, both in the Amendolata and Squillace canyon, biodiversity trend showed a general increase from the HC to the DC; probably due to a higher amount of organic compounds dragged along the canyon and accumulated more at the DC level.

The deepest depth of the canyon would act as sediment and organic matter deposition site (Canals et al., 2006).

4.2.2 Zooplankton

An opposite abundance trend, expressed as number of individuals/1000 m^3, was observed in the zooplanktonic assemblage, with a general decrease moving to the deepest site of the canyons.

Amendolara, as in the case of suprabenthos, was the canyon where a higher biodiversity, in terms of Shannon-Wiever diversity index, was observed.

The reason of this opposite biodiversity trend, compared to the suprabenthic assemblage, was probably due the differences between the BBL and DDL. The BBL fauna (suprabenthos) was conditioned more by the canyon, which is involved in the traponsportation and accumulation of the organic materials (Canals et al., 2006). The DDL fauna (zooplankton) is more affected, in terms of abundance and biodiversity, by the vertical fluxes of fitodetritus (primary production) along the water column (Cartes et al., 2013). The higher primary productivity, in terms of Chl*a* concentration at surface obtained by satellite data (*giovanni.gsfc.nasa.gov/giovanni/*), at Amendolara and Squillace conditioned, in this way, the zooplanktonic distribution along the water column (see below); being more abundant at the sites in which a greater concentration of Chl*a*, as a proxy of primary production, was recorded.

4.3 Suprabenthic and zooplanktonic food web fuctioning

A different food-web functioning was observed between suprabenthos and zooplankton, with a higher heterogeneity of feeding modes observed in the suprabenthic taxa than in the zooplankton. Within the suprabenthic community, a large amount of detritivorous species were generally observed, with the presence of some carnivores on small zooplankton or meiobenthos, mainly amphipods (i.e. *Rhachotropis* spp.), and some higher trophic level carnivore such as the decapod species *Richardina fredericii* and *Aristaeus andtennatus*. The high abundance of detritivores can be due to the transportation of organic matter by the canyons through the deepest bathymetries (Vetter and Dayton, 1998; Puig et al., 2000 and 2003; Canals et al., 2006). Indeed a large amount of organic materials, of both terrestrial and marine origins, was observed in suprabenthic samples and this can explain such high feeding-mode complexity. In the case of zooplankton, a net predominance of carnivores was observed (most copepods, hyperiid amphipods and euphausiids), particularly at the HC and MC sites of the canyon were a high concentration of Chl*a* at surface was observed based on satellite data. These abundances were probably related to the presence, at these sites, of small zooplankonic preys whose dynamics depended on the up-take of phyto-detritus from the water column, and conditioning, in this way, the dynamics of carnivore meso-/macrozooplakton.

Because the analysed zooplanktonic samples were collected distant from the seabed, their dynamics depended less on the advective flux.

4.3.1 Feeding mode determination of suprabethic species

Several suprabenthic analysed taxa had an unknown feeding mode, and the cluster analysis allowed to understand their possible feeding (**Chapter 3**, **Fig. 3.5.1.a,b**). Psaeudocalanidae clustered together with some species which are considered to be omnivores (i.e. *Bruzelia typica*), and can be average considered omnivores as well. *Epimeria parasitica* is an amphipod reported in literature to be a parasite of holothurians (Coleman, 1990) justifyng, in this way, the low TL.

The species *Campylaspis horridoides*, *Bathymedon monoculodiformis*, *Campylaspis glabra* resulted to be close, in the cluster, to the deposit feeders *Leucon longirostris* and *Munnopsurus atlanticus*; being deposit feeders as well. *Monoculodes packardi* clustered with high-TL species such as the carnivore *Rhachotropis rostrata* and the ecto-parasite *Natatolana borealis*. The copepod *Paracalanus pygmaeus,* with unknown feeding mode, clustered with the filter feeder *Vibilia cutripes* while other two species with unknown feeding mode, *Campylaspis vitrea* and *Paracentromedon crenulatum* were close to *Rhachotropis* spp. (carnivore) and *Stegocephaloides christianensis* (omnivore), thus can be considered carnivores/omnivores as well. Copepods of Aetideidae

family (indicated as Aetidsp.1), showed a high TL (= 5), and clustered with other carnivores (i.e. *Rhachotropis integricauda*). A group of unidentified copepods clustered with the carnivore *Rhachotropis integricauda*, suggesting these unidentified copepods to be composed by carnivore species. Ostracods clustered with the filter feeder *Boreomysis arctica* suggesting a filter feeding mode. *Makrocylindrus* sp. seemed to be carnivore, due to its clustering with *Rhachotropis integricauda*; and a clustering between the uknown *Iphimedia jugoslavica* and the parasite *Aega* sp. was noticed. Due to the absence of any informations about the alleged parasitism of *Iphimedia jugoslavica*, and due to its high TL value, a carnivore feeding mode can be suggested.

4.3.2. Feeding mode determiantion of zooplanktonic species

Several zooplanktonic analysed taxa had an unknown feeding mode and the cluster analysis allowed to understand their possible feeding behaviour (**Chapter 3**, **Fig. 3.5.2.a,b**). The unidentified Ostracoda appeared to be close to the filter feeders. *Pyrosoma atlanticum* is reported in literature to be also a bacteria filter (Drits and Arashkev, 1992) justyifing, in this way, the high TL value and the clustering with the hyperiid species and the carnivore-on-salps *Phronima sedentaria. Pleuromamma gracilis* clustered together with the carnivore *Heterorhabdus papilliger*, suggesting a carnivore feeding mode of *Pleuromamma gracilis*.

The very rare hyperiid *Streetsia challengeri* grouped with the *Euchaeta spinosa*, suggesting to be carnivore as well. A clustering between some carnivores (i.e. *Gennadas elenans, Nematoscelis megalops*, *Cyclothone braueri*, etc.) and *Acartia* sp. and *Candacia longimana*, suggested that these copepods were carnivores.

Chapter five

CONCLUSIONS

This study confirms the important role of canyon in the transportation and burial of organic carbon from the land to the deep sea.

The Amendolara and Squillace canyon are located in an oligotrophic area of the Mediterranean Sea (the eastern Mediterranean), and their activity strongly affects the deep-sea faunal assemblages.

Other studies can be done, in the future, on these two canyons; in order to increase the knowladges about bentho-pelagic coupling, and to better understand the vertical and horizontal fluxes of organic matter and their consequences on BBL and DDL faunal diversity. Would be necessary an in-depth study relating to the determination of the organic matter present within the sediment.

In the case of animals, the fatty acids content determination can be done in order to support the isotopic data and to have a real representation of the diet of these organisms.

This study confirmed the precence of multiple trophic levels both in suprabenthos and zooplankton. This fact can have several implications in the use of some fishing models (such as ECOPATH, which considers suprabenthos and zooplankton being part of one only trophic level).

Furthermore, because of the intensive activity of the Amendolara and Squillace canyon, future studies aimed at investigating the impact o human activity on suprabenthic and zooplanktonic communities (i.e. microplastics and contaminants determination) and then on the whole food webs, will be desirable.

A multidisciplinary approach is the key to understand the environmental functioning of the deep-sea environments.

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Julian Sozio

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ANNEXES

Annex. 1: Suprabenthic taxa abundances obtained from Amendolara and Squillace canyon, expressed as number of individuals/100 m^2 (continued on next page).

Taxa	Amendolara			Squillace		
	HC N/100 m^2	MC N/100 m^2	DC N/100 m^2	HC N/100 m^2	MC N/100 m^2	DC N/100 m^2
***Phylum* CNIDARIA**						
Class HYDROZOA						
Order SIPHONOPHORAE						
Chelophyes appendiculata	-	-	-	-	-	0.0060
Siphonophora unid.*	0.0060	-	-	-	-	-
TOT. SIPHONOPHORAE	***0.0060***	***0***	***0***	***0***	***0***	***0.0060***
Phylum* MOLLUSCA						
Class BIVALVIA	0.0687	0.0454	0.0556	0.2165	0	0
Class CAUDOFOVEATA	0.0239	0.0097	0.0101	0.0541	0	0
Class GASTROPODA	0.0746	0.0519	0.0253	0	0	0
TOT. MOLLUSCA	***0.1672***	***0.1070***	***0.0910***	***0***	***0***	***0***
***Phylum* ANELLIDA**						
*Class POLYCHAETA**						
Sternaspis scutata	-	-	-	0.0541	-	-
Aricidea (Acmira) sp.	0.0179	-	-	-	-	-
Aphroditidae	-	-	0.0556	-	-	-
Cauleriella sp.	0.0090	-	-	-	-	-
Capitellidae	-	-	0.0152	-	-	-
Lumbrineridae	0.0030	-	-	-	-	-
Maldanidae	0.0030	-	-	-	-	-
Terebellidae	0.0418	-	-	0.0677	-	-
Polychaeta unid.	0.0030	0.0162	0.0051	0.0406	0.3259	0.0101
TOT. POLYCHAETA	***0.0776***	***0.0162***	***0.0758***	***0.1624***	***0.3259***	***0.0101***
Phylum* SIPUNCULA						
Aspidosiphon sp.	-	0.0065	-	-	-	-
Sipuncula unid.						
TOT. SIPUNCULA	***0***	***0.0065***	***0***	***0***	***0***	***0.0040***
***Phylum* ARTHROPODA**						
Subphylum CRUSTACEA						
Subclass COPEPODA*						
Order CALANOIDA						
Acartia longiremis	-	0.0032	-	-	-	-
Aetideidae	0.0328	0.1329	0.1213	-	-	-
Calanus helgolandicus	-	-	0.0455	-	-	-
Calanidae	-	-	0.0051	-	-	-
Candacia longimana	0.0030	-	-	-	-	-
Candaciidae	-	0.0032	-	-	-	-
Centropages typicus	0.0030	-	-	-	-	-
Centropages sp.	0.0030	-	-	-	-	-
Euchaeta spinosa	-	-	0.0202	-	-	-
Euchaeta sp.	0.0030	-	0.0101	-	-	-
Euchaetidae	-	0.0162	-	-	-	-
Heterorhabdus papilliger	-	0.0097	-	-	-	-
Heterorhabdidae	-	-	0.0051	-	-	-
Lucicutia sp.	0.0030	-	-	-	-	-
Paracalanus pygmaeus	-	-	0.0101	-	-	-
Paracalanus sp.	0.0119	-	-	-	-	-

Annex 1 (continued)

Taxa	Amendolara			Squillace		
	HC N/100 m^2	MC N/100 m^2	DC N/100 m^2	HC N/100 m^2	MC N/100 m^2	DC N/100 m^2
Paracalanidae	-	0.0065	-	-	-	-
Parvocalanus sp.	-	-	0.0051	-	-	0.0202
Pseudocalanidae	0.0179	0.0551	-	-	-	-
Scolecitrix sp.	-	-	0.0202	-	-	-
Scolecithricidae	-	0.0227	-	-	-	-
Temora longicornis	-	0.0032	-	-	-	-
Temora stylifera	-	-	0.0051	-	-	-
Temora sp.	-	-	-	-	0.0638	-
Copepoda unid.	-	-	0.3488	4.9124	-	0.2117
TOT. CALANOIDA	***0.0776***	***0.25***	***0.5965***	***4.9124***	***0.0638***	***0.2318***
Order CYCLOPOIDA						
Cyclops longicaudata	-	-	-	0.0135	-	0.0040
Coryceaus flaccus	-	0.0032	-	-	-	-
Coryceaus limbatus	-	0.0032	-	-	-	-
Coryceidae	-	-	0.0051	-	-	-
Oncaceidae	0.0051	0	0	0	0	0
Sapphirina iris	-	-	0.0253	-	-	-
Sapphirina lactens	-	-	0.0051	-	-	-
Sapphirina opalina	-	-	0.0051	-	-	-
Sapphirina sp.	-	0.0032	-	-	-	-
TOT CYCLOPOIDA	***0.0051***	***0.01***	***0.0404***	***0.0135***	***0***	***0.0040***
*Order HARPACTICOIDA**	***0***	***0***	***0.0051***	***0***	***0***	***0***
Class MALACOSTRACA						
Superorder EUCARIDA**						
Order DECAPODA						
Aristeus antennatus	-	-	0.0051	-	-	0.0302
Monadeus couchi	-	-	-	0.1083	-	-
Richardina fredericii	-	-	-	-	-	0.0081
TOT. DECAPODA	***0***	***0***	***0.0051***	***0.1083***	***0***	***0.0383***
Order EUPHAUSIACEA						
Euphausiacea unid.	0.0030	-	-	-	-	-
Furcilia	-	-	0.0354	0.0541	0.0071	-
TOT. EUPHAUSIACEA	***0.0030***	***0***	***0.0354***	***0.0541***	***0.0071***	***0***
Superorder PERACARIDA						
Order AMPHIPODA (Gammaridea)						
Andaniexis mimonectes	-	0.0032	-	-	-	-
Arrhis mediterraneus	-	0.0032	-	-	-	-
Bathymedon acutifrons	-	0.0032	-	-	-	-
Bathymedon banyulsensis	-	0.0032	-	0.0406	-	-
Bathymedon monoculodiformis	-	0.0130	-	-	-	-
Bathymedon sp.	-	-	0.0051	0.0135	-	-
Bruzelia typica	-	0.0486	-	-	-	0.0060
Epimeria parasitica	-	0.0162	0.0051	-	-	0.0101

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Annex 1 (continued)

Taxa	Amendolara			Squillace		
	HC N/100 m^2	MC N/100 m^2	DC N/100 m^2	HC N/100 m^2	MC N/100 m^2	DC N/100 m^2
Eriopisa elongata	-	-	-	0.0406	0.0035	-
Eusirus longipes	-	-	-	-	-	-
Harpinia antennaria	-	0.0065	-	-	-	-
Iphimedia jugoslavica	-	-	-	-	-	0.0020
Kuerguelenia reducta	-	0.0032	-	-	-	-
Leucothoe euryonyx	-	-	0.0051	-	-	-
Leucothoe lilljeborgi	-	0.0097	0.0051	0.0135	-	-
Leucothoe sp.	-	0.0065	-	-	-	-
Lysianassidae	-	-	0.0051	-	-	0.0020
Moloculodes griseus	-	0.0130	-	-	-	-
Monoculodes acutipes	-	-	-	-	-	0.0020
Monoculodes grifens	-	-	-	0.0135	-	-
Monoculodes packardi	-	0.0162	0.0051	-	-	-
Monoculodes sp.	0.0149	0.0227	0.0051	-	-	-
Oediceropsis brevicornis	0	0.0032	-	-	-	-
Oedicerotidae	0.0418	0.1102	0.0253	-	-	0.0060
Paracentromedon crenulatum	-	0.0065	-	-	-	0.0060
Perioculodes longimanus	-	-	-	0.0135	-	0
Phoxocephalidae	-	-	-	-	-	0.0060
Rhachotropis caeca	-	0.0194	0.0404	0.0541	-	0.0040
Rhachotropis glabra	-	0.0032	0.0404	-	-	0.0020
Rhachotropis grimaldii	0.0298	0.0583	-	0.1218	0.0213	0.0020
Rhachotropis inermis	-	-	-	-	-	0.0020
Rhachotropis integricauda	0.0149	0.2172	0.5661	0.0271	-	0.0443
Rhachotropis rostrata	0.0030	0.0194	0.0051	-	-	0.0040
Rhachotropis sp.	0.0597	0.3500	0.4044	0.2301	0.0106	0.0081
Stegocephalidee	-	-	-	-	0.0035	-
Stegocephaloides christianensis	-	0.0097	0.0354	-	-	0.0161
Triphosites alleni	-	0.0130	-	-	-	-
Triphosites longipes	-	-	-	-	-	0.0040
Tryphosella caecula	-	0.0130	-	-	-	-
Tryphosella minima	-	0.0065	-	-	-	-
Weswoodilla rectirostris	-	-	-	0.0541	-	-
Gammaridea unid.	0.1373	0.5964	-	0.1624	0.0106	0.0101
TOT. AMPHIPODA Gammaridea	***0.3015***	***1.5947***	***1.1525***	***0.7849***	***0.0496***	***0.1371***
*Order AMPHIPODA (Hyperidea)**						
Hyperia galba	-	-	-	-	0.0035	-
Hyperia schizogeneios	-	0.0065	-	-	-	0.0020
Hyperia sp.	0.0060	0.0032	0.0051	-	-	-
Phronima atlantica	-	-	0.0101	-	-	-
Platyscilus senatulus	-	-	-	-	0.0035	-
Primno macropa	-	0.0032	0.0202	-	0.0035	0.0020
Vibilia cutripes	-	-	0.0455	-	-	-
Hyperidea unid.	-	-	0.0101	-	-	-
TOT. AMPHIPODA (Hyperidea)	***0.0060***	***0.0130***	***0.0910***	***0***	***0.0106***	***0.0040***

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Annex 1 (continued)

Taxa	Amendolara			Squillace		
	HC N/100 m^2	MC N/100 m^2	DC N/100 m^2	HC N/100 m^2	MC N/100 m^2	DC N/100 m^2
Order CUMACEA						
Campylaspis glabra	0.0657	0.1070	0.1213	-	-	-
Campylaspis horridoides	-	0.0227	-	-	-	-
Campylaspis verrucosa	-	0.0032	-	-	-	-
Campylaspis vitrea	-	-	-	-	-	0.0040
Cumellopsis puritani	-	0.0065	-	-	-	-
Cyclaspis longicaudata	-	0.0065	-	0.0135	-	0.0040
Dyastilis tumida	0.0030	-	-	-	-	-
Dyastilidae	0.0030	-	-	-	-	-
Leucon affinis	-	-	-	0.0406	-	0.0141
Leucon longirostris	0.0239	0.0843	-	-	-	-
Leucon macrorhinus	0.0119	0.0194	-	-	-	-
Makrocylindrus josephinae	-	0.0065	-	-	-	-
Makrocylindrus longipes	-	0.0130	-	-	-	0.0020
Makrocylindrus sp.	-	0.0032	-	-	-	-
Platysympus typicus	-	0.0259	-	-	-	0.0081
Procampylaspis armata	-	0.0097	-	-	-	0.0040
Procampylaspis bonnieri	0.0269	0.0454	0.0152	-	-	-
Cumacea unid.	-	0.0810	-	-	-	-
TOT. CUMACEA	***0.1343***	***0.4343***	***0.1365***	***0.0541***	***0***	***0.0363***
Order ISOPODA						
Aega strauni	-	-	-	-	-	0.0020
Aega sp.	-	-	-	0.0135	-	-
Eurycope sp.	0.0388	0.0551	-	-	-	0.0141
Gnathia maxillaris	-	0.0065	0.0051	-	-	-
Gnathia sp.	-	-	-	0.1759	-	0.0040
Iliarachna sp.	-	0.0065	-	-	-	0.0101
Munnopsurus atlanticus	0.0358	0.1394	0.1769	-	-	0.0060
Natatolana borealis	-	0.0162	-	-	-	0.0101
Isopoda unid.	-	-	-	0.0271	-	-
TOT. ISOPODA	***0.0746***	***0.2236***	***0.1820***	***0.2165***	***0***	***0.0464***
Order MYSIDA						
Boreomysis arctica	0.0149	0.0259	0.0910	0.0135	-	0.0302
Dyastiloides serrata	-	-	-	0.2571	-	-
Mysidacea unid.	-	0.0227	0.0051	-	-	-
TOT. MYSIDA	***0.0149***	***0.0486***	***0.0960***	***0.2707***	***0***	***0.0302***
*Order TANAIDACEA**						
Apseudes spinosus	0.0060	-	-	-	-	-
Tanaidacea unid.	-	0.0032	0.0051	-	-	-
TOT. TANAIDACEA	***0.0060***	***0.0032***	***0.0051***	***0***	***0***	***0***
Class OSTRACODA *						
Cyprinidae	***0.0060***	***0.1070***	***0.0101***	***0***	***0***	***0***

(continued on next page)

Annex 1 (continued)

Taxa	Amendolara			Squillace		
	HC N/100 m^2	MC N/100 m^2	DC N/100 m^2	HC N/100 m^2	MC N/100 m^2	DC N/100 m^2
Phylum* CHETOGNATHA	***0***	***0***	***0***	***0***	***0.0283***	***0***
***Phylum* CHORDATA**						
Subphylum VERTEBRATA						
Superclass PISCES*						
Class ACTINOPTERYGII						
Pisces larvae	***0***	***0***	***0***	***0***	***0.0035***	***0***
TOT. PER DEPTH	**0.88**	**2.82**	**2.52**	**6.85**	**0.49**	**0.55**
TOT. PER CANYON		**6.22**			**7.88**	
* non-suprabenthic taxa collected during sampling ** *non-permanent* suprabenthos or *near-bottom* zooplakton						

Annex 2: Suprabenthic taxa biomasses obtained from Amendolara and Squillace canyon, expressed as grams of wet weight/100 m^2.

Taxa	Amendolara			Squillace		
	HC gWW/100 m^2	MC gWW/100 m^2	DC gWW/100 m^2	HC gWW/100 m^2	MC gWW/100 m^2	DC gWW/100 m^2
***Phylum* CNIDARIA**						
Class HYDROZOA						
*Order SIPHONOPHORAE**						
Chelophyes appendiculata	-	-	-	-	-	0.0000059
Siphonophora unid.	0.0000003	-	-	-	-	-
TOT. SIPHONOPHORAE	***0.0000003***	***0***	***0***	***0***	***0***	***0.0000059***
Phylum* MOLLUSCA						
Class BIVALVIA	0.0002158	0.0029099	0.0074369	0.0005751	0	0
Class CAUDOFOVEATA	0.0000125	0.0000039	0.0000081	0.0000392	0	0
Class GASTROPODA	0.0002833	0.0014067	0.0001589	0	0	0
TOT. MOLLUSCA	***0.0005116***	***0.0043205***	***0.0076039***	***0.0006144***	***0***	***0***
***Phylum* ANELLIDA**						
*Class POLYCHAETA**						
Sternaspis scutata	-	-	-	0.0004776	-	-
Aricidea (Acmira) sp.	0.0000259	-	-	-	-	-
Aphroditidae	-	-	0.0002401	-	-	-
Cauleriella sp.	0.0000039	-	-	-	-	-
Capitellidae	-	-	0.0000066	-	-	-
Lumbrineridae	0.0000013	-	-	-	-	-
Maldanidae	0.0000013	-	-	-	-	-
Terebellidae	0.0001609	-	-	-	-	-
Polychaeta unid.	-	0.0001033	0.0000022	0.0405985	0.0020736	0.0015607
TOT. POLYCHAETA	***0.0001933***	***0.0001033***	***0.0002488***	***0.0410760***	***0.0020736***	***0.0015607***
Phylum* SIPUNCULA						
Aspidosiphon sp.	-	0.0003556	-	-	-	-
Sipuncula unid.	-	-	-	-	-	0.0000146
TOT. SIPUNCULA	***0***	***0.0003556***	***0***	***0***	***0***	***0.0000146***
***Phylum* ARTHROPODA**						
Subphylum CRUSTACEA						
Subclass COPEPODA*						
Order CALANOIDA						
Acartia longiremis	-	0.0000003	-	-	-	-
Aetideidae	0.0000143	0.0001334	0.0000945	-	-	-
Calanus helgolandicus	-	-	0.0000233	-	-	-
Calanidae	-	-	0.0000005	-	-	-
Candacia longimana	0.0000003	-	-	-	-	-
Candaciidae	-	0.0000003	-	-	-	-
Centropages typicus	0.0000003	-	-	-	-	-
Centropages sp.	0.0000003	-	-	-	-	-
Euchaeta spinosa	-	-	0.0000091	-	-	-
Euchaeta sp.	0.0000003	-	0.0000005	-	-	-
Euchaetidae	-	0.0000139	-	-	-	-
Heterorhabdus papilliger	-	0.0000065	-	-	-	-
Heterorhabdidae	-	-	0.0000005	-	-	-
Lucicutia sp.	0.0000003	-	-	-	-	-
Paracalanus pygmaeus	-	0.0000003	0.0000091	-	-	-
Paracalanus sp.	0.0000116	0.0000003	0.0000005	-	-	-

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Annex 2 (continued)

Taxa	Amendolara			Squillace		
	HC gWW/100 m²	MC gWW/100 m²	DC gWW/100 m²	HC gWW/100 m²	MC gWW/100 m²	DC gWW/100 m²
Paracalanidae	-	0.0000003	-	-	-	-
Parvocalanus sp.	-	0.0000000	-	-	-	0.0000250
Pseudocalanidae	0.0000197	0.0001563	-	-	-	-
Scolecitrix sp.	-	-	0.0000005	-	-	-
Scolecithricidae	-	0.0000036	-	-	-	-
Temora longicornis	-	0.0000003	-	-	-	-
Temora stylifera	-	-	0.0000005	-	-	-
Temora sp.	-	-	-	-	0.0000204	-
Copepoda unid.	-	-	0.0001259	0.0010828	-	0.0000883
TOT. CALANOIDA	***0.0000472***	***0.0003166***	***0.0002719***	***0.0010840***	***0.0000204***	***0.0001133***
Order CYCLOPOIDA						
Cyclops longicaudata	-	-	-	0.0000012	-	-
Coryceaus flaccus	-	0.0000003	-	-	-	-
Coryceaus limbatus	-	0.0000003	-	-	-	-
Coryceidae	-	-	0.0000005	-	-	-
Oncaceidae	-	-	0.0000005	-	-	-
Sapphirina iris	-	-	0.0000043	-	-	-
Sapphirina lactens	-	-	0.0000009	-	-	-
Sapphirina opalina	-	-	0.0000009	-	-	-
Sapphirina sp.	-	0.0000003	-	-	-	-
TOT CYCLOPOIDA	***0***	***0.0000010***	***0.0000070***	***0.0000012***	***0***	***0***
*Order HARPACTICOIDA**	***0***	***0***	***0.0000005***	***0***	***0***	***0***
Class MALACOSTRACA						
Superorder EUCARIDA**						
Order DECAPODA						
Aristeus antennatus	-	-	0.0002184	-	-	0.0043381
Monadeus couchi	-	-	-	0.0017976	-	-
Richardina fredericii	-	-	-	-	-	0.0000754
TOT. DECAPODA	***0***	***0***	***0.0002184***	***0.0017976***	***0***	***0.0044136***
Order EUPHAUSIACEA						
Euphausiacea unid.	0.0000003	-	-	-	-	-
Furcilia	-	-	0.0000081	0.0000708	0.0000034	-
TOT. EUPHAUSIACEA	***0.0000003***	***0***	***0.0000081***	***0.0000708***	***0.0000034***	***0***
Superorder PERACARIDA						
Order AMPHIPODA (Gammaridea)						
Andaniexis mimonectes	-	0.0000088	-	-	-	-
Arrhis mediterraneus	-	0.0000003	-	-	-	-
Bathymedon acutifrons	-	0.0000052	-	-	-	-
Bathymedon banyulsensis	-	0.0000382	-	0.0000073	-	-
Bathymedon monoculodiformis	-	0.0000564	-	-	-	-
Bathymedon sp.	-	-	0.0000006	0.0000073	-	-
Bruzelia typica	-	0.0000302	-	-	-	0.0000082
Epimeria parasitica	-	0.0009668	0.0000256	-	-	0.0005979

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Annex 2 (continued)

Taxa	Amendolara			Squillace		
	HC	MC	DC	HC	MC	DC
	gWW/100 m²	gWW/100 m²	gWW/100 m²	gWW/100 m²	gWW/100 m²	gWW/100 m²
Eriopisa elongata	-	-	-	0.0000106	0.0000040	-
Eusirus longipes	-	-	-	-	-	-
Harpinia antennaria	-	0.0000055	-	-	-	-
Iphimedia jugoslavica	-	-	-	-	-	0.0000157
Kuerguelenia reducta	-	0.0000003	-	-	-	-
Leucothoe euryonyx	-	-	0.0000035	-	-	-
Leucothoe lilljeborgi	-	0.0000088	0.0000038	0.0000024	-	-
Leucothoe sp.	-	0.0000003	-	-	-	-
Lysianassidae	-	-	0.0000025	-	-	0.0000145
Moloculodes griseus	-	0.0000091	-	-	-	-
Monoculodes acutipes	-	-	-	-	-	0.0000032
Monoculodes grifens	-	-	-	0.0000055	-	-
Monoculodes packardi	-	0.0000959	0.0000080	-	-	-
Monoculodes sp.	0.0000045	0.0000162	0.0000016	-	-	-
Oediceropsis brevicornis	0.0000000	0.0000224	0.0000000	-	-	-
Oedicerotidae	0.0000257	0.0000451	0.0000005	-	-	0.0000085
Paracentromedon crenulatum	-	0.0000003	-	-	-	0.0000232
Perioculodes longimanus	-	-	-	0.0000027	-	-
Phoxocephalidae	-	-	-	-	-	0.0000232
Rhachotropis caeca	-	0.0000703	0.0000263	0.0000319	-	0.0000002
Rhachotropis glabra	-	0.0000068	0.0000581	0.0000000	-	0.0000002
Rhachotropis grimaldii	0.0000284	0.0002279	-	0.0004621	0.0000095	0.0000002
Rhachotropis inermis	-	-	-	-	-	0.0000002
Rhachotropis integricauda	0.0000045	0.0006324	0.0017585	0.0000125	-	0.0001921
Rhachotropis rostrata	0.0000003	0.0001112	0.0000005	-	-	0.0000006
Rhachotropis sp.	0.0000307	0.0003209	0.0002964	0.0001284	0.0000045	0.0000067
Stegocephalidee	-	0.0000110	0.0000596	-	-	0.0000475
Stegocephaloides christianensis	-	-	-	-	0.0000007	-
Triphosites alleni	-	0.0000382	-	-	-	-
Triphosites longipes	-	-	-	-	-	0.0000133
Tryphosella caecula	-	0.0000250	-	-	-	-
Tryphosella minima	-	0.0000113	-	-	-	-
Weswoodilla rectirostris	-	-	-	0.0000413	-	-
Gammaridea unid.	0.0000472	0.0002463	-	0.0000759	0.0000038	0.0000119
TOT. AMPHIPODA Gammaridea	***0.0001412***	***0.0030111***	***0.0022456***	***0.0007880***	***0.0000225***	***0.0009672***
*Order AMPHIPODA (Hyperidea)**						
Hyperia galba	-	-	0.0000111	-	0.0000019	-
Hyperia schizogeneios	-	0.0000071	-	-	-	0.0000002
Hyperia sp.	0.0000003	0.0000068	-	-	-	-
Phronima atlantica	-	-	0.0000005	-	-	-
Platyscilus senatulus	-	-	-	-	0.0000349	-
Primno macropa	-	0.0000182	-	-	0.0000077	0.0000002
Vibilia cutripes	-	-	0.0001031	-	-	-
Hyperidea unid.	-	-	0.0000005	-	-	-
TOT. AMPHIPODA (Hyperidea)	***0.0000003***	***0.0000321***	***0.0001152***	***0***	***0.0000445***	***0.0000004***

(continued on next page)

Annex 2 (continued)

Taxa	Amendolara			Squillace		
	HC	MC	DC	HC	MC	DC
	gWW/100 m²	gWW/100 m²	gWW/100 m²	gWW/100 m²	gWW/100 m²	gWW/100 m²
Order CUMACEA						
Campylaspis glabra	0.0000116	0.0000296	0.0000637	-	-	-
Campylaspis horridoides	-	0.0000314	-	-	-	-
Campylaspis verrucosa	-	0.0000003	-	-	-	-
Campylaspis vitrea	-	-	-	-	-	0.0000053
Cumellopsis puritani	-	0.0000004	-	-	-	-
Cyclaspis longicaudata	-	0.0000126	-	-	-	0.0000039
Dyastilis tumida	0.0000003	0.0000000	-	-	-	-
Dyastilidae	0.0000003	0.0000000	-	-	-	-
Leucon affinis	-	0.0000000	-	0.0000061	-	0.0000041
Leucon longirostris	0.0000042	0.0001027	-	-	-	-
Leucon macrorhinus	0.0000057	0.0000039	-	-	-	-
Makrocylindrus josephinae	-	0.0000301	-	-	-	-
Makrocylindrus longipes	-	0.0001050	-	-	-	0.0000021
Makrocylindrus sp.	-	0.0000075	-	-	-	-
Platysympus typicus	-	0.0000318	-	-	-	0.0000084
Procampylaspis armata	-	0.0000061	-	-	-	0.0000014
Procampylaspis bonnieri	0.0000084	0.0000204	0.0000017	-	-	-
Cumacea unid.	-	0.0000188	-	-	-	-
TOT. CUMACEA	***0.0000304***	***0.0004007***	***0.0000654***	***0.0000061***	***0***	***0.0000252***
Order ISOPODA						
Aega strauni	-	-	-	-	-	0.0003356
Aega sp.	-	-	-	0.0006331	-	-
Eurycope sp.	0.0000134	0.0000318	-	-	-	0.0000023
Gnathia maxillaris	-	0.0000117	-	-	-	-
Gnathia sp.	-	-	0.0000042	0.0000503	-	0.0000038
Iliarachna sp.	-	0.0000003	-	-	-	0.0000046
Munnopsurus atlanticus	0.0000051	0.0000865	0.0002270	-	-	0.0000065
Natatolana borealis	-	0.0002013	-	-	-	0.0000051
Isopoda unid.	-	-	-	0.0000027	-	-
TOT. ISOPODA	***0.0000185***	***0.0003316***	***0.0002312***	***0.0006861***	***0***	***0.0003578***
Order MYSIDA						
Boreomysis arctica	0.0000119	0.0004320	0.0000627	0.0000051	-	0.0003624
Dyastiloides serrata	-	-	-	0.0000506	-	-
Mysidacea unid.	-	0.0000003	0.0000101	-	-	-
TOT. MYSIDA	***0.0000119***	***0.0004324***	***0.0000728***	***0.0000558***	***0***	***0.0003624***
Order TANAIDACEA						
Apseudes spinosus	0.0000110	-	-	-	-	-
Tanaidacea unid.	-	0.0000031	0.0000049	-	-	-
TOT. TANAIDACEA	***0.0000110***	***0.0000031***	***0.0000049***	***0***	***0***	***0***
class OSTRACODA *						
Cyprinidae	***0.0000003***	***0.0001277***	***0.0000005***	***0***	***0***	***0***

(continued on next page)

Annex 2 (continued)

Taxa	Amendolara			Squillace		
	HC	MC	DC	HC	MC	DC
	gWW/100 m^2	gWW/100 m^2	gWW/100 m^2	gWW/100 m^2	gWW/100 m^2	gWW/100 m^2
Phylum* CHETOGNATHA	***0***	***0***	***0***	***0***	***0.0000405***	***0***
***Phylum* CHORDATA**						
Subphylum VERTEBRATA						
Superclass PISCES*						
Class ACTINOPTERYGII						
Pisces larvae*	***0***	***0***	***0***	***0***	***0.0000247***	***0***
TOT. PER DEPTH	**0.0010**	**0.0094**	**0.011**	**0.046**	**0.002**	**0.008**
TOT. PER CANYON		**0.0215**			**0.056**	
* non-suprabenthic taxa collected during sampling						
** *non-permanent* suprabenthos or *near-bottom* zooplakton						

Annex 3: Zooplanktonic taxa abundances obtained from Amendolara and Squillace canyon, expressed as number individuals/1000 m^3 (continued on next page).

Taxa	Amendolara			Squillace		
	HC N/1000 m^3	MC N/1000 m^3	DC N/1000 m^3	HC N/1000 m^3	MC N/1000 m^3	DC N/1000 m^3
***Phylum* CNIDARIA**						
Class HYDROZOA						
Order SIPHONOPHORAE	***0.0001591***	***0***	***0***	***0***	***0***	***0***
***Phylum* ARTHROPODA**						
Subphylum CRUSTACEA						
Class BRACHIOPODA						
Superorder CLADOCERA	***0.0025450***	***0.0003362***	***0***	***0***	***0***	***0***
Subclass COPEPODA						
Order CALANOIDA						
Acartia discaudata	0.0002651	0.0000112	-	-	-	-
Acartia longimana	-	-	-	-	0.0000862	-
Acartia sp.	0.0001591	0.0002354	-	0.0001352	0.0004523	-
Aetideidae	0.0001591	0.0000112	-	-	-	-
Calanus brevicornis	0.0001591	-	-	-	-	-
Calanus helgolandicus	0.0094378	0.0007509	-	0.0016218	0.0004954	-
Candacia longimana	0.0002651	0.0000785	-	0.0000541	0.0004308	-
Centropages hamatus	0.0001591	0.0000224	-	-	-	-
Centropages typicus	0.0001591	0.0000224	-	0.0000541	-	-
Euchaeta hebes	0.0001060	-	-	-	-	-
Euchaeta marina	0.0002651	0.0000336	-	0.0000541	0.0000646	-
Euchaeta spinosa	0.0016437	0.0002017	-	0.0002703	0.0002585	-
Euetideus giesbrechti	0.0001060	0.0000224	-	-	-	-
Gaetanus sp.	0.0008483	0.0002129	-	0.0000541	-	-
Gaidius sp.	-	0.0000112	-	-	0.0002585	-
Heterorhabdus papilliger	0.0011665	0.0002017	-	0.0001622	0.0007539	-
Heterorhabdidae	0.0011665	0.0000224	-	0.0002703	-	-
Lucicutia clausi	0.0000530	0.0000336	-	-	0.0000431	-
Paracalanus parvus	0.0000530	-	-	-	-	-
Paracalanus sp.	0.0003181	-	-	-	-	-
Paracalanidae	0.0000530	0.0000000	-	-	-	-
Pleuromamma gracilis	0.0016967	0.0001121	-	0.0000000	0.0012493	-
Scolecithricidae	0.0002651	-	-	-	-	-
Temora stylifera	0.0002121	0.0000448	-	-	-	-
Copepoda nauplii	0.0002651	0.0000112	-	0.0000811	0.0000431	-
Copepoda unid.	0.0482492	0.0039451	0.0011421	0.0078388	0.0217768	-
TOT CALANOIDA	***0.0672308***	***0.0059849***	***0.0011421***	***0.0105959***	***0.0259124***	***0***
Order CYCLOPOIDA						
Corycaeus limbatus	0.0007423	0.0001009	-	0.0003784	-	-
Corycaeus sp.	0.0003181	0.0000112	-	-	-	-
Oithona sp.	-	-	-	0.0001892	-	-
Oncaea sp.	0.0244427	0.0022191	-	0.0010542	0.0051696	-
TOT CYCLOPOIDA	***0.0255032***	***0.0023312***	***0***	***0.0016218***	***0.0051696***	***0***

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Annex 3 (continued)

Taxa	Amendolara			Squillace		
	HC N/1000 m^3	MC N/1000 m^3	DC N/1000 m^3	HC N/1000 m^3	MC N/1000 m^3	DC N/1000 m^3
Class MALACOSTRACA						
Superorder EUCARIDA						
Order DECAPODA						
Gennadas elegans	0.0000530	-	-	-	-	-
Zoea	-	0.0000112	-	-	-	-
TOT DECAPODA	***0.0000530***	***0.0000112***	***0***	***0***	***0***	***0***
Order EUPHAUSIACEA						
Meganycthiphanes norvegica	0.0001591	0.0000785	-	-	0.0000862	0.0002042
Nematoscelis megalops	0.0001060	0.0000112	-	-	-	0.0000255
Stylocheiron sp.	-	-	-	0.0000270	-	-
TOT EUPHAUSIACEA	**0.0002651**	**0.0000897**	**0**	**0.0000270**	**0.0000862**	**0.0002298**
Superorder PERACARIDA*						
Order AMPHIPODA (Gammaridea)						
Epimeria parasitica	-	-	0.0000231	-	-	-
Rhachotropis sp.	-	-	0.0000115	-	-	-
TOT AMPHIPODA (Gammaridea)	***0***		***0.0000346***	***0***	***0***	***0***
Order AMPHIPODA (Hyperidea)						
Hyperia galba	-	-	-	-	0.0000215	-
Hyperia schizogeneios	-	-	-	0.0000541	-	-
Hyperia sp.	-	-	-	-	-	-
Phronima sedentaria	-	-	-	-	0.0000431	-
Primno macropa	0.0001060	0.0000336	-	0.0000541	0.0000431	-
Scina borealis	-	-	-	-	-	0.0000255
Streetsia challengeri	0.0001060	-	-	-	-	-
Vibilia jeangerardi	-	-	-	-	-	0.0000255
TOT AMPHIPODA (Hyperidea)	***0.0002651***	***0.0000336***	***0***	***0.0001081***	***0.0001077***	***0.0000511***
Order TANAIDACEA*						
Tanais sp.	**0**	**0**	**0**	**0**	**0.0000431**	**0**
Class OSTRACODA	***0.0011665***	***0.0004259***	***0.0001269***	***0.0001352***	***0.0003877***	***0***
***Phylum* CHORDATA**						
Subphylum TUNICATA						
Class THALIACEA						
Pyrosoma atlanticum	***0.0001591***	***0***	***0.0000692***	***0.0000541***	***0***	***0.0007914***
Subphylum VERTEBRATA						
Superclass PISCES						
Class ACTINOPTERYGII						
Order STOMIFORMES						
Cyclothone braueri	***0.0001591***	***0***	***0.0000692***	***0.0000541***	***0***	***0.0007914***
TOT. PER DEPTH	**0.098**	**0.009**	**0.001**	**0.013**	**0.032**	**0.0019**
TOT. PER CANYON		**0.108**			**0.046**	
*Non-zooplanktonic taxa collected during sampling						

Annex 4: Zooplanktonic taxa biomasses obtained from Amendolara and Squillace canyon, expressed as grams of wet weight/1000 m^3 (continued on next page).

Taxa	Amendolara			Squillace		
	HC gWW/1000 m^3	MC gWW/1000 m^3	DC gWW/1000 m^3	HC gWW/1000 m^3	MC gWW/1000 m^3	DC gWW/1000 m^3
***Phylum* CNIDARIA**						
Class HYDROZOA						
Order SIPHONOPHORAE	***0.000000005***	***0***	***0***	***0***	***0***	***0***
***Phylum* ARTHROPODA**						
Subphylum CRUSTACEA						
Class BRACHIOPODA						
Superorder CLADOCERA	***0.000000005***	***0.000000001***	***0***	***0***	***0***	***0***
Subclass COPEPODA						
Order CALANOIDA						
Acartia discaudata	0.000000801	0.000000001	-	-	0.000000101	-
Acartia longimana	-	0.000000000	-	-	-	-
Acartia sp.	0.000000239	0.000000216	-	0.000000170	0.000000252	-
Aetideidae	0.000000016	0.000000001	-	-	-	-
Calanus brevicornis	0.000000074	-	-	-	-	-
Calanus helgolandicus	0.000005117	0.000000442	-	-	0.000000209	-
Candacia longimana	0.000000207	0.000000062	-	0.000000846	0.000000230	-
Centropages hamatus	0.000000016	0.000000002	-	-	-	-
Centropages typicus	0.000000159	0.000000041	-	0.000000004	-	-
Euchaeta hebes	0.000000080	-	-	-	-	-
Euchaeta marina	0.000000318	0.000000033	-	0.000000035	0.000000034	-
Euchaeta spinosa	0.000001294	0.000000195	-	0.000000287	0.000000276	-
Euetideus giesbrechti	0.000000005	0.000000001	-	-	-	-
Gaetanus sp.	-	0.000000111	-	0.000000005	0.000000069	-
Gaidius sp.	-	0.000000001	-	-	-	-
Heterorhabdus papilliger	0.000000589	0.000000207	-	0.000000105	0.000000252	-
Heterorhabdidae	0.000000769	0.000000001	-	0.000000062	-	-
Lucicutia clausi	0.000000005	0.000000001	-	-	0.000000002	-
Paracalanus parvus	0.000000005	-	-	-	-	-
Paracalanus sp.	0.000000080	-	-	-	-	-
Paracalanidae	0.000000005	-	-	-	-	-
Pleuromamma gracilis	0.000001872	0.000000113	-	-	0.000000984	-
Scolecithricidae	0.000000011	-	-	-	-	-
Temora stylifera	0.000000016	0.000000010	-	-	-	-
Copepoda nauplii	-	-	-	-	-	-
Copepoda unid.	0.000003081	0.000000600	0.000000053	0.000000492	0.000001346	-
TOT CALANOIDA	***0.000014756***	***0.000002038***	***0.000000053***	***0.000002007***	***0.000003757***	***0***
Order CYCLOPOIDA						
Corycaeus limbatus	0.000000033	0.000000001	-	0.000000030	0.000000013	-
Corycaeus sp.	0.000000014	0.000000001	-	-	-	-
Oithona sp.	-	-	-	0.000000003	-	-
Oncaea sp.	0.000000196	0.000000035	-	0.000000054	0.000000056	-
TOT CYCLOPOIDA	***0.000000244***	***0.000000037***	***0***	***0.000000086***	***0.000000069***	***0***

(continued on next page)

Annex 4 (continued)

Taxa	Amendolara			Squillace		
	HC gWW/1000 m^3	MC gWW/1000 m^3	DC gWW/1000 m^3	HC gWW/1000 m^3	MC gWW/1000 m^3	DC gWW/1000 m^3
Class MALACOSTRACA						
Superorder EUCARIDA						
Order DECAPODA						
Gennadas elegans	0.000004067	-	-	-	-	-
Zoea	-	0.000000007	-	-	-	-
TOT DECAPODA	***0.000004067***	***0.000000007***	***0***	***0***	***0***	***0***
Order EUPHAUSIACEA						
Meganycthiphanes norvegica	0.000006522	0.000000839	-	-	0.000000261	0.000004327
Nematoscelis megalops	0.000000201	0.000000108	-	-	-	0.000000240
Stylocheiron sp.	-	-	-	0.000000530	-	-
TOT EUPHAUSIACEA	***0.000006723***	***0.000000947***	***0***	***0.000000530***	***0.000000261***	***0.000004567***
Superorder PERACARIDA *						
Order AMPHIPODA (Gammaridea)						
Epimeria parasitica	-	-	0.000001575	-	-	-
Rhachotropis sp.	-	-	0.000000063	-	-	-
TOT AMPHIPODA (Gammaridea)	***0***	***0***	***0.000001638***	***0***	***0***	***0***
Order AMPHIPODA (Hyperidea)						
Hyperia galba	-	-	-	-	-	-
Hyperia schizogeneios	-	-	-	0.000000057	-	-
Hyperia sp.	0.000000005	-	-	-	-	-
Phronima sedentaria	-	-	-	-	0.000011610	-
Primno macropa	0.000000111	0.000000093	-	0.000000181	0.000000078	-
Scina borealis	-	-	-	-	-	-
Streetia challengeri	0.000007725	-	-	-	-	0.000000237
Vibilia jeangerardi	-	-	-	-	-	0.000000230
TOT AMPHIPODA (Hyperidea)	***0.000007842***	***0.000000093***	***0***	***0.000000238***	***0.000011690***	***0.000000467***
Order TANAIDACEA*						
Tanais sp.	***0***	***0***	***0***	***0***	***0.000000037***	***0***
Class OSTRACODA	***0.000000493***	***0.000000176***	***0.000000008***	***0.000000038***	***0.000000084***	***0***
***Phylum* CHORDATA**						
Subphylum TUNICATA						
Class THALIACEA						
Pyrosoma atlanticum	***0***	***0.000006357***	***0***	***0***	***0***	***0***
Subphylum VERTEBRATA						
Superclass PISCES						
Class ACTINOPTERYGII						
Order STOMIFORMES						
Cyclothone braueri	***0.000001463***	***0***	***0.000000331***	***0.000002038***	***0***	***0.000031977***
TOT. PER DEPTH	**0.0000278**	**0.0000097**	**0.0000020**	**0.0000049**	**0.0000159**	**0.0000370**
TOT. PER CANYON		**0.0000394**			**0.0000578**	
*Non-zooplanktonic taxa collected during sampling						