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Demersal fishes from the Antarctic shelf and deep sea: A diet study based on fatty acid patterns and gut content analyses

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ABSTRACT

The gut contents and fatty acid composition of 49 fish belonging to five Antarctic demersal families (Nototheniidae, Macrouridae, Channichtyidae, Bathydraconidae and Artedidraconidae) sampled at two stations at the Southern Ocean shelf and deep sea (600 and 2150 m) were analysed in order to identify their main food resource by linking trophic biomarkers with the dietary items found in the fish guts. Main food items of most fish analysed were amphipod crustaceans (e.g. in 63% of *Trematomus bernachii* guts) and polychaetes (e.g. in 80% of *Bathydraco* sp. guts), but other food items including fish, other crustaceans and gastropods were also ingested. The most prominent fatty acids found were 20:5($n-3$), 16:0, 22:6($n-3$) and 18:1($n-9$). The results of gut content and fatty acid analyses indicate that all fish except the Channichthyidae share similar food resources irrespective of their depth distribution, i.e. benthic amphipods and polychaetes. A difference of the dietary spectrum can be observed with ontogenetic phases rather than between species, as high values of typical calanoid copepod marker fatty acids as 22:1($n-11$) indicate that younger (smaller) specimens include more zooplankton in their diet.

1. Introduction

The Antarctic continental shelf is distinctive in being depressed by the weight of the continental ice and heavily scoured by previous extensions of the continental ice sheet. It can exceed 1000 m in depth, which increases the distance from the seabed to the euphotic zone compared to continental shelves elsewhere in the world. Similar to other high-latitude ecosystems, the major pelagic herbivores are copepods, euphausiids and salps (Hunt et al., in press; Flores et al., 2011; Brandt et al., 2011). Intense pulses of particulate organic matter to the shelf floor originating from seasonal water-column production are responsible for high organic carbon fluxes to the shelf sea floor (Bathmann et al., 1991; Fischer et al., 2000; Isla et al., 2006), from where the majority of samples analysed in this study originates. Additionally, the Maud Rise seamount was sampled, regularly appearing as a region of reduced ice coverage (De Steur et al., 2007), with intermediate to high annual primary production rates (Wefer and Fischer, 1991). In marine polar regions, the structure and biomass of the benthic community depend on multiple, interdependent factors, such as hydrography, ice coverage, light, temperature and the structure of the pelagic food web regulating the food supply to the benthic realm (Grebmeier and Barry, 1991; Clarke and Arntz, 2006). However, it appears that the organic matter reaching the continental shelf seabed has a long half-life, leading to a food bank for deposit feeders and thereby providing comparably stable conditions for the benthic fauna (Mincks et al., 2005; Clarke and Arntz, 2006; Isla et al., 2006).

Fish play an important role as top predators in marine systems, a fact that is also true for the Antarctic shelf and deeper waters. Some studies investigating the diet of Antarctic fishes have been conducted, in some cases including deep sea species, and it has been shown that different feeding strategies exist reaching from sediment browsing to active hunting (Daniels, 1982; Gon and Heemstra, 1990; Pakhomov and Tseitlin, 1991; Gartner et al., 1997; Pakhomov, 1997).

The Notothenioidei, a suborder of the Perciformes, form the dominant component of the fish community of the Antarctic continental shelf and upper slope (DeWitt, 1971; Andriashev, 1987; Eastman and Clarke, 1998; Dettaï and Lecointre, 2004). This suborder features unique adaptations such as the presence of antifreeze proteins and the loss of haemoglobin (Eastman, 1993). Notothenioids lack a swim-bladder, but can achieve buoyancy by lipid storage and reduced skeletal calcification. The former is possibly also a strategy to survive long periods of limited food supply during austral winter by relying on these energy-rich deposits (Eastman 1988, 1990, 1993; DeWitt et al., 1990; Hagen et al., 2000). Four families investigated in this study belong to this suborder, including the Nototheniidae (cod icefishes), with the two species *Trematomus scotti* and *T. bernachii*, the Channichthyidae (Antarctic icefishes, *Chionodraco myersi* and *Cryodraco antarcticus*),

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the Artedidraconidae (barbeled plunderfishes, one individual of *Artedidraco orianae*) and the Bathydraconidae (Antarctic dragonfishes, *Bathydraco antarcticus* and *Bathydraco* sp.). The fifth family analysed in this study is the Macrouridae (rattails), belonging to the order Gadiformes.

The traditional way of estimating fish diets is the analysis of stomach contents. However, this method faces some constraints, as it can only provide information on recently ingested food items. Thus, more rapidly digested items might be underestimated compared to slowly digested ones. Furthermore, gas bladders expanding upon retrieval to the surface (for example in macrourid fishes) often cause regurgitation of gut contents. An approach that can be used in addition to clarify which feeding sources have been utilised by an organism integrated over longer time spans is the analysis of its fatty acid (hereafter FA) composition. This method has become an established tool to gain information on food preferences and feeding history of marine organisms (e.g. Sargent, 1976; Sargent and Whittle, 1981; Graeve et al., 1994; Iverson et al., 2002), since FAs of potential food items have specific signatures that are not degraded during digestion, and can accumulate in the tissues of consumers. Some FAs can function as biomarkers for certain food categories, and help interpreting the specific FA composition of an organism. Widely used are the phytoplankton marker FAs 20:5($n-3$), 16:1($n-7$), 18:1($n-7$) and 22:6($n-3$) (Dunstan et al., 1994; Sargent et al., 1995; Falk-Petersen et al., 1998); high 18:1($n-9$) values accompanied by low 18:1($n-7$) values indicative for carnivory (e.g. Graeve et al., 1997; Auel et al., 2002), or FAs synthesised by polar calanoid copepods, such as 20:1($n-9$) and 22:1($n-11$) (Sargent, 1976; Hagen et al., 1993).

Knowing the pathways of energy transmission from lower trophic levels to higher predators is an important prerequisite to understand the quantitative functioning of marine ecosystems. The objectives of this study are to (i) compare the diet composition of benthic fishes, both on the Antarctic shelf and in the deep sea; (ii) evaluate the (short-term) diet composition from gut content analysis in the light of (long-term) results from FA analysis.

2. Material and methods

2.1. Sampling

The studied material originates from the ANDEEP-SYSTCO expedition (ANT XXIV/2 from 28 November 2007 to 4 February 2008) on board of RV *Polarstern*. Samples were collected at two stations in the Weddell Sea. One deep sea station (PS71/39; 64°28′S, 02°52′E) located on the plateau of the Maud Rise seamount at 2150 m depth was sampled on January 1, 2008. One shelf station close to the Antarctic shelf ice edge (PS71/48; 70°02′S, 08°02′W) in 600 m depth was sampled on January 12, 2008 (Fig. 1).

In total, 49 fish belonging to five families were analysed (Table 1). The fish were caught at daytime by a deep-water bottom trawl (3.2 × 1.6 m opening, 10 mm mesh size) and a Rauschert-dredge (0.43 × 0.18 m opening, 0.5 mm mesh size). Species were identified, and the individual fish were immediately measured (for all macrourids total length, TL; for other taxa standard length, SL; both to the nearest mm). In order to investigate ontogenetic differences, the fish were separated into juveniles and adults where possible. Small pieces of white muscle tissue from under the posterior dorsal fin were dissected from each fish for FA analysis and frozen at −80 °C. The fish bodies were frozen at −80 °C for further analysis.

2.2. Gut content analyses

The fish bodies were thawed individually. Guts were removed and stomach contents of each fish sorted, prey items counted and identified to different taxonomic levels, depending on the condition of the items. The degree of gut filling was estimated visually (expressed in %). The percentage frequency of occurrence of food items (number of guts containing a particular prey item as a percentage of the total number of guts examined) was determined for each fish species.

2.3. Fatty acid analysis

Prior to FA analysis the muscle tissue samples were freeze dried, weighed and allowed to extract in dichloromethane–methanol (v:v/2:1) for at least 48 h. Lipid extraction was performed with minor modifications as described in Folch et al. (1957) and analysis of FA composition was performed with modifications as described in Kattner and Fricke (1986) utilising GC-FID. FAMEs and fatty alcohols were detected by flame ionisation and identified by comparing retention times with those derived from standards of known composition. For quantification of FAs, tricosanoic acid was used as an internal standard. The FAs 18:5($n-3$) and 20:1($n-9$) showed identical retention times and are therefore presented together as 20:1($n-9$)[18:5($n-3$)]. For a detailed method description, see Würzberg et al. (2011).

2.4. Statistical methods

Principal component analysis (PCA) was performed using the SPSS software package (SPSS version 16.0) to investigate the variation in FA signatures between species and to identify the FAs most responsible for this variation. The PCA was performed unrotated based on the correlation matrix with eigenvalues >1 extracted. FAs with proportions lower than 1% of total FAs were excluded prior to analysis. Eleven FAs were chosen as variables for

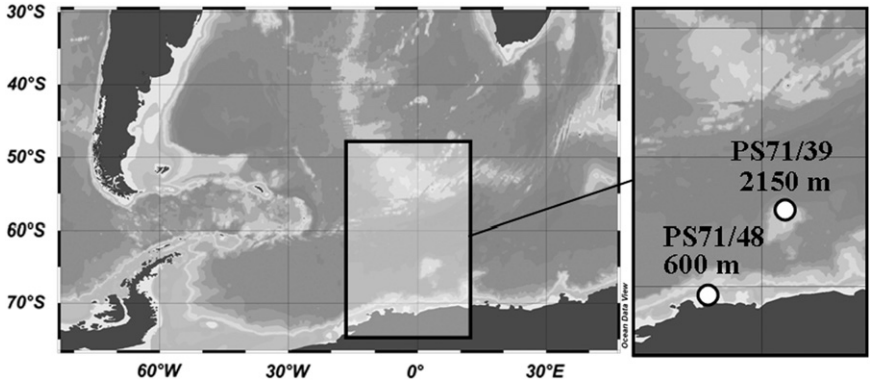

Fig. 1. Position of the sampled shelf (PS71/48, 600 m depth) and deep sea (PS71/39, 2150 m depth) station.