

## Patterns of abundance and diversity from the abyss - polychaetes from northeastern Atlantic abyssal plains

Gordon L. J. PATERSON\*, John D. GAGE\*\*, P. LAMONT\*\*  
B. J. BETT \*\*\* & M. H. THURSTON\*\*\*

\* The Natural History Museum, London SW7 5BD

\*\* Scottish Marine Biological Association

PO Box 3, Oban, Argyll PA34 4AD

\*\*\* Institute of Oceanographic Sciences Deacon Laboratory  
Brook Road, Wormley, Godalming, Surrey GU8 5UB, U.K.

### ABSTRACT

Preliminary results are presented from an intensive study of three abyssal plain sites in the NE Atlantic. The aim of this study was to assess the similarity of polychaete faunas from sites with different trophic characteristics. Analysis of polychaete families from the Porcupine, Madeira and Tagus abyssal plains showed differences in composition and richness. Comparisons with other deep abyssal studies provide further evidence that polychaete faunas of abyssal basins vary regionally.

### RÉSUMÉ

#### Abondance et diversité des Polychètes des plaines abyssales du nord-est atlantique

Les résultats préliminaires d'une étude intensive de trois sites des plaines abyssales de l'Atlantique nord-est sont présentés. Le but de cette étude était d'évaluer la similarité des faunes de polychètes provenant d'emplacements aux caractéristiques trophiques différentes. L'analyse de quelques familles de polychètes des plaines abyssales de Porcupine, de Madère et du Tage a montré des différences de composition et de richesse. Des comparaisons avec d'autres travaux en zone abyssale profonde apportent des preuves supplémentaires sur la variation régionale des faunes de polychètes des bassins abyssaux.

### INTRODUCTION

The abyssal plains of the world ocean represent approximately 40 % of the surface of the Earth, making them one of the largest habitats on the planet. They have been perceived as vast open, physically monotonous habitats without definable limits. However, pan-ocean studies carried out by the former Soviet Union have detected broad patterns of animal distributions (VINOGRADOVA, 1979) and have lead to general trophic classifications of the deep

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ocean fauna (SOKOLOVA, 1972). Despite these studies our understanding of the processes which operate within deep-ocean basins, and of local scales of faunal distributions, remains poor. To date there have been relatively few quantitative studies which have concentrated on a single abyssal plain site, e.g. HESSLER & JUMARS (1974, Climax site - North Pacific); KHRIPOUNOFF *et al.* (1980, Vema Fracture Zone); LAUBIER & MONNIOT (1985, Bay of Biscay); NOWELL & HOLLISTER (1985, HEBBLE, Northwestern Atlantic), SIBUET *et al.* (1984, Demerara Abyssal Plain), THIEL *et al.* (1989, BIOTRANS site - Northeastern Atlantic) and WILSON & HESSLER (1987, ECHO - N. Pacific).

In 1989, as part of a European Community Marine Science and Technology (MAST) programme, three Northeastern Atlantic abyssal plains were selected for intensive study. Each site was characterised by differences in the trophic regime. An aim of this continuing programme is to assess how differences in the physical environment, particularly nutrient flux, affect the abundance, diversity and trophic structure of the benthic populations.

We present, herein, a preliminary analysis of the polychaete fauna at these sites, concentrating on the familial similarity. We ask a basic question: are the polychaete faunas of abyssal plains dominated by the same families? Several authors have noted that nearly all polychaete families have representatives in the deep sea, e.g. ELIASON (1951) and HARTMAN (1965, 1971), but it is less clear whether certain families predominate. Answering such a question is a first step in assessing biodiversity amongst the sediment dwelling fauna of deep ocean basins.

To broaden the scope of our study, we compare our results with published data from two other deep abyssal sites, HEBBLE in the Northwestern Atlantic and ECHO in the eastern tropical Pacific.

## STUDY SITES

The three sites investigated were: Porcupine Abyssal Plain (PAP) - 48°50'N 16°30'W, c.4,850 m; Madeira Abyssal Plain (MAP) - 31°10'N 21°10'W, c.4,900m and Tagus Abyssal Plain (TAP) - 38°00'N 11°40'W, c. 5080 m. Studies on the PAP and MAP sites were initiated as part of the Institute of Oceanographic Sciences Deacon Laboratory Deepseas programme, while the Tagus was studied as part of the Scottish Marine Biological Association deep-sea benthos programme.

The PAP and MAP sites were selected to be: distant from the continental margin, of comparable depth, as representative of flat abyssal plains, and under oceanic regions exhibiting markedly different depths of winter mixing (A. L. RICE, pers. comm.). Surface productivity is somewhat greater over the PAP site than at the MAP (BERGER, 1989). Data from nearby sites suggest that PAP and MAP experience seasonal fluxes of organic matter, with lower values at MAP reflecting lower surface productivity (LAMPITT, 1992; HONJO & MANGANINI, 1993). Seasonal deposition of phytodetritus, characteristic of northeastern Atlantic waters (BILLETT *et al.*, 1983; RICE *et al.*, 1986; THIEL *et al.*, 1988/89) occurs at PAP but not at MAP (A. L. RICE, pers. comm.). TAP is a semi-enclosed abyssal basin. Overlying productivity values suggests a nutrient regime intermediate or higher than MAP and PAP (BERGER, 1989; KOBLENZ-MISHKE *et al.*, 1970). It is not known if there is a seasonal component to nutrient flux in the benthos.

There are comparable published data on the polychaete fauna from two other abyssal sites: HEBBLE (42°24'N 63°7.4'W and 42°24'N 63°9.6'W, 4,626 m NOWELL & HOLLISTER, 1985), which although not strictly on the abyssal plain, lies at a similar depth to our sites; and ECHO in the equatorial eastern Pacific (14°40'N: 125°25'W, c.4,500 m SPIESS *et al.* 1987). HEBBLE is subject to extreme physical disturbance which structures the community (THISTLE *et al.*, 1985) making an interesting comparison with the more quiescent NE Atlantic sites. ECHO lies in an oligotrophic to mesotrophic region of the eastern Pacific and was the site of a manganese nodule mining trial (WILSON & HESSLER, 1987). In the present comparison, data from the six control samples, collected at a distance from the trial site, were used.

## MATERIALS & METHODS

Samples from PAP and MAP were taken with a modified 0.25 m<sup>2</sup> USNEL spade box corer (SBC). Cores were sectioned into 0-1, 1-3, 3-5 and 5-10 cm layers, and washed through 1, 0.5, 0.3 and 0.25 mm sieves. One core from PAP (0.25 m<sup>2</sup>) and three cores from MAP (0.75 m<sup>2</sup>) were analysed. TAP samples were taken with a vegematicmodified SBC, with the inner nine cores, each 0.01 m<sup>2</sup>, processed through a 0.3 mm sieve. Five cores from TAP were analysed (0.45 m<sup>2</sup>). All samples were preserved in 4 % buffered formaldehyde on the ship then



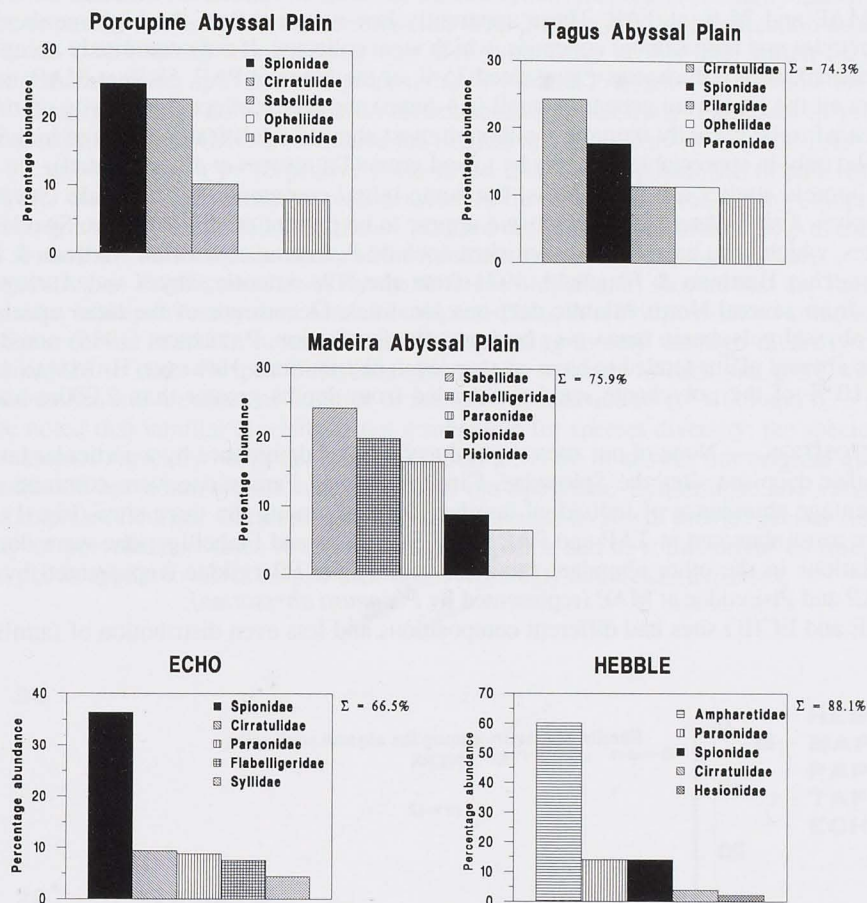


FIG. 1. — A comparison of familial abundance at each of the NE Atlantic sites studied. The five most abundant families were compared. Also shown is the familial abundances of the HEBBLE high energy site, NW Atlantic and ECHO, an equatorial eastern Pacific manganese nodule mining site. The total percentage abundance of the five dominant families is also given.

sorted and identified in the laboratory. Analyses were carried out on pooled data. The number of samples used from each site is given in figure 3. Only specimens retained on 0.3 mm sieve were used. Where more than one sieve size was used, i.e. PAP and MAP, all specimens were counted from the 0.3 mm and greater sieves. Analysis of familial similarity and richness at the different sites utilized methods which were relatively sample-size independent to avoid biases due to differences in sample abundances. Familial richness was analysed using Hurlbert rarefaction (SANDERS, 1968 - as modified by HURLBERT, 1971). Comparisons of family compositions were made using Normalised Expected Species Shared (NESS) - GRASSLE & SMITH (1976). NESS is based on the probability of the number of Operational Taxonomic Units (OTU i.e. species, trophic groups, family groups) expected to occur in common between random sub-samples drawn from the original samples. The size of the sub-sample can be determined by varying the number of individuals to be compared,  $m$ . Where  $m$  is large, up to half the size of the original sample, NESS is sensitive to the less abundant OTUs. Where  $m$  is low, NESS similarity will be based on the dominant OTUs. NESS sub-sample value,  $m$ , was set at 42 individuals. Group average clustering was used to classify the sites.

## RESULTS AND DISCUSSION

GENERAL OBSERVATIONS. — Polychaetes represented 17 % of all metazoans retained on a 0.3 mm sieve at PAP, 27 % at MAP and 25 % at TAP. These apparently low values reflect the high numbers of meiofauna, particularly nematodes and harpacticoid copepods, which were collected. If only commonly accepted macrofaunal groups are considered, then polychaetes represented 35 % of the fauna at PAP, 58 % at MAP and 49 % at TAP. Polychaetes from all the sites were generally small (c.1-5mm) and were collected primarily on the 0.3 mm sieve. Specimens appeared to be sexually immature, although most showed adult features. Large individuals were rare and were collected only in appreciable numbers by towed gears (THURSTON *et al.*, submitted).

Detailed taxonomic studies are in progress, but some initial comments can be made. Several undescribed species of *Sigambra*, *Aphelocheata* and *Prionospio* appear to be present at all three sites. Species recorded from other abyssal sites, which have been found at our sites, include *Pisionura abyssorum* Hartman & Fauchald, 1971, *Aricidea tetrabanchia* Hartman & Fauchald, 1971 from the NW Atlantic, abyss and *Aurospio dibranchiata* Maciolek, 1981 from several North Atlantic deep-sea localities. Occurrence of the latter species suggests that elements of the abyssal polychaete fauna may have a wide distribution. PATERSON (1985) noted that ophiuroids from the Atlantic abyssal plains tended to have cosmopolitan distributions. However, HARTMAN (1971) estimated that fewer than 10 % of the polychaete species recorded from depths greater than 2,000m had cosmopolitan distributions.

FAMILY COMPOSITION. — None of our sites showed any marked dominance by a particular family although in common with other deep-sea sites the Spionidae, Cirratulidae and Paraonidae were common elements of the fauna. The percentage abundance of individual families differed among the three sites (Fig. 1). Spionidae and Cirratulidae were most abundant at TAP and PAP while Sabellidae and Flabelligeridae were dominant at MAP. There were variations in the other abundant families, notably the Pilargiidae (represented by one species of *Sigambra*) at TAP and Pisionidae at MAP (represented by *Pisionura abyssorum*).

The HEBBLE and ECHO sites had different compositions and less even distribution of families compared to

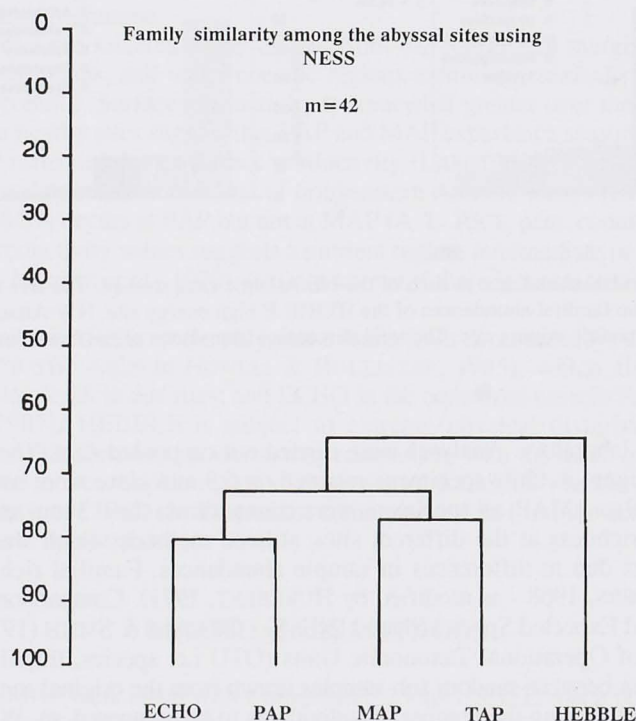


FIG. 2. — A classification of the abyssal plain sites studied using NESS similarity measure,  $m=42$ , and clustered using group average clustering.



the NE Atlantic sites (Fig. 1). HEBBLE was dominated by one species of ampharetid accounting for c. 60 % of the macrofauna (THISTLE *et al.*, 1985), and had three of the dominant families in common with our NE Atlantic sites, whereas ECHO shared four families (WILSON & HESSLER, 1987). Familial similarity among all the sites was high as might be expected at this level of discrimination (Fig. 2). The NESS classification separated HEBBLE first. THISTLE *et al.* (1985) noted low diversity and high dominance at this site, which they linked to high disturbance. The remaining sites split into two groups: the first linked PAP and ECHO while the second grouped TAP and MAP. These groupings do not appear to reflect surface productivity. Estimates of productivity in the waters over these sites suggest ECHO would have the highest at  $125 \text{ g. Cm}^{-2} \text{ y}^{-1}$ , while PAP, TAP and MAP have 40-60, 60-90 and  $40 \text{ gC. m}^{-2} \text{ y}^{-1}$  respectively. However, relating composition to trophic regimes is difficult. For example, ECHO was subject to sediment resuspension due to the action of the mining equipment (WILSON & HESSLER, 1987) so it is possible that this disturbance affected the benthos in a similar way to the dramatic inputs of phytodetritus at the PAP, hence the similarity of the familial fauna between these two sites.

**FAMILIAL RICHNESS.** — Rarefaction curves for the different sites (Fig. 3) showed that the Tagus and Porcupine Abyssal plains had a higher diversity than Madeira Abyssal Plain. It is not possible to compare TAP and PAP directly because the curves intersect, nevertheless, it is interesting to note the high diversity of PAP from the single sample analysed to date. Despite differences in sample numbers at each site there was no correlation between sample number and numbers of families or numbers of individuals ( $r^2 = 0.3$  and  $0.35$  respectively, d.f. = 3). It should be noted that familial diversity is not a substitute for species diversity; the species to family ratio estimated from samples currently being analysed is at least 2 : 1. So to answer our original question: the same polychaete families do not dominate the fauna although the Spionidae, Cirratulidae and Paraonidae are often among the most abundant families. Continuing studies at the species level will provide greater resolution to assess how biodiversity of polychaetes varies in different abyssal plains and how this might be linked to the trophic regime. Abyssal plains appear to differ despite their open, seemingly featureless expanses.

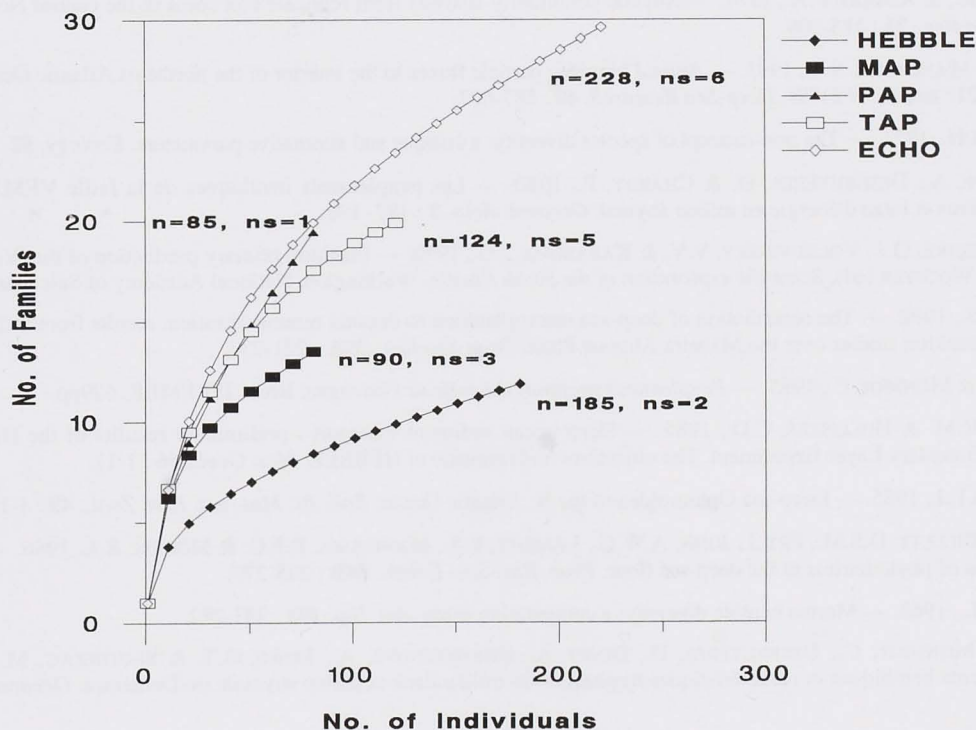


FIG. 3. — Family richness curves using rarefaction. n = total number of individuals, ns = number of samples pooled. There was no correlation between number of samples and number of families or number of individuals.

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