

EFFECT OF WATER QUALITY PARAMETERS ON THE DISTRIBUTION OF PLEUROMAMMA (COPEPODA-CALANOIDA) SPECIES IN THE INDIAN OCEAN: A STATISTICAL APPROACH

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Abstract Region between 10°N and 10°S latitude was known to be congenial for distribution of Pleuromamma species. Diel and ontogenetic migrations were observed for *Pleuromamma xipias*. Multivariate analyses such as factor analysis on species' abundance and predictive step-up multiple regression models of water quality parameters: temperature, salinity, dissolved oxygen, NO_3^- and PO_4^{3-} and their first order interaction effects on Pleuromamma species' abundance, were carried out in the regions off 10°N, 10°N to 10°S, 10°S to 30°S, along the Somali Coast, (38°S–40°S) and a 5th region along the western boundary of the above 4 regions. Relation between Pleuromamma species' abundance and the water quality parameters showed a decreasing trend in the variability explained (VE) from region 1 (VE=55.19%) to region 4 (VE=31.15%) in the models, indicating that the influence of other ecological factors was of higher significance in the south than in the north, with a north– south gradient. Indices of diversity (Shannon–Weaver) and evenness (Heips) were calculated and lognormal distributions fitted for these indices were found to be a good fit ($p < 0.05$). The five regions were compared, based on critical ratio of the diversity index. Shannon–Weaver diversity showed higher values during night collections than day collections, justifying the tendency for diurnal variations. Diversity and dominance were highly ($r=0.95$) correlated. A multilinkage cluster analysis by group averaging method for the species, based on the standardised values of $\log_{10}(X + 1)$ transformed species' abundance, showed that *P. indica*, *P. gracilis* and *P. abdominalis* were not segregated in any of the 5 regions. Bray–Curtis coefficient of similarity for the species in the 5 regions combined together, showed 50% similarity for the cluster containing circum–global species, *Pleuromamma piseki*, *P. gracilis*, *P. abdominalis* and *P. borealis*. The species, *P. indica* and *P. xipias* entered this cluster at 22% similarity level. Multivariate factor analysis by row normalisation (for species) and column normalisation (for stations), using varimax rotation to simple structure for unique grouping of species as well as stations, carried out in the five regions, showed that the maximum number of species' clusters were obtained in region 2, indicating a higher variability in the ecological conditions in this region than in the other 4 regions. The significance of the factor model and the differential factor groups of species were also determined in the studied regions. On a broader scale, based on the ecological aspect, the first four regions could be reduced to 2 regions, viz, region 1 including the north off 10°N, central Indian Ocean and the area of subtropical convergence, and region 2 consisting exclusively of the equatorial region between 10°N and 10°S based on distribution of pleuromamma species. The plot of the species abundance with respect to latitude also showed such a demarcation.

Keywords: Pleuromamma. Distribution. Lognormal. Community Structure. Multilinkage clustering. Differential factor. Environmental parameters.

1 Introduction

Pleuromamma, a marine calanoid copepod genus, are known for their marked diel changes exhibited by most species in vertical distribution. Pleuromamma species play an important role in marine food chain, because they constitute the main food item for fishes (Palma, 1990, Yoon, 1995, Gasser et al, 1998). Earlier studies on Pleuromamma species distribution in the Indian Ocean were those of Wolfenden (1906), De Decker (1964,1973), Grice and Hulsemann (1967) and Haq *et al.* (1973). The ecology of *Pleuromamma indica* was described by Saraswathy (1986) and, Saraswathy and Krishna Iyer (1986). The quantitative distribution and bathymetric distribution was described by Jayalakshmy and Saraswathy (1990) and Jayalakshmy (1991). The present work is a statistical study of the ecology through a multivariate approach, the sexual segregation and spatial distribution of community structure indices of the seven species of Pleuromamma along the north-south transect and along the western boundary of the north-south transect. This paper is a contribution to the knowledge of ecology of the Pleuromamma (Copepoda - Calanoida) species of the Indian Ocean by means of quantitative analysis. This work is part of an interdisciplinary programme undertaken by UNESCO, which led to the IIOE. The aim of this work is to analyse the Pleuromamma community structure of the Indian Ocean in relation to water quality parameters quantitatively. In this community, several studies on this species were previously available, which has resulted in certain thrilling observations both qualitatively (Saraswathy, 1986) such as isolation of *P. indica* in the northern Indian Ocean and quantitatively (Jayalakshmy and Saraswathy,1990, Jayalakshmy,1991), estimating the importance of the average values of the parameters in predicting the Pleuromamma total abundance, indicating that this copepod group shows vertical migration, and also the bathymetric variations in its distribution. This study is important in the sense that it gives a predictive model for estimating the total Pleuromamma species' abundance from the environmental parameters and their first order interaction effects, because the Pleuromamma community is governed by the outcome of interactive effects of several environmental parameters. Hence the analysis of individual variables may not provide a complete representation of changes in the Pleuromamma density status.

In this study, the areas included are Arabian Sea and Bay of Bengal in the north and waters of the Southern Indian Ocean in the south. They present a highly varied environment with respect to distribution of Pleuromamma species. Evidently, in the previous studies, not much work has been done on the relationship of the various environmental parameters with the abundance of this genus, except rarely (Jayalakshmy, 1990), which however considers only the linear relationship with single environmental factors but not the interaction effects between the input independent factors. Hence the principal objectives of this study are :

- To verify the ecological factors controlling the Pleuromamma species abundance in terms of interaction effects of environmental parameters. (Wyrski, 1971, 1973) Jayalakshmy, 1998).
- To determine the differential groups of species so as to extract the maximum information about their distribution in the areas of study (Gooday, 1957).
- To identify the theoretical population from which this genus has been collected, using the type of distribution of the factor scores calculated from the factor analysis model, and to classify it as a population with a continuously varying distribution, a population with a homogeneous distribution or a population with a distribution which highlights the signal of any sort of unexpected changes in the study area during the period of study (Angel and Fasham, 1973)
- To study the lognormal distribution pattern of diversity and equitability coefficients (Snedecor and Cochran, 1967)
- To assess species niche breadth and its relation with species abundance (Lydia Ignatiades, 1994).

2. Material And Methods

The study area has been geographically divided into five regions: (1) north of 10°N, (2) area between 10°N and 10°S, (3) area between 10°S and 30°S (4) area of the subtropical convergence which lies between 38°S and 40°S, and (5) the region along the east coast of Africa which comprises the western boundary areas of the previous four regions (Fig. 1).

A total of 579 zooplankton samples collected during IIOE formed the basis of this study. Samples were collected in a uniform manner, using the Indian Ocean standard net (Currie, 1963). Of the total collected samples, 397 samples were obtained from a 200m water column in the five regions mentioned earlier. This comprises 104 sampling stations from region 1, 129 sampling stations from region 2, 65 sampling stations from region three, 32 sampling stations from region 4, and 67 sampling stations from region 5, all of which included both day and night collections. The details of sampling and mode of analysis were as per IOBC (1969). Sorted copepods were again subsorted into different groups, including the genus *Pleuromamma*, which was then studied. Zooplankton samples were collected during the cruises 2, 3, 4A and 5 of R.V. *Anton Bruun* in the western Indian Ocean between 40° and 80°E and they are available at the Smithsonian Oceanographic Sorting Center, Washington, D.C., USA. Details of these samples are mentioned in the cruise reports published by the Woods Hole Oceanographic Institute (Anonymous, 1964-65). *Pleuromamma* species were separated into males and females, except for prediction. In addition to

the depth in each region, environmental parameters like temperature, salinity, dissolved oxygen, phosphate phosphorus and nitrate nitrogen were considered to determine the extent to which they control the total Pleuromamma species' abundance. Seven species and one type of genus *Pleuromamma* were considered. They are *Pleuromamma abdominalis* (PA), *P. xipias* (PX), *P. quadrangulata* (PQ), *P. indica* (PI), *P. gracilis* (PG), *P. borealis* (PB), *P. piseki* (PP) and a genus *P. abdominalis abyssallis* (PAA). Males and females of these species were separately dealt with.

Multiple regression model fitted is of the form

$$Y = a_0 + \sum_{i=1}^{i=k} a_i X_i + \sum_{i=1}^{i=k} \sum_{j=1, i < j}^{j=k} b_{ij} X_i X_j \dots\dots\dots (1)$$

Where $a_i, b_{ij}, i, j = 1, 2, 3, \dots$ and $i < j$ are the regression coefficients of the individual effects and the corresponding interaction effects respectively. Independent variables as well as dependent variables are standardized using the transformation,

$$Z_i = (X_i - \mu_i) \div \sigma_i \dots\dots\dots (2)$$

$$\text{and } Z = (Y - \mu) \div \sigma \dots\dots\dots (3)$$

where $\mu_i, \mu =$ arithmetic mean of X_i, Y and σ_i, σ is the standard deviation of X_i and Y respectively. Then the regression coefficients are called standard partial regression coefficients or the relative importance of the independent variables. In this study the X_i 's are standardised individually but not the products, $X_i * X_j$. The model is fitted by least square method considering the parameters and also their interaction effects of first order as the independent variables. In this model, a provision was made to screen out all those models which were less significant than the best selected, by means of the *Student's t* statistic for standardised regression coefficients (Paul(1954);Richard & morris(1981)).

The Students' 't' statistic is

$$t_i = a_i' \div S_{ei} \dots\dots\dots (4)$$

$$t_{ij} = b'_{ij} \div S_{eij} \dots\dots\dots (5)$$

where a'_i is the estimated value of the i^{th} regression coefficient and b'_{ij} is the estimated value of the $(ij)^{\text{th}}$ interaction effect, S_{ei} and S_{eij} are the standard errors of the regression coefficients.

$$S_{ei} = S(C_{ii}) * 0.5 \dots\dots\dots (6)$$

where S^2 is the deviation mean square and C_{ij} is the i^{th} diagonal element in the inverse of the matrix of sum of squares and products (Sokal and Rohlf, 1981). Similarly for S_{eij} .

When k parameters are considered there will be $k(k-1)/2$ interaction effects and total number of parameters for the model will be $(k+k(k-1)/2)$, ie; $(k(k+1)/2)$ and total number of regression models fitted is (2^k-1) . The regression model of Y (dependent variable) on all the parameters (individual effects only) is also determined. From these 2^k predictive models $((2^k-1)+1)$, that model with highest value for the explained variability (V.E), calculated as,

$$V.E. = [100 - (MDSS \div MTSS) * 100] \dots\dots\dots(7)$$

where $MDSS$ = Mean deviation sum of squares and $MTSS$ = Mean total sum of squares, is considered. Further, the above analysis is repeated with different transformations (Colebrook, 1960) for Y and X_i as

$$PO_4^{3-}$$

Y on X_i , $\log Y$ on $\log X_i$, \sqrt{Y} on X_i , \sqrt{Y} on $\sqrt{X_i}$, Y on $\sqrt{X_i}$ and $\log Y$ on X_i

To sum up, a maximum of $2^5 \times 6 = 192$ models are fitted to choose the best predictive model for each of the 5 regions. Among these, that model which explains the maximum variability is considered as the best predictive multiple regression model. In this model, the insignificant regression coefficients are deleted based on the t statistic, thereby reducing the number of parameters included in the model equation. Having determined the best model, the parameters in the model are arranged based on the relative importance which is calculated as *relative importance* = [(regression coefficient * σ of independent variable) \div σ of dependent variable] (converted to percent)(8)

The environmental parameters already mentioned and their first order interaction effects formed the fifteen parameters (5 individual parameters and $5C_2=10$ interaction effects of first order). Multiple regression analysis was carried out using the programme MULTIREG.FOR (Snedecor and Cochran, 1967; Jayalakshmy, 1998), Thus, In this programme, a set of 2^k models, (considering all possible combinations of the input independent parameters including that of input parameters without interaction effects also), were fitted, where k is the number of input parameters. For this step up multiple regression model, only 73 stations from region 1, 77 from region 2, 44 from region 3, 32 from region 4 and 58 from region 5 were considered based on the availability of the environmental parameters. Biodiversity was studied by defining the community structure in terms of 4 diversity indices calculated for each of these samples:

1. Shannon – Weaver (1963) diversity index is:

$$H(S) = -\sum_{i=1}^{i=S} [p_i \log_2(p_i)] \dots\dots\dots(9)$$

where $p_i = (n_i/N)$, n_i is the number of individuals of the i^{th} species, N is the total number of individuals of all species, and S is the total number of species observed. The importance of this diversity index is that it has a probability distribution and hence can be used for comparison of stations using critical ratio tests unlike other diversity indices.

Shannon – Weaver diversity index $H(S)$ is however, a biased estimate of the population index of diversity. Hence the expected value (Hutcheson, K. (1970)) of $H(S)$ is

$$E[H(S)] = \left[-\sum_{i=1}^{i=S} p_i (\log_2 p_i) \right] - \left[(S-1) \div (2N) \right] + \left[1 - \sum_{i=1}^{i=S} (1/p_i) \right] / (12N^2) \dots\dots\dots(10)$$

corrected to third term in the expansion.

The variance of the estimate $H(S)$ is given by

$$Var[H(S)] = \sum_{i=1}^{i=S} [p_i (\log_2 p_i)^2] - \left[\sum_{i=1}^{i=S} p_i (\log_2 p_i) \right]^2 \div N + (S-1) \div (2N^2) \dots\dots\dots(11)$$

corrected to second power on N . When N is very large, the first term is sufficient (Hutcheson, 1970). $E[H(S)]$ and $Var.[H(S)]$ were calculated for each region for the purpose of comparison between stations. Variance of the biased diversity index is important because it enables comparison of the sampling stations in terms of diversity index for the observed difference in the distribution of Pleuromamma species' total abundance.

2. Margalef's (1957) richness index is defined as

$$d = (S - 1) \div \ln N \dots\dots\dots(12)$$

where S is the total number of species in a sample, d is richness measurement and N is the total number of individuals of all the species in a sample.

3. Evenness index given by Heip's (1974) formula is :

$$\varepsilon = [EXP[H(S) - 1]] \div (S - 1) \dots\dots\dots(13)$$

where $e^{H(S)}$ is the equivalent number of equally distributed species. Equitability is defined as the ratio of the number of species observed to the number of species that are theoretically required by MacArthur's model to achieve the same diversity with equitable (or even) distribution of individuals among the species in a population (Howard, 1960; Lloyd and Ghelardi, 1964). Log normal distribution is fitted for both diversity and evenness indices (Snedecor and Cochran, 1967)

4. Species niche breadth nb_i , was calculated as

$$nb_i = EXP \left\{ - \sum_{j=1}^{j=n} \left[\left(\frac{n_{ij}}{N_j} \right) * \ln \left(\frac{n_{ij}}{N_j} \right) \right] \right\} \dots \dots \dots (14)$$

where n_{ij} = number of individuals of the i^{th} species in the j^{th} station of each region. Species niche breadth is plotted against total abundance of the species. The diversity and evenness indices as well as niche breadth for the species were calculated using the programme NICHE.FOR (Jayalakshmy, 1998).

For grouping of species as well as stations, factor analysis by varimax rotation to simple structure (Rummel, 1975) for Q-mode (species) as well as R mode (stations) was adopted. A frequent feature of faunal data is that many species are absent from a majority of samples, which lead to zero values in more than half of the data matrix. Transformation of data does not alter this. The measures which take into account the joint absences are not robust enough to be generally applicable (Field et al. 1982). Therefore the measure used by Bray and Curtis (Clifford and Stephenson, 1975) has been applied here, because it is not affected by joint absences (Field and McFarlane, 1968) and therefore sufficiently robust for faunal data. Yet it gives more weight to abundant species than to rare ones. In representative stations group linkage cluster analysis was carried out using Bray Curtis similarity index on standardized 4throot transformed abundance of species to see the species clustering/ specificity at different regions using Plymouth Routine in Marine Environmental Research (PRIMER v5.; Clarke and Gorley, 2001). The primary goal of this similarity matrix is to detect meaningful underlying dimensions that allow the researcher to explain observed similarities or dissimilarities (distances) between the investigated objects. Cluster analysis attempts to arrange 'objects' (in the present case males and females of pleuromamma species in the different regions) in a space so as to reproduce the observed similarities. As a result we can explain the distances in terms of dissimilarity between species occurring in the different stations. In more technical terms, it uses a function minimization algorithm that evaluates different configurations with the goal of maximization of the goodness of fit or minimizing the lack of fit. (see <http://www.statsoft.com/textbook/simulsca.html> for further details).

3 Results And Discussion

3.1 Quantitative distribution in the upper 200m water column.

Seven species and one variety of the genus *Pleuromamma* were considered for this analysis. To study the sexual segregation, males and females were separately investigated for species distribution and species coexistence. Among the males, *Pleuromamma indica* was the most abundant and evenly distributed species: in the area north of 10°N (Geometric Mean, GM= 18.54/100m², Coefficient of Variation, CV, =74.53%; in the equatorial region (8.32/100m², 71.70%); in the Central Indian Ocean (2.27/100m², 146.76%) and in the area extending along the east coast of Africa (5.12/100m², 107.22%), whereas *Pleuromamma gracilis* was the dominant species in the area of subtropical convergence (2.63/100m², 177.55%). The rarest and highly dispersed male *Pleuromamma* species in the above 5 regions were *P. abdominalis* (1.08/100m², 597.03%), *P. boreali* (1.04/100m², 870.65%), *P. abdominalis abysallis* (1.05/100m², 484.88%), *P. piseki* (1.35 /100m², 316.07%) and *P. piseki* (1.35/100m², 567.50%), respectively.

Among the female *Pleuromamma* species, the frequently occurring and uniformly distributed species were *P. indica* in the region north of 10°N (57.73/100m², 60.60%), *P. piseki* in the equatorial region (16.11/100m², 61.23%), *P. indica* (4.28/100m², 120.69%) in the Central Indian Ocean and *P. gracilis* in the area of subtropical convergence (4.20/100m², 136.24%), and *P. piseki* (11.27/100m², 85.8%) in the area extending along the east coast of Africa (11.27/100m², 85.18%), while the most rare and highly dispersed distribution was observed for *P. borealis* (1.09/100m², 601.97%) in the north of 10°N, *P. piseki* (1.98/100m², 607.97%) in the equatorial region, *P. xipias* (1.75/100m², 222.50%) in the Central Indian Ocean, *P. indica* (1.30/100 m², 321.28%) in the area of subtropical convergence and *P. xipias* (2.40 / 100m², 159.85%) in the area extending along the east coast of Africa. It has been noticed that, in the study area during *Gaveshani* and *Sagar Kanya* cruises, a preponderance of females was discernable; the males of *P. piseki*, *P. quadrungulata* and *P. borealis* were not recorded, but in the case of the other species, males of *P. xipias* were comparatively higher in the collections.

3.2 Distribution of environmental parameters and their relation with *Pleuromamma* species :

The range of variations in the distribution of the environmental parameters are given in table 1. The highest variation in salinity was observed in region 1 and the least in region 4. Similarly the highest variation in temperature was observed in region 5 and the least in region 1. The dissolved oxygen varied over a wide scale in regions 1 and 2, and over a narrow scale in region 4. Regarding the PO_4^{3-} distribution, high dispersion was observed in the regions 1 and 5, whereas the distribution was more or less uniform in regions 4 and 2. High variation in NO_3^- was found in regions 1 and 5

whereas in region 2, NO_3^- varied over a small range. In general, the highest range in the distribution of parameters other than dissolved oxygen was observed in the region north of 10°N where *Pleuromamma indica* was the dominant species implying that this species can tolerate a wide range for all water quality parameters other than dissolved oxygen, and furthermore indirectly implying that a major contribution in controlling the distribution of *P. indica* is that of dissolved oxygen.

Species abundance when plotted against latitude showed a normal pattern of distribution with unimodal distribution for *Pleuromamma xipias*, *P. quadragulata*, *P. piseki* and *P. abdominalis abyssalis* and it showed bimodal distribution for *P. borealis* from south to north, whereas the trend was an increasing parabolic function towards north, for *P. indica* (Fig. 2). On plotting species abundance against dissolved oxygen, it showed a trend opposite to that observed for latitude, from low oxygen level to high oxygen level (Fig. 3). *P. abdominalis*, *P. xipias*, and *P. quadragulata* preferred low oxygen in the range of 3.0 to 4.0 whereas *P. borealis* and *P. abdominalis abyssalis* were highly scattered, showing that factors other than dissolved oxygen were controlling their abundance. *P. indica* preferred dissolved oxygen in the range 2.5 to 3.5 mostly, gradually decreasing with increasing oxygen, and almost totally absent for dissolved oxygen exceeding 4.5. *P. gracilis* and *P. piseki* showed more of a platykurtic type of distribution with respect to dissolved oxygen, showing a wider range extending from 2.5 to 4.5 indicating a wide range of tolerance.

3.3 Step up predictive Multiple regression model

In Regions 1, 2 and 3 the parameters considered were temperature, salinity, dissolved oxygen, PO_4^{3-} and NO_3^- and their first order interaction effects, but in regions 4 and 5 only the first three parameters and their interaction effects were considered. In all the models, the abundance was transformed to log values, and then all the input variables (dependent variable, Pleuromamma species' total abundance, (Y) and independent variables (water quality parameters, X_i , $i=1,2,3,4,5$) were standardised and normalised (Sokal and Rohlf, 1981).

In region 5, the western boundary of the 4 regions considered, the temperature, salinity and dissolved oxygen were determined to be not sufficient enough for estimating the Pleuromamma species abundance from their single factor effects and interaction effects ($P>0.05$). This implies that other parameters such as growth rate, rate of assimilation of nutrients by the species and competition between species may be the controlling/limiting factors. In the region 5, the leading parameters were T*DO and salinity, and the order of importance of the parameters was

$$T*DO > S > S*DO > DO > T > T*S.$$

However, these factors alone were found to be insufficient to predict the *Pleuromamma* abundance in this region with high precision. Because nitrogen compounds were not considered, and the other parameters considered could not predict the total abundance with significant precision, the possibility for nutrients to be the leading influencing parameters, could not be ruled out.

In region 1, north of 10°N, among the parameters considered, the ecological factors as obtained from the model could be given as

$$T * S > NO_3^- > S * PO_4^{3-} > T * PO_4^{3-} > (DO * NO_3^-) > (PO_4^{3-} * NO_3^-) > (DO * PO_4^{3-}) > S * DO > T * DO$$

Predictive regression equation containing the first 8 important model parameters is

$$Y = -0.03965 - 0.52740(T * S) - 0.45192 NO_3^- + 0.3993(S * PO_4^{3-}) + 0.3882(T * PO_4^{3-}) + 0.3745(DO * NO_3^-) - 0.3603(PO_4^{3-} * NO_3^-) - 0.3238(DO * PO_4^{3-}) \dots\dots\dots(15)$$

This model explained about 55.19% of the variations in the *Pleuromamma* species distribution ($P < 0.05$), $F_{(15,56)} = 4.5981$. Since this region contains high nutrient low oxygen waters, and because interaction of temperature and PO_4^{3-} was an important controlling factor, it could be stated that (Greze, 1984) the assimilation of nutrients by the *Pleuromamma* species, which increases during low temperature and decreases during hot periods in a zooplankton community (Morris and Lewis, 1992), was the ecological factor controlling the *Pleuromamma* abundance. Also, because Interaction of temperature and salinity was an important limiting factor it implied that density of water masses was also determining the *Pleuromamma* abundance, with high abundance in low density waters. This region, being dominated by *Pleuromamma indica*, was characterised by high productivity and a strong oxygen minimum above 500m depth and salinity ranges from 32.32 to 36.62 PSU (Saraswathy, 1986).

In region 2, The most significant model for predicting *Pleuromamma* species abundance was also a fifteen parameter model, explaining about 34.32% of the variations in the distribution of abundance, $F_{(15,61)} = 2.1246$, ($P < 0.05$). The order of importance of the parameters was

$$(S * DO) > (DO * NO_3^-) > (T * DO) > (T * PO_4^{3-}) > (T * NO_3^-) > (S * NO_3^-) > NO_3^- > (PO_4^{3-} * NO_3^-)$$

This gradation showed that the efficiency of the model will not be reduced even when the parameters, such as the individual effects of the input parameters and the first order interaction effects of: (1) phosphate with dissolved oxygen, (2) phosphate with salinity and also (3) temperature with nitrate, were removed from the model ($t < 2.201$)

The model equation containing the first 6 important model parameters was

$$Y = 0.1980 - 0.615(S * DO) + 0.4873(DO * NO_3^-) - 0.3767(T * DO) - 0.3725(T * PO_4^{3-}) + 0.3635(T * NO_3^-) - 0.3365(S * NO_3^-) \dots\dots\dots(16)$$

Because the regression coefficients are partial regression coefficients, smaller the value for the coefficients, lesser will be the importance of the model parameter. Nutrients interaction was an important limiting factor. It determined (Kautsky, 1981) the outcome of the interspecies competitions at different nutrient concentrations because the intake of these parameters are species specific to a large extent, this region being comprised of low nutrient high oxygen waters as indicated by the relative importance of the non-bold model parameters. The region between 10°N and 10°S latitude which comprises the Somalia coast at its western boundary, is an area with majority of the species having higher relative abundance. During the SW monsoon when the North Equatorial current is easterly, deriving in part from the north easterly Somalia current, and also when the flow north of the equator is westerly during the NE monsoon period, high concentration of *P. piseki* was found north of the equator. The southern edge of the easterly Equatorial current during the NE monsoon and the northern edge of the westerly South Equatorial current during the SW monsoon lie in this region to the south of the equator. The south tropical gyre extends south of 10°S, and the hydrochemical front at 10°S separates the low nutrient high oxygen waters of the subtropical gyre from the high nutrient low oxygen waters of the monsoon gyre in the northern Indian Ocean, north of 10°S, thus acting as a barrier. When nutrients were the leading parameters, it followed that the main role of the microbial loop (Wylie and Currie, 1991) in aquatic food web was rapid remineralization of organic nutrients with little carbon being transferred to higher trophic levels and also that transfer of carbon from diatoms to crustaceans was equally inefficient. In a copepod dominated crustacean community, bacteria and picoplankton contributed an insignificant amount of carbon to crustaceans as indicated by the low value for the prediction efficiency where only nitrate and phosphate compounds were leading parameters. Because salinity was an important factor, growth rate of dominant phytoplankton species (Qasim et al, 1972a) on which *Pleuromamma* species feed, can be introduced as an ecological factor, replacing the effect of salinity-dissolved oxygen interaction. The remaining part of the variability could be explained if currents were also considered as a model parameter because there is the influence of the North equatorial currents and Somali currents in this region.

In region 3 the grading for the model parameters could be given as

$$(DO * PO_4^{3-}) > (S * DO) > S > DO > (T * PO_4^{3-}) > (T * DO) > PO_4^{3-} > T > (T * S) > (S * PO_4^{3-})$$

with the remaining four factors insignificant, implying that density of water remained as a homogeneous factor and so cannot be an indicating factor in the Pleuromamma species distribution. The prediction equation with the first 5 important model parameters was

$$Y = 0.34223 + 1.3559(\text{DO} * \text{PO}_4^{3-}) + 1.1035(\text{S} * \text{DO}) + 0.5533\text{S} - 0.4821\text{DO} + 0.2762(\text{T} * \text{PO}_4^{3-}) \dots\dots\dots(17)$$

This model explained about 32.73% of the variations in the distribution of Pleuromamma species' total abundance, $F_{(10,33)} = 1.6058$. As observed at region 2, in this region also since salinity was an important factor, growth rate of dominant phytoplankton species (Qasim et al. 1972a) on which Pleuromamma species feed, can be introduced as an ecological factor replacing the effect of salinity-dissolved oxygen interaction, provided it can be estimated very precisely. Since phosphate is not a limiting factor, it can be suggested that differences in nutrient limitation are supposed to be the result of the differences in the ratio of total nitrogen to total phosphorus in nutrient inputs to the system, and also be due to the differences in the internal biogeochemical processes which include nitrogen fixation and a variety of recycling processes (Currie, 1990; Howarth,1988; Kiefer and Atkinson, 1984) . In region 4, a three parameter model supported by three interaction effects had been found to be the best model. The order of importance of the parameters was

DO > **(T*DO)** > **(T*S)** > **S** > **(S*DO)** > **T** in which, the last two factors could be deleted without affecting the significance of the estimated abundance ($t < 1.96$). The equation of the model with the first 4 important model parameters was

$$Y = -0.2039 - 0.3739\text{DO} - 0.2866(\text{T} * \text{DO}) + 0.2578(\text{T} * \text{S}) - 0.1424\text{S} \dots\dots\dots(18)$$

This equation explained about 31.15% of the variations. $F_{(6,25)} = 1.8849$, ($P < 0.10$). In the relative importance of the model parameters, those given in bold letters are limiting factors, and the others are controlling factors. In this region also temperature and oxygen act in concert with each other as observed by Clifford et al. (1995) in the study of population dynamics of bacterioplankton in an oligotrophic lake. This may be possible because in Arabian Sea, biological activity appears to play a predominant role in controlling the oxygen content whereas in the open ocean oxygen distribution is mainly governed by the water movements circulation and mixing (Panakkala Rao and Jayaraman, 1970). Errhif, et al. (1997) showed that in the Antarctic waters the distribution of copepods appeared to be unrelated to chlorophyll concentrations and on a larger scale the distribution was related to hydrologic characteristics as observed in this study. In all cases except region 3, all the leading parameters are limiting factors in the sense that their shortage reduces the abundance of the Pleuromamma species.

3.4 Species composition and coexistence

Among the seven species of *Pleuromamma*, *P. quadrungulata* was totally absent in regions 1, 3, 4 and 5 and male species of *P. borealis* was completely absent in region 1. About 68.18%, 73.31%, 85.5%, 97.5% and 65.8% of the species coexisted in the 5 regions, 1 to 5 respectively.

A special feature of regions 2, 3, 4 and 5 was that no significant predator–prey relation ($r \geq 0$) was observed. There appeared to be a latitudinal gradient of increasing coexistence of species towards the South with decreasing abundance of *Pleuromamma indica*. This indicated that *Pleuromamma* species coexisting in the same area, are all exposed to the same environmental characteristics and food resources (Leonardo et al, 1991) and identical tolerance shows a north–south range (Fig. 2 & Fig. 3). Dendrogram drawn for each region showed that males and females of *P. indica*, *P. gracilis* and *P. abdominalis* were always together in the 4 regions. In region 1, *P. piseki* males were widely segregated from its females whereas in region 1 and 4, *P. piseki* and *P. xipias* females were extensively associated with males and females of *P. indica* and *P. abdominalis*, respectively. In region 2, *P. borealis*, *P. xipias* and *P. piseki* females were linked more closely with males and females of *P. abdominalis*. *P. borealis* males were widely separated from the major cluster of *Pleuromamma* species in region 3. Roe (1972) has described in detail the vertical segregation of species of *Pleuromamma* in the Atlantic Ocean. The vertical segregation was found to be clear during day, but during night, due to the upward migration of all the species, the distinctive feature was not evident (Saraswathy, 1986). In this study, segregation was evident in the case of males of *P. piseki* and *P. xipias* and of *P. borealis* to some extent. Dendrogram drawn for the whole study area, showed >95% similarity between *P. piseki* and *P. gracilis*. *P. indica* showed 40% similarity (Fig. 4) with the cluster of circum global species: *P. xipias*, *P. piseki*, *P. gracilis*, *P. abdominalis* and *P. borealis*. This clustering obtained was well defined with respect to both latitude and dissolved oxygen (Fig. 2 & Fig. 3).

Regarding the geographical distribution of the *Pleuromamma* species, it was observed that nearly 90% of the species occurred in the western and eastern boundary of the Indian ocean along the African and Australian coasts, respectively and in lesser degree along the eastern boundaries, from the Andaman Sea to the South of Java. *P. xipias*, *P. gracilis*, *P. abdominalis abyssalis*, and *P. piseki* were observed in the south east Bay of Bengal. Except for a few stray records, *P. borealis* and *P. quadrungulata* were very rare in the Bay of Bengal and in the Arabian Sea. *P. quadrungulata* occupied a specialised position due to the presence in the isolated area of Equatorial belt and it is almost absent along the Somalia and the Agulhas current regions (Fig. 2 & Fig. 3).

3.5 Diversity, evenness and niche breadth in the distribution of *Pleuromamma* species

Shannon–Weaver diversity index (Shannon and Weaver, 1963, Monte Lloyd and Ghelardi, 1964) and Heip's evenness index (Heip, 1975), was used to study the diversity and equitability in the distribution of species in the different areas. Majority of the stations lying between 10°N and 20°N had diversity ranging between 0.4 and 1.0 in region 1, whereas in region 2 the diversity ranged between 1.0 and 3.4. In region 3, 4 and 5 the corresponding values were 1.0–3.0, 1.4–2.6 and 1.4–2.8 respectively (Fig. 5). As far as diversity is concerned Region 1 is quite different from the other 4 regions which are almost similar. Species evenness was high in regions 2 and 4 (0.3–0.9) (Figure 6) The diversity index was more consistent (1.4–2.5) in majority of the stations in region 5. On testing the significance of the difference between the sample diversity and the theoretical diversity for all the regions it was observed that in no station the difference was highly significant ($P > 0.05$) (Table 2).

Based on the richness factor, it follows that region 1 was the least diverse, followed by regions 4, 2 and 3, respectively. In region 1, Vinogradov and Voronina (1961) had observed that the spread of *P. xipias* to the northeast Arabian Sea was limited by approximately 0.5 ml/l and of *P. gracilis*, by 0.15 ml/l of oxygen. *P. indica* was observed even when oxygen was less than 0.1 ml/l. The regions 3, 2 and 4 are almost similar, leading to the inference that there is higher diversity towards the south than towards the north. The diversity and evenness are particularly taken to study the form of the statistical distribution rather than just the diversity. The lognormal distribution (Gupta, 1980) fitted for diversity index (Fig. 5) and evenness index (Fig. 6) showed that this distribution was a good fit for H(S) only in regions 2, 3 and 5 whereas for evenness, lognormal distribution was a good fit only in region 5 (Calculated value of $X^2 >$ tabled value of X^2 ($P > 0.05$)). The Agulhas current which is the western boundary current in the southwest part of the Indian ocean draws its water essentially from the south Equatorial current and represents a southward extension of tropical and subtropical water which carries within its core several tropical species. Thus the currents in the western boundary help in the dispersal of species over a wider area rather than the water quality parameters which were found to be least important ($P > 0.05$) in predicting *Pleuromamma* species' total abundance in region 5.

According to Lydia Ignatiades (1994) classification of assemblages based on species niche breadth, there are no species with narrow breadth (<3). Region 4 contains all species with moderate (4–8) niche breadth, whereas regions 1 and 3 contains 66.6% and 29% of the species with moderate niche breadth, and region 2 contains all species with broad (>8) niche breadth. Niche breadth could be taken as an index of the spread of the species. Narrower the niche breadth, smaller will be the rate of migration (table 3).

Relation between niche breadth and total abundance is given by the equation

$$Y = 16.1518 - 0.014459X + 9.617803X10^{-6}X^2 - 1.329045X10^{-9}X^3 + 5.043930X10^{-13}X^4 \dots\dots\dots(18)$$

where Y is the species niche breadth, and X is the species total abundance in a region. This relation explains about 34.42% of the spatial variability ($F_{(4,23)}=4.5435$). Thus species niche breadth has divided the species into two scales of hierarchy, i.e., a background population formed by broad breadth and high abundance species (35%) and a population with species demonstrating moderate breadth and low abundant species (65%). This division combines regions 1, 3 and 4 forming the second category, with region 2 falling exclusively in the first category.

3.6 Factor analysis

Based on the Q-mode factor analysis by varimax rotation to simple structure, it was possible to delineate 4 significant factor groups in region 1, 10 in region 2, 5 in region 3, 6 in region 4 and 5 in region 5. The differential groups were constituted by factor 1 in regions 1 and 2 and factors 1 and 2 in regions 3, 4 and 5 (Table 4). The significant factor groups presented a closeness ratio of 97%, 98%, 68%, 98% and 85% in the 5 regions (Table 5). The five areas were demarcated with respect to the number of differential groups also. Only one (73.27%), one (55.8%), two(52.06%), two(65.10%) and two (60.93%) differential groups were sufficient to extract the maximum information about the distribution of this genus in these regions (Table 5).

Factor analysis shows that the eigen values are maximum in region 4 and least in region 3. There is a decreasing gradient for the closeness ratio from region 1 to region 5, with an asymptotic nature from region 3 to region 5 for each factor. The number of species in the factor group decreases steadily from factor 1 to the last significant factor group in that area. Lesser the number of significant factor groups more is the uniformity in the spatial distribution. More the number of factors more the variability in the spatial distribution and less the information gathered from the latitudinal distribution. Regions 1 and 2 are similar in the sense that the first factor group itself is enough to describe that region. The differential groups are constituted by different species and this characteristic demarcates the five regions qualitatively. Regarding the sexual segregation, it is observed that the females and males of the same species are included in the same factor groups in region 2 than in regions 1, 3 and 4, sexual segregation being less in the north than in the south except for the species *P. abdominalis* for which males and females are always found together irrespective of the region they occupy (Table 4). Sexual segregation obtained from the Bray–Curtis similarity index was almost similar to that delineated from the factor analysis. But the latter method is preferable, because it could be associated with a significance value for the significance of the factor model

($P < 0.05$) unlike the former method, which is purely nonparametric. Similar to niche breadth, factor grouping also delineated more similarity among the regions 1, 3 and 4, based on the number of significant factor groups.

On a broader scale, based on the ecological aspect, the four regions could be justifiably reduced to 2 regions viz., region 1 comprising the north off 10°N , central Indian Ocean and the area of the subtropical convergence, and region 2 consisting of the equatorial region between 10°N and 10°S . The plot of the species abundance with respect to latitude also showed such a demarcation. On a broader scale, as an application of the distribution of pleuromamma species in forensic studies, it could be stated that adult copepods can be used in studies such as acute toxicity of polycyclic aromatic hydrocarbons (PAH's) associated (Carlos Barata et al, 2005) with the oil spill either as single substances or in mixtures through motility of copepods. Quantitative structure activity regression models can be applied for predicting the toxicity of the PAH's compounds in copepod species using the relation between acute toxicity of the tested PAH's compounds and their octanol-water partition coefficients.

Conclusion

P. quadrangulata was totally absent in regions 1, 3, 4 and 5 and male species of *P. borealis* was completely absent in region 1. About 68.18%, 73.31%, 85.5%, 97.5% and 65.8% of the species coexisted in the 5 regions, 1–5 respectively. No significant predator–prey relation ($r \geq 0$) was observed in regions 2, 3, 4 and 5 based on the Pleuromamma species distribution.

Highest range in the distribution of parameters other than dissolved oxygen was observed in the region north of 10°N where *Pleuromamma indica* was the dominant species, implying that this species can tolerate a wide range for all water quality parameters other than dissolved oxygen, indirectly implying that a major contribution in controlling the distribution of *P. indica* is that of dissolved oxygen.

Relation between Pleuromamma species' abundance and the water quality parameters showed a decreasing trend in the variability explained (VE) from region 1 (VE=55.19%) to region 4 (VE=31.15%) in the models, indicating that the influence of other ecological factors was of a higher order in the south than in the north, with a north–south gradient. Indices of diversity (Shannon and Weaver) and evenness (Heips) were calculated for sampling stations, and lognormal distribution fitted for these indices were observed to be a good fit for regions 2,3 and 5 for diversity and only for region 5 in the case of evenness($P < 0.05$).

Species niche breadth has divided the species into two scales of hierarchy i.e., a background population formed by broad breadth and high abundance species (35%), and a population with

species demonstrating moderate breadth and low abundant species (65%). This division combines regions 1, 3 and 4 forming the second category, and region 2 falling exclusively in the first category.

The females and males of more numbers of species are included in the same factor groups in regions 1 and 2, compared to regions 3, 4 and 5. Sexual segregation being less in the north than in the south, except for the species *P. abdominalis* for which males and females are always found together, irrespective of the region it occupies.

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Table 1 - Range of temperature, salinity, dissolved oxygen, PO₄-P and NO₃-N

Region	Salinity (PSU)		Temperature.(°C)		Diss.Oxy.(μmol /L)		PO ₄ -P(μmol /L)		NO ₃ -N (μmol /L)	
	Max	Min	Max	Min	Max	Min	Max	Min	Max	Min
1.	36.64	32.32	27.99	19.06	04.85	01.82	01.92	00.10	22.90	00.01
2.	35.78	32.88	29.52	17.33	04.37	02.34	01.18	00.46	21.10	08.00
3.	35.69	34.38	24.51	14.97	05.40	03.07	01.21	00.20	14.20	01.30
4.	35.79	34.93	19.85	10.52	05.94	03.97	00.54	00.26	05.50	01.40
5.	36.64	34.95	27.04	12.25	05.56	02.25	01.92	00.26	20.40	02.30

Table-2 showing the average values and coefficient of variation (CV%)of diversity indices

index	Region 1		Region 2		Region 3		Region 4	
	Average	CV%	Average	CV%	Average	CV%	Average	CV%
Richness	2.064	52.25	3.073	45.14	3.422	52.18	2.631	41.13
Diversity	0.954	68.36	1.405	115.52	1.522	32.48	1.124	43.99
Evenness	1.027	65.75	1.3989	30.66	1.384	30.74	1.080	39.56

Table 3 species niche breadth

Species	Region 1	Region 2	Region 3	Region 4
PA	7.624	34.273	9.947	3.655
PX	4.703	33.913	9.945	6.346
PQ	-----	46.779	-----	-----
PI	13.233	57.337	8.558	4.212
PG	-----	31.299	7.909	3.268
PB	9.922	50.973	10.768	5.728
PAA	7.848	47.151	16.961	4.134
PH	7.928	33.154	9.953	5.328

Table 4- Grouping of Pleuromama species based on Q-mode factor analysis

Region 1	Region 2	Region 3	Region 4	Region 5
Cluster (1)	Cluster (1)	Cluster (1)	Cluster (1)	Cluster (1)
<i>P. gracilis</i> (m)	<i>P. abdominalis</i> (m,f)	<i>P. abdominalis</i> (m,f)	<i>P. abdominalis</i> (m,f)	<i>P. abdominalis</i> (m,f)
<i>P. piseki</i> (m,f)	<i>P. indica</i> (m,f)	<i>P. xipias</i> (m)	<i>P. xipias</i> (m,f)	<i>P. gracilis</i> (m,f)
<i>P. borealis</i> (m)	<i>P. gracilis</i> (m,f)	<i>P. gracilis</i> (m)	<i>P. gracilis</i> (m,f)	<i>Pa. Abyssalis</i>
	<i>P. piseki</i> (m,f)	<i>P. piseki</i> (m,f)	<i>Pa. abyssalis</i>	<i>P. xipias</i> (f)
	<i>P. xipias</i> (f)	<i>P. quadrangulata</i> (f)	<i>P. piseki</i> (f)	<i>P. piseki</i> (f)
		<i>P. indica</i> (f)		<i>P. borealis</i> (f)
		<i>P. borealis</i> (f)		
Cluster (2)	Cluster (2)	Cluster (2)	Cluster (2)	Cluster (2)
<i>P.abdominalis</i> (m,f)	<i>P. borealis</i> (m,f)	<i>P. indica</i> (m)	<i>P. piseki</i> (m)	<i>Pf. Indica</i> (m,f)
<i>P. xipias</i> (m,f)	Cluster (3)	<i>P. abdominalis</i> (f)	<i>P. borealis</i> (m)	<i>P. Piseki</i> (m)
<i>P. indica</i> (m,f)	<i>P. xipias</i> (m)			
	<i>Pa. abyssalis</i>			
	Cluster (4)			
	<i>P. indica</i> (m)			
	<i>P. piseki</i> (f)			

m.- male, f. – female.

Table 5 - Eigen values (λ) and closeness ratio (CR%) by Q-mode factor analysis for species grouping

Region Factors	Region 1		Region 2		Region 3		Region 4		Region 5	
	λ	CR%	λ	CR%	λ	CR%	λ	CR%	λ	CR%
1.	49.09	73.27	61.91	55.70	06.20	41.48	164.3	39.49	25.59	44.11
2.	06.63	83.17	17.76	71.76	01.53	52.06	104.5	65.10	09.75	60.93
3.	05.53	91.41	09.67	80.47	01.43	61.62	58.29	79.40	06.30	71.78
4.	03.82	97.10	06.26	86.11	01.08	68.79	37.82	88.20	04.90	80.22
5.			04.44	90.11			27.11	94.72	02.53	84.58
6.			02.99	92.80			16.88	98.77		
7.			02.07	94.67						
8.			01.60	96.11						
9.			01.41	97.31						
10.			01.14	98.41						

LEGEND TO FIGURES

Figure 1- Station locations

Figure 2 - Pleuromamma species' abundance plotted against latitude for the pooled data of regions 1–4.

Figure 3 – Pleuromamma species' abundance plotted against dissolved oxygen for the pooled data of regions 1–4

Figure 4 - Dendrogram for species coexistence using Bray Curtis coefficient of similarity in regions 1–5

Figure 5- Lognormal distribution fitted for Shannon–Weaver Diversity index in region 1 to region 5.

Figure 6– Lognormal distribution fitted for Heips evenness index in region 1 to region 5.

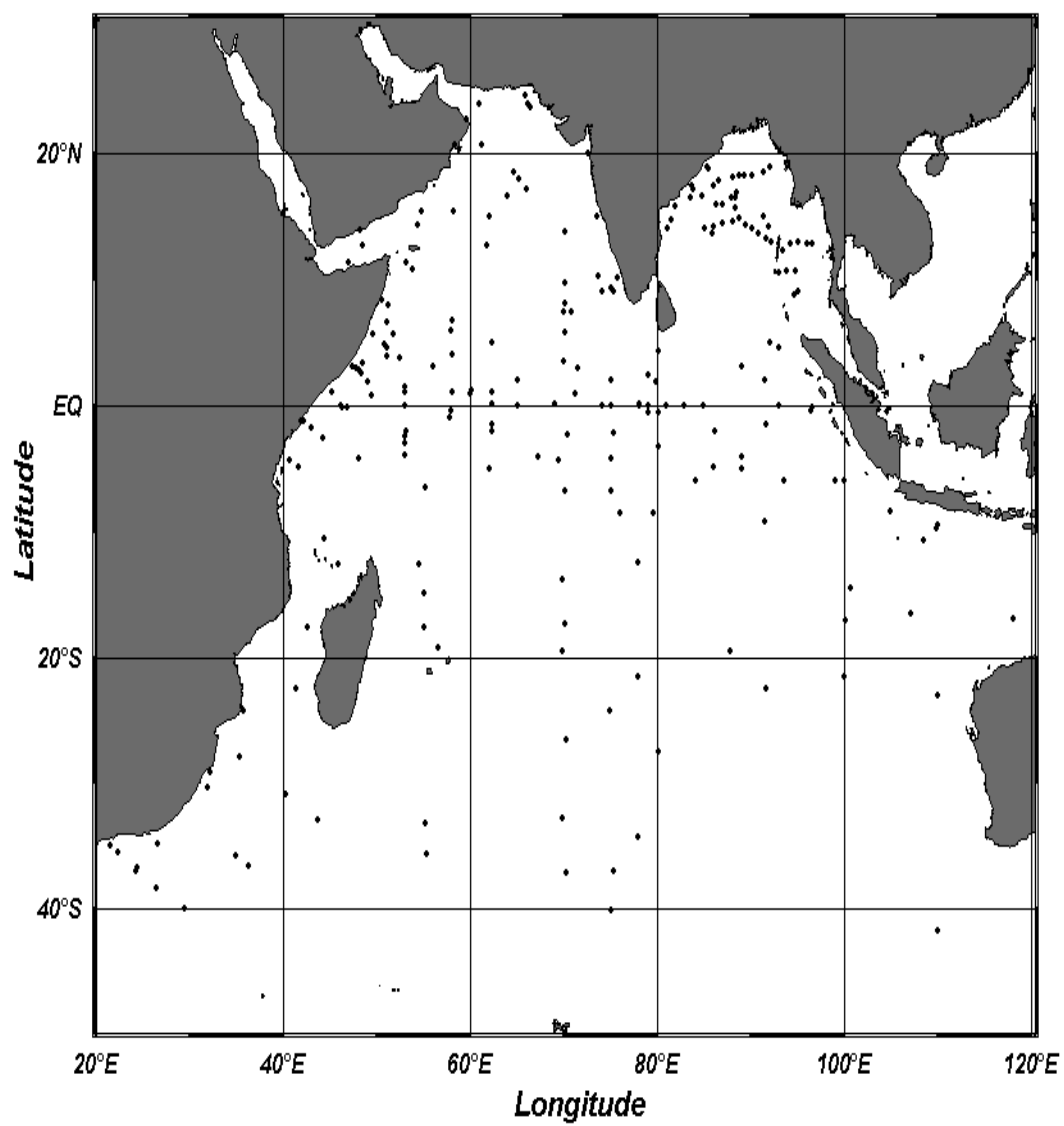


Figure 1

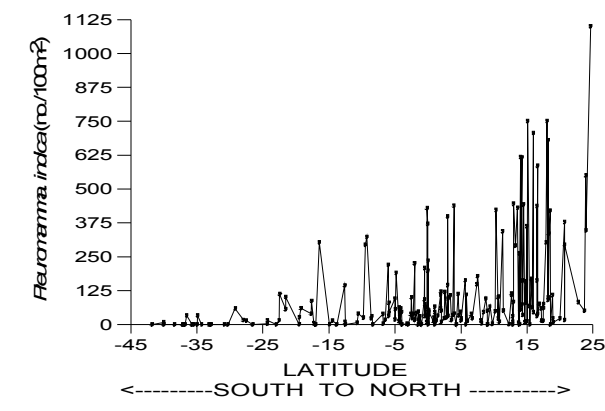
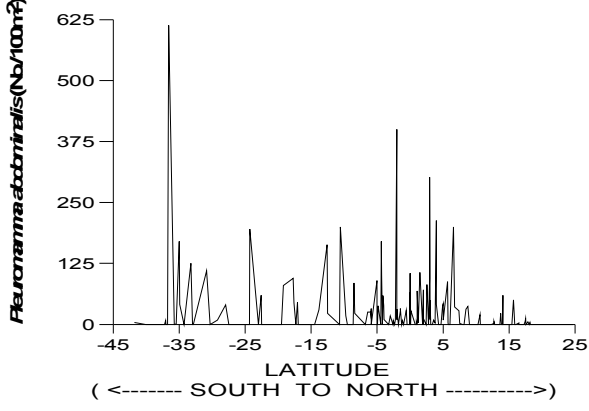
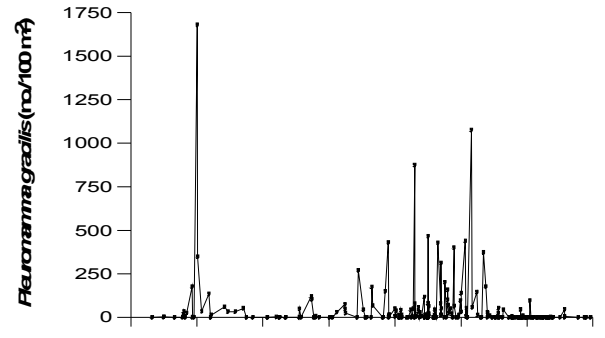
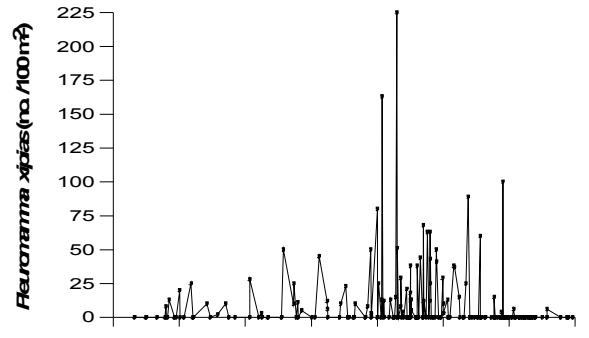
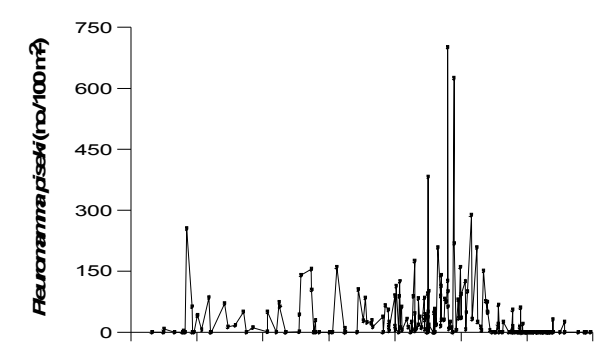
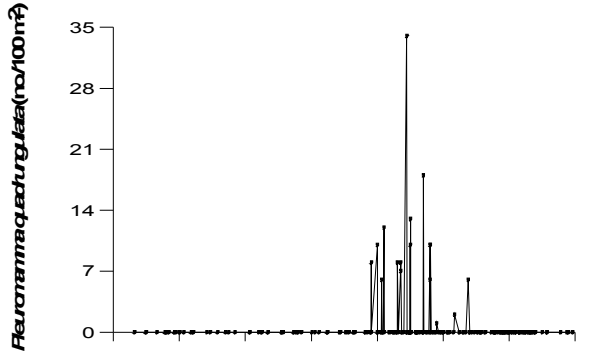
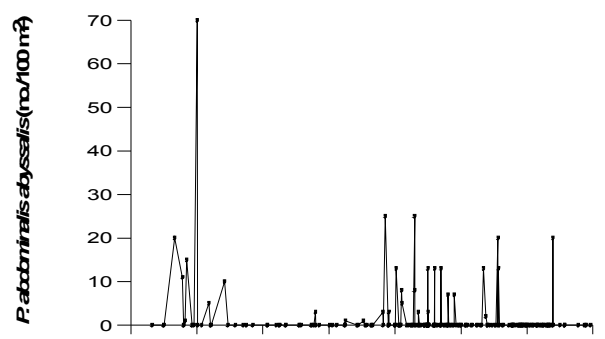
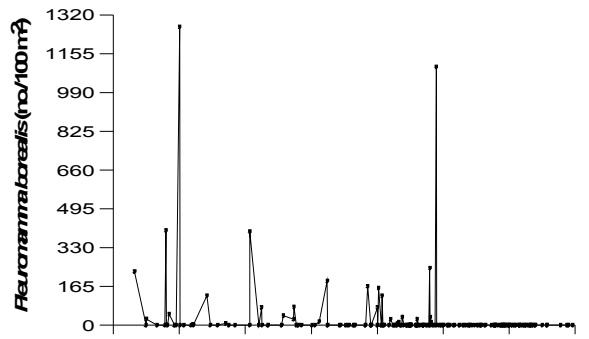


Figure 2

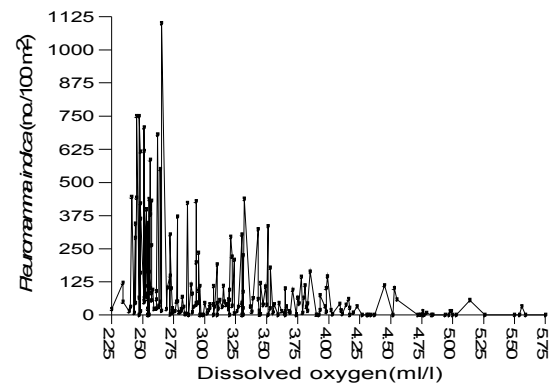
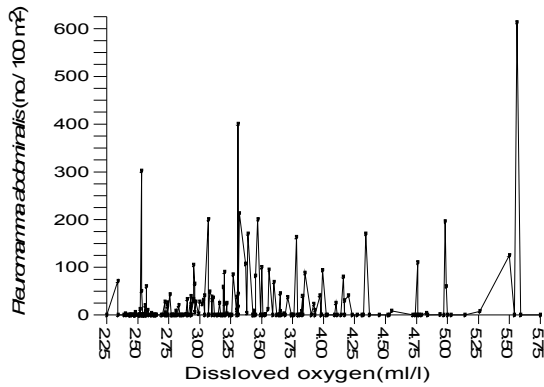
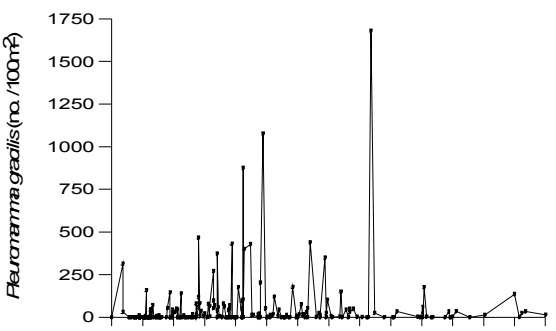
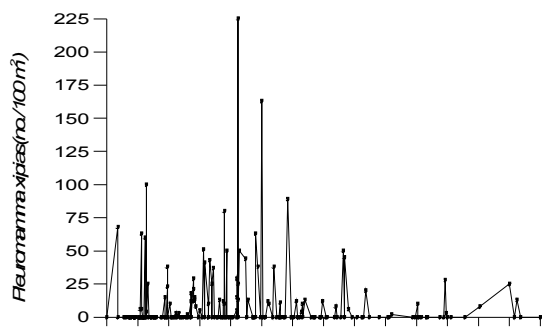
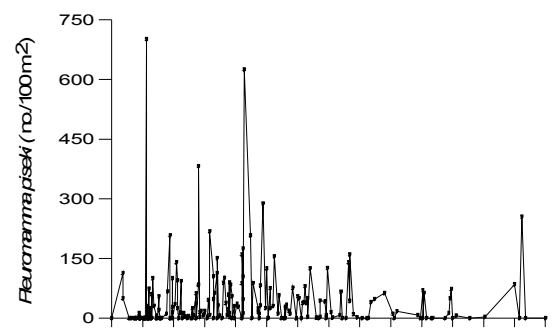
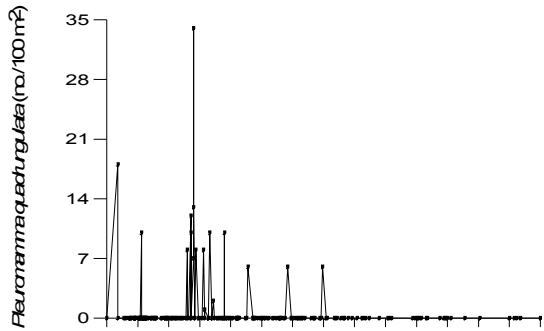
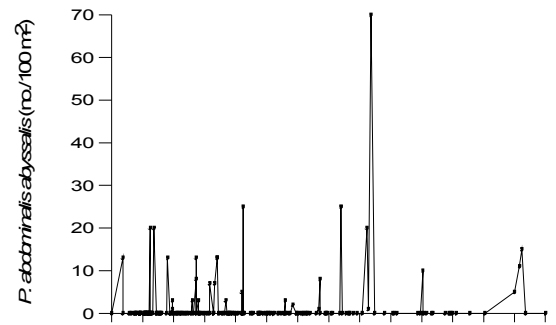
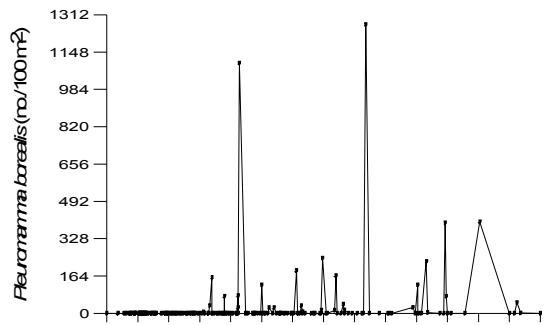
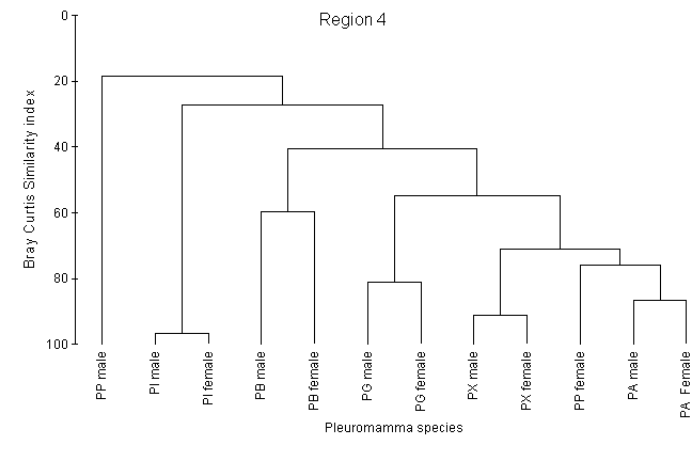
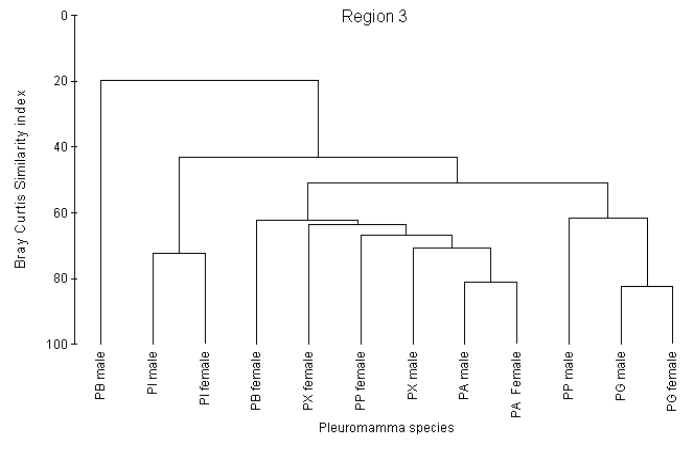
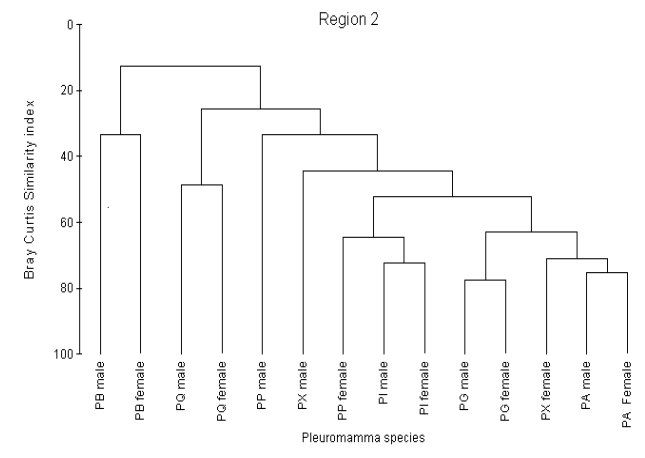
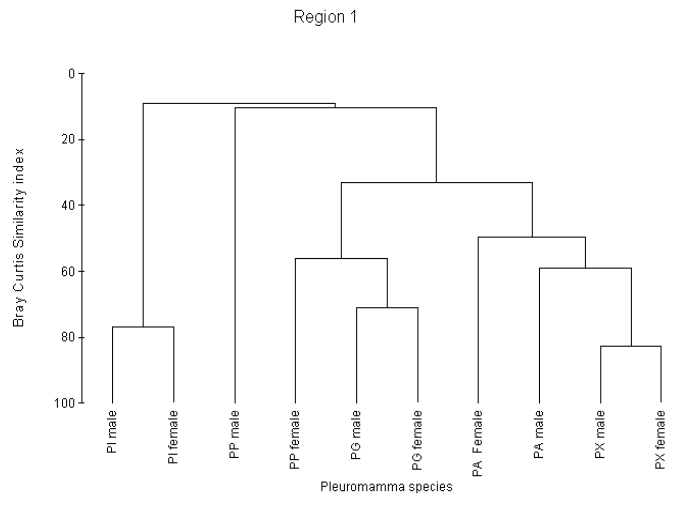


Figure 3



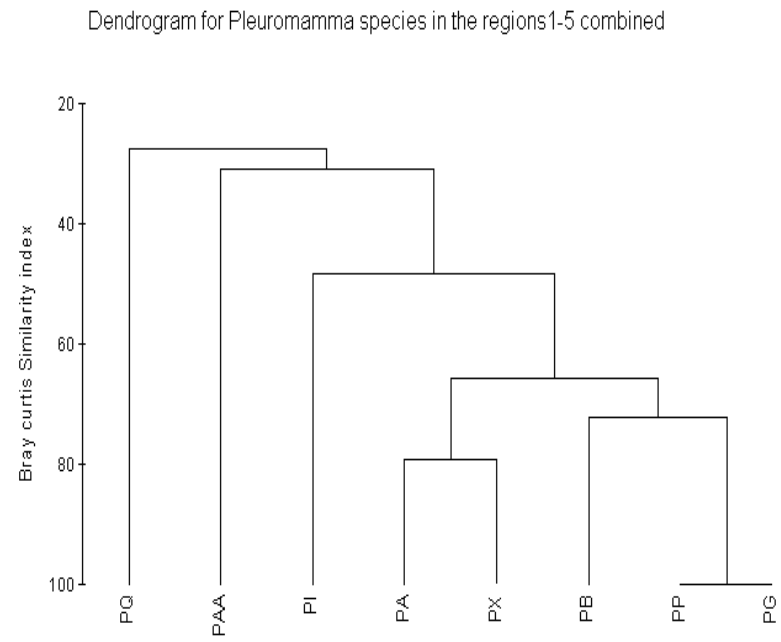


Figure 4

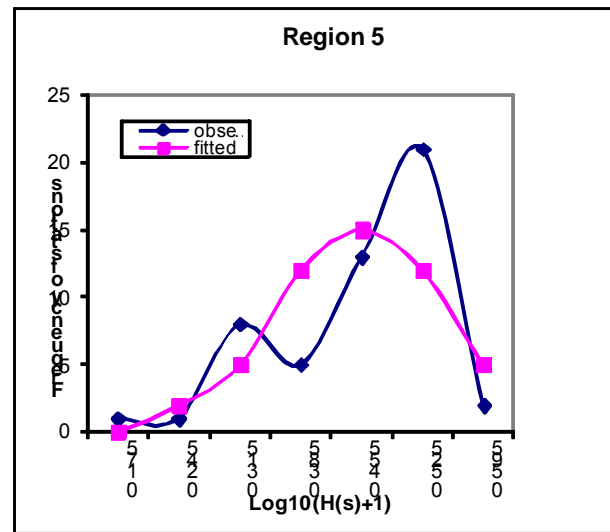
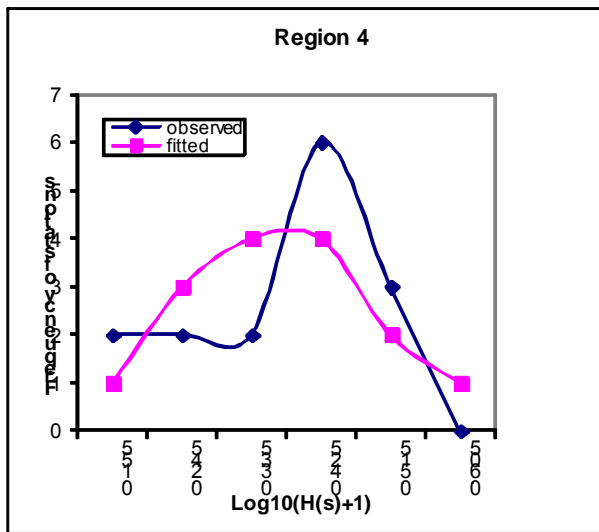
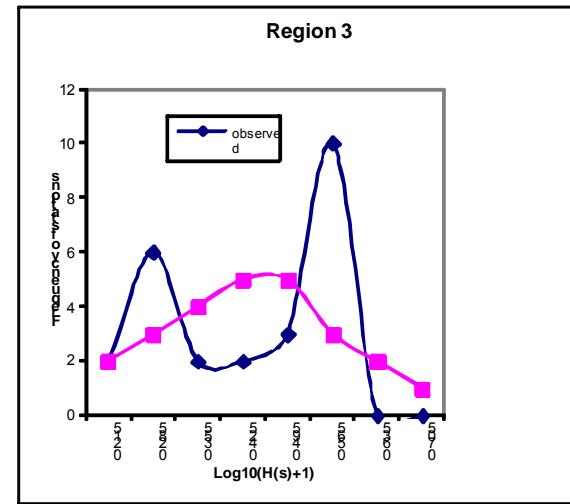
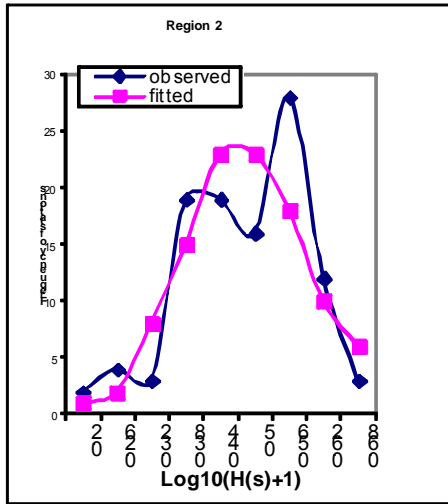
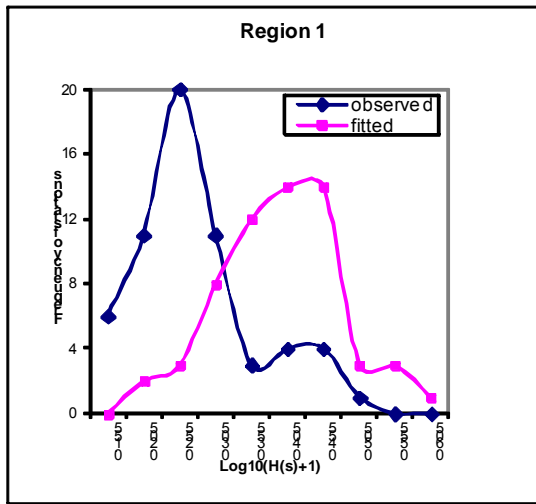


Figure 5

