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Microbial Populations in Deep Sea Water and Fish of South East Arabian Sea with Special Emphasis on Escherichia coli & Coliphages

B. Madhusudana Rao* and P.K. Surendran

Microbiology, Fermentation & Biotechnology Division, Central Institute of Fisheries Technology, Cochin - 682 029, India

Deep sea fish, deep sea surface water (DSW) and deep sea water from 200m depth (DSW₂₀₀) and littoral sea water (LSW) of the Arabian Sea (8-13°N Latitude, 74-76°E Longitude) were analyzed for faecal indicators. E.coli could not be detected in DSW200: However, two deep-sea fish, Psenopsis cynea and Heterocarpus woodmasoni had low levels of E.coli, 0.3 MPN/ g and 0.7 MPN/g, respectively, at the time of harvest. Ecoli strains isolated from deep sea environment have been found to be indistinguishable from terrestrial forms, either morphologically or biochemically. DSW had almost equal proportions of Gram -ve (22%) and Gram +ve (20%) bacteria whereas DSW₂₀₀ had a high percentage of Gram +ve (46%) bacteria. In deep-sea fish, Gram -ve were almost double of Gram +ve bacteria. Pseudomonas was the predominant bacterial genus in deep-sea water samples whereas Vibrio was preponderant in deep-sea fish. DSW₂₀₀ had significant proportions of Arthrobacter (24%) and filamentous bacteria (17%). Yeasts were detected only in deep-sea fish samples. LSW collected from a location 15 nautical miles off Quilon had high levels of faecal pollution. In LSW predominant (16%) whereas Pseudomonas (13%) and Gram +ve bacterial genus was Micrococus Enterobacteriaceae (10%) were the prominent Gram -ve groups. E.coli and coliphages could not be detected in deep-sea waters. A few deep-sea fish at the time of harvest showed low levels of faecal pollution and were within the stipulated limits. The study showed that high count of E.coli and coliphages in deep-sea fish procured from landing centres is not due to polluted deep-sea fish or polluted deep-sea waters.

Key Words: Deep sea, Escherichia coli, coliphages, faecal pollution

Arabian sea has potentially rich unexploited deep sea fish resources. In the South East Arabian sea (8-13°N latitude, 73-76°E longitude) *Chlorophthalmus* formed the most dominant species. Other major exploitable species included *Cubiceps, Neopinnula orientalis, Psenopsis cynea, Chascanopsetta lugubris* and *Priacanthus hamrur* (Khan *et al.*, 1996). In the 200 - 500m depth region, the potential for deep sea fish resources is higher in South West Coast than in North West, Lower East and Upper East Coasts (Sudarsan *et al.*, 1990).

Monitoring the sanitation quality of water and fish is necessary for predicting

potential public health hazards. bacteria viz., faecal coliforms and E.coli are by far the most commonly used indicators of faecal contamination. Regulatory agencies had fixed the admissible level for these in water and food intended for human consumption (European Economic Communities, 1980; GOI, 1995). Salinity, light intensity, lack of adequate amounts of nitrogen, phosphorous, iron and low organic matter content of the sea water contribute significantly to the death of coliforms in marine environment (Borrego et al., 1983, Lei et al., 2000). As such very low counts of E.coli are expected in deep sea fish. However, when deep sea fish procured from fish landing centers at Cochin were analyzed, we found that all the samples had very high numbers of faecal coliforms, *E.coli* and coliphages (Table 1). In order to ascertain whether *E.coli* and coliphages were present in the deep sea fish at the time of harvest and whether deep sea waters harbour these organisms, the present work was undertaken. Additionally, study on the microbial populations and generic distribution of bacteria in deep sea water and deep sea fish of the southwest coast was taken up, as the information available on this aspect was limited.

Materials and Methods

Deep sea fish and deep seawater samples were collected from the South East Arabian sea during Cruise 191 of FORV Sagar Sampada, in January, 2001, the area of operation being 8-13°N latitude, 74-76°E longitude and depths of 227m to 324m for deep sea samples and 51 to 70 m for littoral sea samples. The samples were analyzed in the on-board laboratory, immediately after collection.

Deep sea surface water (DSW) samples were collected from the surface (1-2m deep), at four locations, using presterilized bottles. Deep sea water samples from a depth of 200m (DSW₂₀₀) were collected at three locations using CTD system (Seabird Electronics, USA). Samples were dispensed immediately into presterilized bottles and analyzed. Littoral sea water (LSW) samples were collected from the surface (1-2m deep) at two locations, using presterilized bottles.

Five species of fish (Psenopsis cynea, Chlorophthalmus agasizzi, Priacanthus hamrur, Trichurus lepturus, Neopinnula orientalis), three species of prawn (Plesionika ensis, Heterocarpus woodmasoni, Heterocarpus gibbosus) and one species of lobster (Panulirus sewelli) were obtained from six locations from deep sea by

bottom trawling using high speed demersal trawl (fish version), high opening trawl and high speed demersal trawl. Immediately after hauling, the fish were aseptically picked from the trawl net, transferred into sterile plastic bags and analyzed microbiologically.

Two samples of fish (*Priacanthus hamrur*), four samples of shrimp (*Heterocarpus woodmasoni*, *Heterocarpus* sp. *Solenocera crassicornis*), two samples of lobster (*Panulirus sewelli*, *Panulirus polyphagus*), one sample of squid (*Loligo duvaucelli*) and one sample of oyster (*Crassostrea* sp.) were procured from fish landing centres in Cochin and were analyzed.

Aerobic Plate Count (APC) was done by pour plate method using sea water agar (peptone 0.5g, ferric phosphate 0.01g, agar 1.5g, aged seawater 100ml, pH 7.5±0.1). Aged sea water was autoclaved and used as diluent for homogenization. Plates were incubated aerobically at room temperature (26 – 28°C) for 10-12 days (ZoBell, 1990).

Original isolates from TPC plates were randomly picked using Harrison's disc (Harrigan and McCance, 1976b) and plated out to obtain a pure culture and put through a series of operations – microscopy (Gram's reaction, morphology) and biochemical reactions (Kovac's oxidase test, catalase test, Hugh & Leifsons glucose oxidation & fermentation reaction, sensitivity to 2.5 units of penicillin, growth at 0% NaCl) (Surendran & Gopakumar, 1981). The cultures were identified as per Surendran & Gopakumar, (1981); Bergey's Manual of Systematic Bacteriology Vol 1 & Vol 2, (1986a).

Total Coliforms, Faecal Coliforms and *E.coli* were determined by Most Probable Number (MPN) method (3step, 3tube MPN). MacConkey broth, brilliant green lactose bile broth 2%, EC broth and tryptone broth were

the media used. The incubation temperature for Step I and II was 37° C whereas for Step III it was $44.5 \pm 0.5^{\circ}$ C (Harrigan and McCance, 1976a).

Total Enterobacteriaceae Count was determined by employing VRBG Agar (Violet red bile glucose agar) using the pour plate method. Colonies that produced acid from glucose were counted as members of *Enterobacteriaceae*. Isolates which were Gram negative rods, oxidase test negative and H&L glucose fermentative were confirmed as members of *Enterobacteriaceae* (Bergey's Manual of Systematic Bacteriology Vol 1, 1986b).

From the positive MPN tubes, *E.coli* was purified by streaking on Levine eosin methylene blue agar (Difco, Becton Dickinson, USA) and confirmed using microscopy and biochemical tests. Isolates which were Gram –ve rods, oxidase –ve, catalase +ve, indole +ve, methyl red +ve, acetoin –ve, citrate –ve, H&L glucose fermentative with gas, gas from lactose at 44.5°C, ONPG +ve, utilised maltose, mannitol, sorbitol, trehalose and could not utilise adonitol and raffinose were

confirmed as typical *E.coli* (Bergey's Manual of Systematic Bacteriology Vol 1, 1986c)

Colonies from sea water agar APC plates were purified and identified as yeast based on their appearance in Gram's staining (blue to blue-black coloured yeast forms with budding and pseudo mycelium formation).

Coliphages were analyzed by single agar layer method (APHA, 1998), using *E.coli* (NCIM 2089) as host strain and nutrient agar medium (Rao & Surendran, 2001). Briefly, 1ml of host *E.coli* culture (24 h in nutrient broth), 5ml of water or 5ml of homogenized fish and 8ml of molten nutrient agar were mixed thoroughly and poured into petridishes and examined for the presence of plaques after 4-6 h.

Results and Discussion

Deep sea generally has none of the bacteria associated with terrestrial origin whereas those caught inshores may be heavily contaminated. Coliform bacteria especially *E.coli* indicates faecal pollution in water and fish. However, almost all samples of deep sea fish (one sample of *Priacanthus*

Table 1. Aerobic Plate Count and Faecal Indicators in Deep Sea Fish procured from Fish Landing Centres

Samples	Aerobic Plate Count	Faecal	E.coli	Coliphages	
(Deep Sea Fish Species)	(cfu/g)	Coliforms (MPN/g)	(MPN/g)	(pfu/g)	
Priacanthus hamrur	7.7 × 10 ⁵	0.7	0.7	NT*	
Priacanthus hamrur	6.7×10^{5}	140+	110	NT*	
Heterocarpus woodmasoni	1.3×10^6	110	110	<i>7</i> 5	
Heterocarpus sp.	3.5×10^6	140+	140+	20	
Heterocarpus sp.	6.0×10^6	140+	140+	4	
Solenocera crassicornis	8.1×10^{5}	45	45	80	
Panulirus sewelli	4.2×10^6	140+	140+	240	
Panulirus polyphagus	4.3×10^7	140+	140+	14	
Loligo duvaucelli	3.7×10^4	140+	45	4	
Crassostrea sp.	1.1×10^8	140+	140+	6	

^{*} NT - Not Tested

Table 2. Aerobic Plate Count and Faecal Indicators in Deep Sea Water and Littoral Sea Water of South East Arabian Sea

Samples	Location Lat. – Long.	Water Depth (m)	Aerobic Plate Count (cfu/ml)	Total Coliforms (MPN/100ml)	Faecal Coliforms (MPN/100ml)	E.coli (MPN/100ml)	Coliphages (pfu/100ml)
DSW 1*	12°30′N 74°11′E	227	8 :	0	0	0	0
DSW 2	12°40′N 74°19′E	284	13	4	4	0	0
DSW 3	8°40′N 75°38′E	318	4	0	0	0	0
DSW 4	9º08′N 75º150E	324	4	3	0	0	0
DSW 1 א	9°22′N 75°47′E	295	1.6×10^3	0	0 .	0	0
DSW2	8°40'N 75°38'E	318	3×10^{5}	0	0	0	0
DSW ₂₀₀ 3	9°08′N 75°50′E	324	4×10^2	0	0	0	0
LSW11	8°52′N 76°18′E	51	2.9×10^4	250	250	45	30
LSW 2	8°39'N 76°20'E	70	2.3×10^4	0	0	0	0

[•] DSW - surface level deep sea water

hamrur, two samples of Heterocarpus sp., one sample each of Heterocarpus woodmasoni, Solenocera crassicornis, Panulirus sewelli, Panulirus polyphagus, Loligo duvaucelli and Crassostrea sp.) procured from fish landing centers at Cochin had very high levels of faecal coliforms, E.coli and coliphages (Table 1). Out of all the landing centre samples tested, only one sample of Priacanthus hamrur (0.7MPN/g) had acceptable levels of E.coli. The present study is undertaken to know the levels of faecal coliforms and E.coli in deep sea fish at the time of harvest and in deep sea waters.

Aerobic Plate Count values were very low in DSW (4 - 13cfu/ml) than in samples collected from 200m below the surface (4 x 10^2 to 3 x 10^5 cfu/ml) [Table 2]. This difference in abundance can be attributed to the concentration of easily assimilable organic matter. The raining down of organic matter, in the form of detritus/dead plankton from the euphotic zone, might have resulted in this high variability in counts. Higher counts of bacteria were reported at the 300m horizon followed by 100m, 25m and the 0m level (Labedeva et al., 1963). Chandrika (1996) reported 108cfu/ml in

Table 3. Aerobic Plate Count and Faecal Indicators in Deep Sea Fish, immediately after harvest

Fish Species	Aerobic Plate Count	Total Coliforms	Faecal	E.coli	Coliphages (pfu/g)	
	(cfu/g)	(MPN/g)	Coliforms (MPN/g)	(MPN/g)		
Psenopsis cynea	2.1×10^{2}	0.3	0.3	0.3	0	
Chlorophthalmus agasizzi	1.4×10^4	0	0	0	0	
Priacanthus hamrur	3.7×10^6	0.9	0	0	0	
Trichurus lepturus	2.5×10^6	0	0	0	0	
Neopinnula orientalis	1.4×10^{3}	0.9	0	0	0	
Plesionika ensis	5×10^4	0	0	0	0	
Heterocarpus woodmasoni	6×10^4	1.5	0.7	0.7	0	
Heterocarpus gibbosus	4×10^{5}	1.5	0.3	0.7	0	
Panulirus sewelli	2.1×10^{5}	, 0	0	0	0	
Range	2.1×10^2 to 3.7×10^6	0 - 1.5	0 - 0.7	0 - 0.7	0	

N DSW - deep sea water collected from a depth of 200m ↑ LSW - surface level littoral sea water

surface and 50m deep waters around Lakshadweep islands but Karthiayani & Iyer (1975) obtained high aerobic plate counts in bottom mud (2.7 x 10⁴ cfu/g) and lowest counts at surface waters (0-90/ml). In LSW samples total bacteria ranged between 2.3 x 10⁴ and 2.9 x 10⁴ cfu/ml (Table 2). Demersal deep sea fish at the time of harvest had APC values ranging between 2.1 x 10² and 3.7 x 10⁶ cfu/g (Table 3). Bacterial load of ocean fresh prawn and fish was reported to be in the range of 10³ to 10⁵ cfu/g (Karthiayani & Iyer, 1975).

E.coli could not be detected in DSW as well as in DSW₂₀₀ samples. However, two of the DSW samples had total coliform levels of 3/100ml and 4/100ml, of which only one sample had faecal coliforms (4/100ml). None of the DSW₂₀₀ samples were positive either for total coliforms or faecal coliforms (Table 2). Five out of nine deep sea fish samples had total coliform levels ranging between 0.3MPN/g and 1.5MPN/g (Table 3). Three samples viz., Psenopsis cynea (0.3/g), Heterocarpus woodmasoni (0.7MPN/g) and Hetrocarpus gibbosus (0.3MPN/g) were positive for faecal Coliforms. E.coli was detected in Psenopsis cynea (0.3/g) and H.gibbosus E.coli, the most commonly used (0.7/g). indicator of faecal pollution, was detected in

two deep sea fish but was absent in deep sea surface waters and 200m deep waters. Till now E.coli was not reported from deep sea fish at the time of harvest. Although E.coli is regarded as unique to the gastrointestinal tract of warm blooded animals (APHA, 1995), studies showed that in natural waters certain cold blooded animals viz., fresh water turtles (Mitchell & McAvoy, 1990) and diamond back estuarine terrapins (Harwood et al., 1999), harbour E.coli as part of commensal flora. The question then was, whether these isolates of E.coli were truly marine. The ability of the isolated E.coli strains to survive and grow rapidly at 0% salt concentration suggests that they might have been of terrestrial origin. E.coli strains isolated from marine environment were found to be indistinguishable from terrestrial forms. Coliforms and E.coli were found to be 100 to 1000 times more abundant in sediment samples than in surface samples and were detected upto 11 km for sediment samples and for sea water upto 5 km from the coastline (Yde et al., 1980).

It can be said that *E.coli* was not present in marine environment either in deep sea fish or deep sea water and if at all present it might have been due to some human intervention. Deep sea fish did not harbour

Table 4. Qualitative distribution of microorganisms in sea water and fish

Littoral sea water (surface)		Deep Sea Water (Surface)		Deep Sea Water (at 200m)		Deep Sea Fish	
Micrococcus	16%	Pseudomonas	7%	Pseudomonas	27%	Vibrio	16%
Pseudomonas	13%	Vibrio	7 %	Arthrobacter	24%	Pseudomonas	9%
Filamentous bacteria	13%	Arthrobacter	7%	Filamentous Bacteria	17%	Filamentous Bacteria	6%
Enterobacteriaceae	10%	Filamentous Bacteria	5%	Acinetobacter	2%	Arthrobacter	2%
Arthrobacter	10%	Enterobacteriaceae	2%	Kurthia	2%	Acinetobacter	1%
Acinetobacter	6%	Photobacterium	2%	Unidentified	2%	Corynebacterium	1%
		Micrococcus	2%			Kurthia	1%
		Kurthia	2%				
		Corynebacterium	%				
Yeast	16%					Yeast	17%
No Growth	16%	No Growth	59%	No Growth	24%	No Growth	44%
Total Isolates	31	Total Isolates	41	Total Isolates	41	Total Isolates	109

E.coli at the time of harvest and wherever present they were within the admissible limits. The high levels of E.coli encountered in the landing center samples might have been due to inadequate hygiene and sanitary practices. It is also possible that improper storage of fish might have helped the E.coli present in small numbers at the time of harvest, to multiply and made the fish unacceptable.

Total Enterobacteriaceae count is used as food safety indicator (Forsythe, 2000). Total Enterobacteriaceae were detected in DSW, DSW₂₀₀, and deep sea fish samples. Fish samples had relatively higher counts of total Enterobacteriaceae. However, on subsequent confirmatory tests it was found that majority were non-members of Enterobacteriaceae. Most of the colonies were either yeasts or filamentous bacteria. Only few were true members of Enetobacteriaceae belonging to the genera Escherichia and Enterobacter. Previous studies did not encounter Enterobacteriaceae in surface and 50m deep waters of Arabian Sea (Chandrika, 1996).

The group wise distribution of microorganisms in deep sea fish and deep sea water samples is shown in Figure 1. The isolates were grouped as Gram -ve, Gram +ve, Yeast and No Growth based on their Gram's staining reaction, morphology and ability to grow on subsequent propagation. DSW had almost equal proportions of Gram -ve (22%) and Gram +ve (20%) bacteria whereas DSW₂₀ had high percentage of Gram +ve (46%) than Gram -ve bacteria (29%). In deep sea fish Gram -ve (26%) were almost double that of Gram +ve (14%) bacteria. 59% of DSW, 44% of deep sea fish and 24% of DSW₂₀₀ colonies from APC plates failed to grow on subsequent culture. Although the fact that, many marine bacteria do not undergo cell division in or on routinely employed bacteriological media (viable but non culturable state) is well known (Roszak and Colwell, 1987) but their ability to grow on initial isolation and failure to grow on subsequent culturing was seldom known. The generic distribution of bacteria in the commensal flora of deep sea fish and water was carried out and summarized in

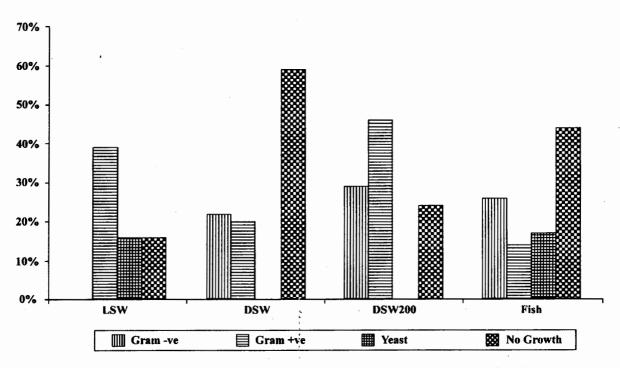


Fig. 1. Occurrence of Different Microbial Groups in Deep Sea Water and Fish

Table 4. Pseudomonas predominated in DSW₂₀₀ (27%) and DSW (7%). In deep sea fish, Vibrio (16%) was preponderant followed by Pseudomonas (9%). The dominance of Pseudomonas was expected as they were nutritionally non-exacting group, which utilize a wide spectrum of substrates. Upto the present, valuable data have accrued from numerous studies showed that the majority of forms cultivated from marine sources were Gram -ve asporogenous rods belonging to the Vibrio and Pseudomonas groups (Liston & Colwell, 1963; Skerman, 1963; Ohwada et al., 1980; Chandrika, 1996). Other Gram -ve bacteria isolated belonged to Acinetobacter and Enterobacteriaceae. DSW₂₀₀ had significant proportions of Arthrobacter (24%) and filamentous bacteria (17%). The Arthrobacter isolates were all orange pigmented while the filamentous forms were highly coiled. Arthrobacter were found in soils where humus was the major ingredient (Schlegel, 1993). Kurthia, Corynebacterium and Micrococcus were the other Gram +ve bacteria observed. Previously, Aeromonas was reported to be the dominant genus in the surface waters of wedge bank region (Shankar, 1990).

Yeasts were noticed only in deep sea fish (17%) and LSW (16%). They could not be detected in DSW and DSW₂₀₀ samples. Yeast populations were reported to be most dense in the inshore waters and decrease progressively with distance from the shore. Yeast were also detected in the gut microflora of deep sea benthic microfauna (Ohwada *et al.*, 1980).

Littoral seawater had relatively higher Gram +ve (39%) than Gram -ve (29%) bacteria. The predominant Gram +ve bacterial genus was *Micrococcus* (16%) whereas *Pseudomonas* (13%) and *Enterobacteriaceae* (10%) were the prominent Gram -ve groups. Littoral sea water collected from a location

(8°52'99"N latitude, 76°18'273"E longitude, 51.2m deep water) which was 15 nautical miles off Quilon (Kerala Coast), a relatively bigger coastal town, had high levels of total coliforms (250/100ml), faecal coliforms (250/ E.coli (45/100ml) and coliphages (30pfu/100ml) [Table 2]. The absence of all these indicators of faecal pollution in the littoral sea water collected from a location (8°36'340N, 76°23'408", 70m deep waters) 16 nautical miles off Neendakara (near Quilon), a small coastal town, suggests that littoral waters off densely populated coastal towns can pollute upto larger distances from the shore. Although our data was limited to arrive at a confirmed conclusion, it was in accordance with other studies which showed high E.coli levels in sea water samples from area with hinterlands of human populations and very low levels of E.coli in samples from areas with a hinterland of natural forest or very few dwellings (Owens, 1978). This assumes significance as the microbial populations in water can influence the microflora of fishes (Colwell & Liston, 1960). High total bacterial counts and *E.coli* counts were reported for different coastal waters (Owens, 1978; Yde et al., 1980; Choi & Kim, 1988; Shin & Jung, 1996; Sunarya et al., 1997; Vaidya et al., 2001).

Coliphages were proposed as indicators of faecal pollution in marine waters (Borrego et al., 1983; Legnani et al., 1998). Coliphages were not detected in any deep sea water and deep sea fish samples. Only one littoral water sample yielded coliphages (30pfu/100ml). This sample had high levels of total coliforms, faecal coliforms and *E.coli* counts (Table 2).

E.coli and coliphages could not be detected in deep sea waters and most of the deep sea fish at the time of harvest or hauling. Few fish showed faecal pollution, although at very low levels and were within

the stipulated limits. The study showed that high count of *E.coli* and coliphages in landing centre samples is not due to the deep sea fish or sea water but could be only from terrestrial sources.

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