II. Review of Literature
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2.1. Impact of dam on aquatic environment

Dams have been constructed for various purposes such as hydroelectricity, irrigation, flood control, drinking water supply, transportation, navigation and recreations. Dams and reservoirs contribute greatly to human prosperity and well-being but they may have effects which are deleterious to the environment and to human welfare. The changes in hydrodynamic characteristics above and below the dam bring about physical and chemical changes, which influence the aquatic biota in various ways. Such effects are more pronounced below a dam, sometimes for hundreds of kilometers. These are mainly due to the action of the reservoir as a source or sink for heat, sediments and solutes, and to changes in the diurnal or annual flooding pattern. In addition to bringing about physical, chemical and biological changes, the dams are also known to induce seismic activity under certain geophysical conditions. Dams have also been criticized for their negative environmental and social impacts and association with spread of communicable diseases due to decrease in the water quality. Schistosomiasis-vector borne diseases have been reported with reservoirs and irrigation projects (Baxter, 1985, Lerer and Scudder, 1999, Soderbaum, 2002). Dam construction leads to inundation of agricultural and forest land thereby causing unemployment problem among farmers (Thomas and Adams, 1996). The ecological problems associated with the action of hydrotechnical structures on the environment are usually considered from the standpoint of hydrological, climatic, and landscape changes in the zone of the hydro development’s influence (Durcheva and Rozhanskaya, 1995). Drinkwater (1988) reviewed the ecological effects of man-made changes in freshwater discharge on the marine environment. The review reports that dam construction result in several ecological impairments like alteration in seasonal pattern of river run-off which disrupts the organisms that have
adopted over a longer period of time. Reduction in total annual freshwater discharge due to evaporation loss and salinity increase has been observed. A well-documented example is that of the Dniester and Dnieper rivers discharging into the Black sea (Tolmazin, 1985).

Major hydroelectric projects in Dniester and Dnieper rivers were begun in the 1950’s and more or less completed by early 1970’s. There was significant loss of water quality, since much of the water from the reservoirs was used in agriculture, industry and by municipalities, returning to the system loaded with various contaminants (Mann and Lazier, 1996). Accumulation of high load of organic waste will affect the process of self-purification. Oxygen concentrations in the lower layers were reduced to zero resulting in mass mortality of inhabitants. The average salinity in the Dnieper estuary increased, with an upstream extension of the near bottom high salinity layer. These environmental disruptions led to the disappearance of many species of zooplankton and fish from the estuary. Nutrients from agricultural run-off and sewage sources accumulated both in the estuary and their plumes. Oxygen concentrations in the lower layers were reduced to zero due to increased stratification caused by increased summer freshwater discharge that resulted in mass mortalities of invertebrates and fish (Mann and Lazier, 1996). The total primary productivity in the estuaries increased, but the changed distribution of salinity and oxygen killed the invertebrates and fish adapted over longer periods to the more natural conditions. The primary production was consumed mainly by bacteria and the commercial fish landings were severely reduced (Mann and Lazier, 1996).

The construction of a dam disturbs the continuity in the river system and the discontinuity in downstream results in changes of physical and biological aspects in regulated streams. “The serial discontinuity concept” was formed based on this fact (Ward and Stanford, 1983). Dams and other
river valley projects interfere with the riverine environment thereby affecting the fisheries resources. These effects may be harmful, beneficial or indifferent, depending on the situation and the fish fauna inhabiting in the river. The obstructional and ecological changes brought about by the dams also adversely affect both migratory and non-migratory species. Fluctuation of water level results in inundation and alteration in the physical and chemical conditions of spawning grounds (Jhingran, 2001). Mastrorillo and Dauba (1999) studied the short-term impact of reservoir cleaning on the microhabitat use of three non-salmonid fishes in a Piedmont river in southwest France. Changes in relative abundance, habitat availability and habitat use of three species of small fishes namely, minnow (Phoxinus phoxinus), gudgeon (Gobio gobio), and stone loach (Barbatula barbatula) was examined at three sites downstream of the dam. After the reservoir cleaning, areas covered by gravel, sand and mud increased significantly as the result of the sediment release. The three species did not react in the same manner to these environmental changes. There was decrease in relative abundance of most sensitive species, stone loach at all sites whereas number of gudgeon species decreased at the most downstream site where large deposits of mud were recorded. The fish species minnow was found to be most resistant.

Effects of damming on river biota include decimation of migratory fauna (e.g., diadromous and potamodromous fishes and crustaceans), lost fisheries, and imperilment of obligate riverine taxa. Dam construction results in alteration of distributions and abundances of migratory fauna, which often provide trophic subsidies and may strongly influence the structure of local habitats and communities in river ecosystems. It is well documented that anadromous fishes can provide a major input of nutrients and energy to freshwater systems when spawning adults return from the sea. Other less-studied taxa that migrate between distinct portions of
riverine systems (e.g., acipencerids, catostomids, prochilodontids) may similarly provide trophic transfers within undammed river systems, in addition to modifying local communities and habitats through feeding and spawning activities. Experimental faunal exclusions have demonstrated strong potential effects of some amphidromous shrimps and potamodromous fishes on benthic organic matter and algal and invertebrate communities. Depletion of these animals above dams is likely to significantly affect ecosystem processes such as primary production and detrital processing. The decline of freshwater mussels isolated by dams from their migratory fish hosts has likely lowered stream productivity, nutrient retention and benthic stability. Greater focus on effects of dams on ecosystem processes, as mediated by faunal change, would improve our ability to assess the costs and benefits of future river management strategies (Freeman et al., 2004).

Several changes were observed regarding physico-chemical characteristics of water in upstream as well as down stream of Petit Saut hydroelectric dam on the Sinnamary River during its 18-month filling period (Richard et al., 1997). Dissolved oxygen levels were found to be high during dry season, when sunlight is maximum and photosynthesis was strong. The oxygenated epilimnion in the stratified lake was increased. The hypolimnion was anaerobic and enriched by inflow of reduced compounds due to organic degradation and matter released from the geological substrate. Water quality in the downstream stretch of the river was ensured artificially by forced oxygenation of the water released from the dam (Richard et al., 1997).

Snow et al., (2000) noted that in Kromme estuary, the amount of fresh water released was insufficient to increase the nutrient content of the water to a level that resulted in a significant increase in primary production. Fluctuations in the physico-chemical and biological parameters in the dam’s
run-off leads to changes in the trophic processes, microbial processing, nutrient content and production profile of coastal waters. Barasseau et al., (1998) have analyzed the morphological and sedimentological changes in the Senegal estuary after the construction of Diama dam. Patel and Sinha (1998) have assessed the pollution load in the ponds of Burla area near Hirakud dam of Orissa. Dumestre et al., (1999) studied the bacterial ecology of a hydroelectric reservoir of Petit Saut in French Guina. Microbial and physico-chemical changes were observed during their study. The whole water column of dam has remained anoxic, with high load of reduced elements originating from degradation of the submerged primary forest. These elements deoxygenated the water drained from the dam, as they were biologically and chemically oxidized in the river. Microbial load of drinking water reservoir tributaries during extreme rainfall and run-off was studied by Kisteman et al., (2002). According to their study, most of the bacteriological parameters such as total counts, coliform, fecal streptococci, Clostridium perfringens levels were increased during extreme run-off events, indicating the substantial share of total microbial load in water courses in drinking water reservoirs results from rainfall and extreme run-off events.

Seasonal variations and modes of riverine input of organic pollutants to the coastal zone were observed by Takada et al., (1992). Coastal areas are often contaminated by dissemination of pathogenic bacteria from terrestrial inputs (Baudart et al., 2000). Lipp (2000) has studied the occurrence, distribution and transport of human pathogens in coastal waters of South-west Florida.

In newly constructed retention dam reservoirs, a marked rise in the amount of bacteria could be observed throughout after initial flooding, followed by clear decline in subsequent years. Total bacterial numbers increased, for example, in the krementshug reservoir of the Dnieper
(Ukraine) from 5.4 to 10.4X10^6/ml in the years 1961 to 1964, and by 1978 had fallen to 2.1X10^6/ml (Michajlenko, 1981).

2.1.1. Impact of dam on primary productivity of coastal waters

Constructing a dam across the river influences the primary productivity in coastal waters (Mann and Lazier, 1996). Dam hinders the process of sedimentation in the coastal waters as much of sediment load accumulates within the dam itself. Quantity of freshwater discharge (river runoff) into the coastal waters greatly reduces. Fluctuations in the physico-chemical and biological parameters in the dam’s run-off is known to bring about changes in the cycling of elements, trophic processes, microbial processing, nutrient content and production profile of coastal waters (Snow et al., 2000).

Photo and chemoautotrophic eubacteria participate to a smaller extent in primary production but in some waters where conditions are favorable; they can develop in large numbers and make a substantial contribution to overall productivity. Cyanobacteria are responsible for a considerable part of the total production of the earth’s organic material (Rheinheimer, 1991). Algae and cyanobacteria play a major role in production of organic material in aquatic environment and microscopically small forms of the phytoplankton contribute to a greater proportion. Higher plants are important only in regions along the shores (Rheinheimer, 1991). The heterotrophic microorganisms play an important role in the remineralization of organic matter (Johannes, 1968). Mainly bacteria, fungi, zooplankton, colorless algae, and animals are involved in process of remineralization (Waksman, 1933, Azam et al., 1983).

Biomass, productivity and bacterial activity were studied during 1995 in the Petit-Saut reservoir and downstream, in Sinnamary River (French Guiana) by Dumestre et al., (1997). Biological analyses showed a regular increase in bacterial abundance, particularly below the oxycline, followed
by a stabilizing trend at the end of the year. A similar increase was observed in the river downstream depending on the evacuated flow, or the residence time of suspended organisms.

The release of freshwater from the Mpofu Dam in November 1998 resulted in a short-term (6 days) longitudinal and vertical gradient of both salinity and nitrate in the estuary. There was significant increase in phytoplankton chlorophyll-a observed during the study. Diatoms and flagellates were dominant group among phytoplankton communities. There was no change in subtidal benthic chlorophyll-a biomass but there was increase in intertidal benthic chlorophyll a from 35.6 mg per m$^2$ before the release, to 63.3 mg per m$^2$ by the sixth day. However, it was concluded that the amount of freshwater released was insufficient to increase the nutrient content of the water to a level that resulted in a significant increase in primary productivity. The length of time that the freshwater influence was present also prevented a significant increase in micro algal growth (Snow et al., 2000).

2.2. Factors affecting the growth of bacteria in aquatic environment

A great variety of physical and chemical factors affects the growth of aquatic microorganisms in a multitude of ways and also acts with or against one another. These factors influence bacterial characteristics such as size, composition, morphology and physiology. Factors like temperature, pH and salinity play a major role in controlling the bacterial metabolism, morphology and reproduction. Variations in the level of these factors result in considerable changes in life cycle of bacteria. The degree of salinity determines to a large extent the living communities in waters. The relatively high NaCl concentration of seawater leads to the development of physiologically different freshwater (halophobic) and marine organisms (halophilic). Light is another important ecological factor in water and inhibits most of non-pigmented bacteria. Biologically effective light
intensity is found in 10-100m depth of water depending on the degree of turbidity. The growth and reproduction of microorganisms is affected by the hydrogen ion concentrations (pH) of the medium. Most bacteria can grow only within the range of pH 4-9 and very few at pH 3 or below. The optimum for most aquatic bacteria is between pH 6.5 and 8.5 (Rheinheimer, 1991).

Other than these physical factors, concentration of certain nutrients and active substances limit the life of organisms to a certain extent. Microorganisms in water are also affected by other inorganic, organic and active substances. Inorganic nitrogen and phosphorus compounds are of particular importance in the productive zone of many waters. Organic substances, dissolved or suspended in water, are particularly important as food for heterotrophic microorganisms. The size and composition of the bacterial populations in an aquatic environment depend to a large degree on the concentration and composition of such substances. Organic compounds have however, other important roles as activating and inhibiting factors (Rheinheimer, 1991).

The life processes of all microorganisms are affected by temperature. Growth rate, nutritional requirements and, to a lesser extent, the enzymatic and chemical composition of cells get affected by the limited range of temperatures lying between the extremes of −10 and +90 C (Precht et al., 1973). The effect of hydrostatic pressure on the biological processes of microorganisms determines their proper niche in different regions of sea. It is an important ecological factor, which considerably influence the life of microorganisms. As 90% of the seas of world are deeper than 1000m hence having the hydrostatic pressure of more than 100 atm., (ZoBell, 1946a). The turbidity of the water also affects the life of aquatic microorganisms. According to observations made by Kang and Seki (1983) in a Japanese sewage pond, the proportion of Gram-positive forms (37.6%) of attached
bacteria was distinctly greater than that of the free-living forms (19.8%) in the yearly average. The effect of the turbidity factor is mainly indirectly by way of its influence on nutritional and light conditions.

2.3. Bacterial profile of rivers

The composition of the bacterial flora differs widely in different kind of water and on the supply of nutrients. Factors like salinity; temperature, pH, organic matter and turbidity play a major role in the life process of bacteria. Sources from where organisms enter the water also influence the bacterial profile of a water body. The distribution of microorganisms in a body of water thus always results from the interaction of biotic and abiotic factors and is constantly subjected to changes. The fluvatile nature of rivers results in low productivity and microbial load because of low organic load. The bacteria living in rivers are different from those of other habitats. Majority of aquatic bacteria are heterotrophic and Gram negative. Morphologically most aquatic bacteria correspond to the basic types of terrestrial bacteria. There exists a relationship between the bacteria flora of rivers and that of terrestrial environment. There are relationships between the bacterial flora of inland water and that of the soil as the flowing waters constantly exposed to infection from soil. Thus, it is difficult to separate soil and aquatic bacteria (Pelczar, 2003)

Diversified groups of bacteria are present in the rivers. The important ones are *Vibrios, Spirilla, Thiobacilli, Micrococci, Spirochetes, Cytophagae*, stalked bacteria like *Hyphomicrobium, Caulobacter, Gallionella, Pseudomonas, Flavobacterium, Acinetobacter, Moraxella* and soil bacteria such as *Azotobacter, Nitrosomonas and Nitrobacter*. Presence of Enterobacteriaceae members and other human pathogens in riverine waters is a result of domestic sewage and other waste discharge into these habitats (Rheinheimer, 1991).
The hydrography of rivers varies considerably hence determination of total bacterial count would not give a comprehensive picture. However, it was estimated to be $3.5 \times 10^6$ to $9.8 \times 10^8$ of bacteria per ml of water in Fulda river (Germany) (Jannasch, 1955) but Schmidt (1970) obtained nearly constant values of between $2.0 \times 10^6$ and $3.0 \times 10^6$ per ml., on repeated investigations in the Rio Negro waters (Brazil). In a small north Swedish river and various north German rivers, the yearly course of total bacterial numbers and bacterial biomass has been established by employing fluorescence microscopic methods (Muller-Haeckel & Rheinheimer, 1983). The load of bacterial biomass of the river Elbe estimated to be 11000 tonnes in the year 1975 at Lauenburg. This corresponds to about 1100 tonnes of carbon. The bacterial biomass, therefore, acquires a considerable significance for the biology of rivers (Schulz, 1961).

Rakesh et al., (1996) monitored the water quality of river Ramganga at Bareilly. Physico-chemical characteristics of the waters were studied during “Gangasnan” (mass bathing) period. Higher values of E.coli count, alkalinity hardness, calcium, magnesium, BOD obtained during Gangasnan and post Gangasnan indicated that the water is highly polluted. Seasonal variations in the physicochemical and bacteriological properties of Ganga river water at Narora and Kachla (UP) were studied. The remarkably high level of coliforms, fecal coliforms and fecal streptococci reflects the poor bacteriological quality of water. Some of the E. coli isolated from the test stretch also exhibited multiple drug resistance which makes the water unfit for drinking and bathing and may pose serious problems related to public health (Qadri et al., 1993). Srivastava et al., (1996) examined the water quality of the river Ganga at Phaphamau (Allahabad) during “Mahakumbh” festival. These studies indicate significant changes in the bacteriological quality of river water due to mass bathing making the river water at Phaphamau not fit for drinking or bathing purposes. The presence of fecal
coli forms in the water also indicated the potential presence of pathogenic microorganisms, which might cause waterborne diseases.

The study made by Chopra and Nirmal (2000) showed that the effluent of domestic sewage coming from Rishikesh town led to a considerable change in microbiological characteristics of Ganga river water at its confluence point near Triveni ghat, Rishikesh. The recovery had started in the river due to its self-purification nature. Though algal pollution index reported upto 1 km downstream from the confluence point, bacterial counts could not be stored. A bacteriological study of river Varuna at Varanasi was conducted by Singh and Singh (1994). The concentration of fecal coliform bacteria is used as an index of fecal pollution, which varies with the season, water current, depth, and physicochemical characteristics of water. Fecal coliform bacteria reach the terrestrial and aquatic ecosystems via alimentary canal of herbivorous animals.

Chinmoy and Raziuddin, (2001) analyzed the bacteriological quality of river water in Asansol town in West Bengal. Studies were conducted with an objective of assessing the bacterial density in water of the river Nunia, polluted with industrial and domestic wastes of Asansol coal and industrial belt. All the samples contained total coliform and fecal coliform bacteria above the safe limits for drinking water standards. Seasonal variations in bacterial density were recorded with maximum density in summer and monsoon seasons and minimum density in winter season. It was inferred that contaminated water of this river is not suitable for human use.

High incidence of plasmid borne enterotoxin producing Escherichia coli (65%) was reported in water and sediment samples of River Bhavani, Tamil Nadu. Most of enterotoxin producer were found to be highly resistant and showed resistance to more than two tested antibiotics. This
higher percentage of multiple antibiotic resistant, enterotoxin producers in river is a high risk source of contamination. They were having high potential to cause public health problem. Therefore, necessary precautionary measures should be taken before using this source for drinking purpose (Gomathinayagam et al., 2001).

2.4. Bacterial profile of estuaries

An Estuary is a semi-enclosed coastal body of water, which has a free connection with the open sea. Estuaries are complex ecosystems, which receive inputs from a variety of sources and are characterized by intensive exchanges of water, energy and materials across the margin between marine and freshwater environments. The estuarine microflora comprising of freshwater, brackish and marine types process the nutrient load discharged from rivers. The processed nutrient load concentrated in this region is finally transported to coastal areas. Thus estuary is the region of higher levels of primary and secondary productions (Pelczar, 2003).

The estuarine bacteria comprise of both heterotrophs and photoautotrophs. Some purple sulphur bacteria (Chromatiaceae) preferentially grow in brackish water, inland and seacoast. A group of brackish-water organisms (Agrobacterium) forming characteristic star-shaped cell aggregates played an important role in the western Baltic (Ahrens, 1968). They were found to be numerous particularly in Bay of Kiel and the adjoining sea areas of salinity 1 to 2.5%. But in places like eastern Baltic (low salinity) and kattegat (high salinity), these bacterial numbers diminished remarkably. Adaptation experiments showed that a least number of bacteria of brackish water have stable salt optima of between 0.5 and 2.0%. (Ahrens, 1969). Rheinhiemer (1970a) reported halophilic bacterial groups in fringe areas of the seas, which carry brackish water along with genuine marine bacteria and salt-tolerant fresh water bacteria. These organisms from brackish water showed either scanty or no
growth in freshwater media and were often, inhibited by salt concentrations above 3%. By contrast, many genuine marine bacteria were markedly inhibited at salt concentrations of 1.5% or below (Larsen, 1962).

The mixing processes occurring in the tidal areas of river estuaries on the east coast of North America in warmer seasons increased the concentration of nutrients resulting in rise in total bacterial numbers (Wright and Coffin, 1983). Ferguson et al., (1996) studied the relationships between indicators, pathogens and water quality in an estuarine system. Water and sediment samples collected from six sites in an urban estuary, Sydney, were examined for the presence of indicator and pathogenic microorganisms. It was found that water quality was affected by rainfall and sewage overflows which were associated with significant increases in the concentration of fecal coliforms, fecal streptococci, *Clostridium perfringens* spores, F-RNA bacteriophage, *Aeromonas* spp., *Giardia* and *Cryptosporidium* spp. However, in sediments, only fecal coliform concentrations were significantly increased by rainfall, although sewage overflow again resulted in increased concentrations of fecal coliforms, fecal streptococci, *C. perfringens* spores and *Aeromonas*. Isolation of *Salmonella* appeared to coincide with wet weather events and occasionally identical serotypes were detected in sediments at several locations within the estuary. *C. perfringens* was identified as the most useful indicator of fecal pollution and was the only indicator significantly correlated to the presence of pathogenic *Giardia* (*r = 0.41, p < 0.05*) and the opportunistic bacterial genus *Aeromonas* (*r = 0.39, p < 0.05*).

Churchland et al., (1982) found variations in the fecal pollution indicators through tidal cycles in the Fraser River estuary. Fecal coliforms were measured on shipboard using the membrane filter technique, and coprostanol and cholesterol were extracted using hexane and analyzed by gas chromatography. Maximum concentrations of fecal sterols and
coli forms occurred after high tide at the station upstream of major sewage outfalls and on the ebb or at low tide at the stations downstream of major sewage outfalls. Fecal coliform counts were highly correlated with coprostanol and cholesterol levels at sites near sewage treatment plants. It was concluded that samples should be collected either randomly in time so that the seasonal or annual mean includes tidal variability or systematically during the ebb tide in order to assess contributions to bathing beaches and shellfish harvesting areas. Fecal sterols deserve consideration as potential indicators of fecal contamination from chlorinated sewage effluents.

Tidally induced changes in bacterial growth and viability in the Macrotidal Han River Estuary, Yellow sea were observed by Hyun et al., (1999). The Han River estuary is a macrotidal (tidal range of 3.5m at neap tide and 8.0 m at spring tide) eutrophic environment. Changes in bacterial growth and viability at different salt concentrations as well as other physico-chemical environmental parameters were investigated at different tidal levels in order to elucidate the major environmental factors controlling the bacterial community. Bacterial growth rate found to be maximum at high tide and minimum at low tide. Bacterial growth was not controlled by the fluctuations of nutrient concentrations in the high nutrient estuary, but the low viable cell number recorded with the increased NaCl concentration indicated that the salinity changes with tidal state was a major environmental factor controlling the viability of the freshwater bacterial populations. Based on the results, the microbial communities in the macrotidal Han River estuary was divided into two distinct groups namely, autochthonous halotolerant estuarine groups and allochthonous halophobic freshwater populations.

2.5. Bacterial profile of coastal waters

The coastal water represents a variety of habitats due to their geographical and climatic peculiarities and salinity variations from 0.1% to
4.4% under the influence of low and high tide. Coastal water being richer in nutrients than the open sea, they are much more colonized by plants and animals. They serve as spawning grounds for fish and also support a rich microflora. Microorganisms are found at all depths and at all latitudes in seawater. They occur in plankton and in the sediment of the ocean floor. The greater volume (70.8% of the surface of the earth) of the open sea provides an environment with less variation in conditions than the other aquatic habitats. In large parts of the open sea, very small forms often dominate the bacterial flora due to lack of nutrients. The highest total bacterial numbers are found in surface regions and numbers decline more or less markedly with increasing depth of water (Rheinheimer, 1991).

The enrichment of coastal waters from different sources such as domestic, agricultural, industrial, atmospheric and terrestrial discharges supports diversified microflora and microfauna. The important members of microflora of coastal waters are *Vibrios, Bacillus, Proteus, Clostridium, Beggiatoa, Thiothrix, Thiobacillus, Caulobacter, Gallionella, Azatobacter and Nitrosomonas* (Pelczar, 2003). Disposal of sewage, which is characteristically having high organic load, creates anaerobic condition in the waters resulting in the growth of anaerobe and facultatively anaerobes such as *E.coli, Salmonella, Streptococcus* and *Clostridium* (Baudart et al., 2000 and Lipp, 2000).

Usually autochthonous marine flora develops in the open sea and most marine bacteria are halophilic. Their optimum salt concentration ranges from 2.5 to 4.0% (ZoBell and Upham, 1944). Larsen (1962) classifies marine bacteria as weakly (salt optima of 2-5%), moderately (5-20%) and extremely halophilic organisms (20-30%) in addition to this there are halotolerant organisms, which are able to grow in freshwater media. These are found mainly near the coasts, particularly in creeks and estuaries (Rheinheimer, 1968a). The majority of marine bacteria are Gram negative.
and halophilic, which thrive optimally at salt concentrations of between 2 and 4% (Oliver et al., 1986) (ZoBell and Upham, 1944). According to Starr et al., (1981), members of the genera Pseudomonas, Beneckea, Vibrio, Spirillum, Alcaligenes, Flavobacterium (in sediments, Bacillus also) and symbiotic luminous bacteria are widely distributed in marine regions. According to ZoBell (1946a) more than half of all viable bacteria living in seawater are pigmented. Photoautotrophic organisms occur wherever there is hydrogen sulphide and sufficient light. Chemoautotrophic bacteria are found in coastal waters as well as in the open sea. Nitrifying bacteria have been demonstrated in the North Sea (Rheinheimer, 1967) and in the Atlantic (Watson, 1963).

Total bacterial numbers in coastal waters of the North Sea and Baltic Sea varies from some hundred thousands to several millions. The bacterial numbers determined by Zimmermann (1977) in water samples sampled monthly from Kiel Bay in 1974 ranged from 4.5X10^5 to 5.67X10^6 per ml. Gast and Gocke, (1988) compared the bacterial populations in aerated and anoxic bodies of water in the middle Baltic Sea and found that the proportion of large cells in the H_2S-containing deep water was particularly high and it had a corresponding effect on the bacterial biomass. But in the deep sea, the concentration of bacteria was generally low with total bacterial numbers less than 1.0 x 10^6 per ml. However, in the region of thermal vents near the Galapagos Islands in the Pacific, high bacterial numbers from 0.5 to 1000 million per ml of water were reported at a depth of about 2500m (Ruby et al., 1981). The highest bacterial numbers were always found in the productive euphotic zone at a depth of 10-50m with regard to vertical distribution. ZoBell (1946a) states that it is often a little below that of the phytoplankton. In the investigations of vertical profile, differing bacterial levels can be encountered in different bodies of water (Rheinheimer and Schmalijohann, 1983).
2.6. Human pathogenic bacteria in aquatic environment

Human pathogenic bacteria get entry into the aquatic system mainly through domestic sewage, and eventually die off. Type of water and prevailing conditions determines the survival rate of pathogen in water. Hence water polluted with sewage become sources of infection. Most frequently isolated pathogenic intestinal organisms in polluted waters are *Salmonella typhi* and *S. paratyphi*, which cause enteric fever and less frequent are *shigellae* (cause of dysentery). Members of genus *Campylobacter* enter waters through excrement of water birds. The spores of pathogenic clostridia such as *Clostridium perfringens*, *C. novyi* and *C. septicum* are always encountered in sewage-loaded waters. These get enriched and remain alive in the sediments for a relatively long time (Bonde, 1967). Haagsma (1991) studied the distribution of pathogenic anaerobes in the environment and the relationship with diseases in animals. The main habitat of clostridia (Gram-positive spore bearing anaerobe) is the soil but they are also found in dust, sewage, rivers, lakes, seawater, milk, vegetables, fresh meat, fish, insects and the intestinal tract. The Gram-negative non-spore-forming anaerobic bacteria are also widely distributed among animals, principally on mucous membranes of the alimentary tract.

Occasionally, infections due to halophilic vibrios from seawater have been reported. Various marine strains of *Vibrio parahaemolyticus* cause intestinal disorders (enteritis) in humans (von Graevenitz and Carrington, 1973). *V. cholerae* in contaminated tropical waters is the causative agent of cholera which occurs epidemically and spread by water contamination. Colwell (1979) reported the incidence of *V. cholerae* in coastal waters where there was no fecal contamination. It shows that *V. cholerae* is a natural inhabitant of brackish water areas. The ecology and microbiology of human pathogenic vibrios have been reviewed by many workers (West, 1989, Chakraborty *et al.*, 1997 and Cottingham *et al.*, 2003). Pathogenic
*Vibrio* species are naturally occurring bacteria in freshwater and saline aquatic environments. Counts of free-living bacteria in water are generally less than required to induce disease. Increase in number of organisms towards an infective dose can occur as water temperatures rise seasonally. *V. cholerae* acts as a typical heterotrophic bacterium in aquatic environments by mineralizing organic matter for reuse within the food web. Several factors link *V. cholerae* in its human and aquatic habitats, especially human activities that influence its growth conditions outside the body. These activities create feedbacks between humans and the environment that are at present not well understood, but which are likely to alter the persistence and spread of the resulting disease.

Ortiz-Roque and Hazen (1987) studied the abundance and distribution of *Legionellae* in Puerto Rican waters. Several species, including *L. bozemanii, L. dumoffii, L. gormanii, L. longbeachae, L. micdadei* and *L. pneumophila*, were widely distributed among all sites along marine and freshwater areas of Puerto Rico. *L. pneumophila* was the most abundant species at all sites, with average densities of $10^4$ cells /ml, very close to the range which is potentially pathogenic for humans. Densities of *L. pneumophila* were highest in sewage contaminated costal waters. The study shows that *L. pneumophila* was a relatively common cause of atypical pneumonia in Puerto Rico and suggests natural aquatic habitats as possible sources or reservoirs of pathogenic *Legionella* spp in the tropics. Quaglio *et al.*, (1989) studied the occurrence of bacteria belonging to the genus *Yersinia* in surface and ground water. *Yersinia* strains were isolated from 37% of the water samples (out of 89 water samples, 55 samples collected from rivers and streams and 34 from wells) with highest incidence of *Y. enterocolitica* (43.8%), followed by *Y. intermedia* (21.9%) and *Y. fredericksenii* (17.1%). However no human pathogenic strain has been
evidenced and all the isolates appeared belonging to environmental biogroups, serogroups and phage-types.

Goyal et al., (1977) studied the occurrence and distribution of bacterial indicators and pathogens in canal communities along the Texas coast. Pollution of canals is potentially hazardous because of their heavy usage for recreational activities. Coliforms, fecal coliforms, and *salmonellae* in the surface water and bottom sediments of 6 selected residential coastal canals were monitored over a period of 17 months. No significant relationship was observed between the organism’s concentrations and physico-chemical parameters. An inverse relationship between the concentration of indicator organism and salinity of water was found. All of the microorganisms studied were found to be present in greater numbers in sediments than in the overlying water. Heavy rainfall resulted in large increases in the number of organisms in both water and sediment samples. These results indicate that bottom sediments in the shallow canal systems can act as reservoirs of enteric bacteria, which may be resuspended in response to various environmental factors and recreational activities.

The occurrence, distribution and transport of human pathogens in coastal waters of Southwest Florida were studied by Lipp (2000). Oceanic and coastal waters are known to harbor and transport microorganisms that cause disease in humans and other animals. It was found that Estuaries of moderate salinities and relatively warm temperatures harbor naturally occurring *Vibrio* spp, which may cause fatal infections in certain high-risk groups. Additionally, estuaries are prone to anthropogenic pollution from septic systems, wastewater treatment and runoff from urban and agricultural areas. The reliance on water quality indicators rather than direct detection of pathogens has resulted in a poor assessment of coastal water quality. It was
suggested that pathogen specific monitoring is needed to develop appropriate models for occurrence and risk assessment.

A large variety of pathogenic organisms capable of transmission by the faecal-oral route found in wastewaters include *Salmonella, Shigella, Vibrio cholerae, Yersinia and Campylobacter*. These pathogens in domestic waste may not be completely removed by conventional sewage treatment processes, including chlorination. Discharge of sludge and raw wastewaters in coastal waters is, therefore, potentially hazardous to human health (Patti and Pana, 1989).

2.7. Prevalence of fecal coliform bacteria in aquatic environment

The Gram-negative bacilli of the genera *Escherichia, Klebsiella, Enterobacter, Serratia, Citrobacter*, and *Proteus* are members of the normal intestinal flora of humans and animals and may be isolated from a variety of environmental sources. With the exception of *Proteus*, they are sometimes collectively referred to as the coliform bacilli because of shared properties, particularly the ability of most species to ferment the sugar lactose. Distribution of these organisms in the aquatic environment is mainly through dissemination from the human and animal excretion hence, referred as ‘fecal coliform’. Though many of these microorganisms were considered as harmless commensals. Now, they are known to be responsible for major health problems worldwide. Included in this group are *E coli, K pneumoniae, Enterobacter aerogenes, Enterobacter cloacae, S marcescens*, and *P mirabilis* which are responsible for most infections. The increasing incidence of the coliforms, *Proteus*, and other Gram-negative organisms in diseases reflects in part a better understanding of their pathogenic potential but more importantly the changing ecology of bacterial disease (Guentzel, 1996).

The sources, distribution and fate of fecal coliform populations in the North Fork of the New River that flows through the city of Fort Lauderdale,
Florida, USA were investigated in a study made by Scarlatos (2001). The dynamics of this brackish river are driven by weak tides, regulated freshwater discharges, overland runoff, storm water drainage from sewers, and groundwater exchange. Extensive field studies failed to document any alleged source of contamination. In order to facilitate field sampling, and support the data analyses efforts, computer simulations (WASP-Water Quality Analysis Simulation Program and Neural network MATLAB) were applied to assess the likelihood of the various possible pollution trends. The numerical results supported the conclusion that fecal coliform were introduced by the animal populations along the riverbanks and by storm water washout of the adjacent drainage basins and the banks. The problem is exaggerated due to the low flashing capacity of the river. Luksamjarulkul et al., (1994) studied the microbiological quality of drinking water and using water of a Chao Phya River community, Bangkok. The contamination of water with infected fecal material is common in areas with poor standards of hygiene and sanitation. The study attempted to determine the HAV (Hepatitis A Virus) and coliform bacterial contamination in drinking water and using water of a Chao Phya River community. The results revealed that the contamination rate (percentage) of coliforms in drinking water, rainwater and used water was higher than that of percentage of HAV.

George et al., (2004) assessed the fecal contamination of rivers in the Seine watershed through soil leaching. Seventy eight small streams located in rural areas were sampled upstream from any wastewater outfall. Culturable fecal coliforms (FC) and beta-D-glucuronidase activity (specific of Escherichia coli) were measured in the samples. Data showed a significant correlation between both estimates of fecal contamination. Fecal bacteria, significantly contaminated most of the small streams in two different areas of the Seine river watershed. Rainfall increased the
suspended solid content of small streams as well as their fecal contamination, as an important fraction of FC was adsorbed on particles. Calculations showed that, at a large watershed scale, the input of FC in rivers through soil leaching was very low when compared to the input through the discharge of treated domestic wastewater but this could not be true at local scale.

Environmental pollution that renders waters along the coastline and beaches unsatisfactory for use by the general public has become a global health problem. A study was conducted to examine the effects of pollution of beach waters and sediment at seven selected locations receiving land drainage along a 45-km stretch of the east coast near Visakhapatnam, India. The Pollution Index (PI) was determined as the ratio of fecal coliform/fecal streptococci. The results suggested that the beach waters in Visakhapatnam are hygienically poor. A high PI of the water in Lawson's Bay indicated that the water was unsuitable for recreation (boating, etc.) (Clark et al., 2003).

The distribution of resistance to ampicillin, chloramphenicol, sulfonamides, tetracycline, and streptomycin among fecal coliforms in sewage, surface waters, and seawater was investigated. The incidence of resistant strains among isolates varied significantly among the water samples, without obvious connection with the water source or the level of pollution. The average frequency of multiple resistance was not always high in the same samples in which the overall resistance was high. The species composition varied considerably in different water samples. A significant correlation was observed between the relative frequency of Klebsiella species and the incidence of ampicillin resistance in water samples. The importance of species composition of fecal coliforms, affected by their source and by the aquatic environment, on the resistance pattern was noted (Niemi et al., 1983)
2.8. Prevalence of fecal streptococci in aquatic environment

The genus *Streptococcus*, a heterogeneous group of Gram-positive bacteria, has broad significance in medicine and industry. Various streptococci are important ecologically as part of the normal microbial flora of animals and humans. However, some are known to cause diseases that range from subacute to acute or even chronic. The nomenclature for streptococci, especially the nomenclature in medical use, has been based largely on serogroup identification of cell wall components rather than on species names. For several decades, interest has focused on two major species that cause severe infections: *S. pyogenes* (group A streptococci) and *S. pneumoniae* (pneumococci). In 1984, two members were assigned a new genus - the group D enterococcal species (which account for 98% of human enterococcal infections) became *Enterococcus faecalis* (the majority of human clinical isolates) and *E. faecium* (associated with a remarkable capacity for antibiotic resistance) (Patterson, 1996). The normal habitat of fecal streptococci is the gastrointestinal tract of warm-blooded animals. The fecal streptococci have been used with fecal coliform to differentiate human fecal contamination from that of other warm blooded animals. The ratio greater than 4 was considered indicative of human fecal contamination, whereas a ratio of 0.7 was suggestive of contamination by animal source (A.P.H.A, 1998).

Ator and Starzyk (1976) have studied sources of bacteriological contamination of rivers as well as the ecology of faecal group D streptococci in natural and contaminated waters. High concentrations of all division II species (*S. faecioum, S. faecium var. casseliflavus, and S. facecioum var. durans*) were found in the water and sediment samples, with *S. faecium* var durans comprising 50% of the total number of isolates. Low concentrations of division I group D streptococci (*S. faecalis* and varieties) and only one isolation of division III group D streptococci (*S. bovis* and *S.
equines) were encountered. Due to low concentrations of fecal coliforms (FC) and fecal streptococci (FS) in river water samples, the FC/FS ratio was shown to be of little value in determining sources of contamination. High concentrations of FC and FS from sediment samples gave more credible FC/FS ratios.

Presumptive fecal streptococci were isolated from environmental samples namely, domestic wastewater, forest industry wastewater, contaminated surface and seawater, well water, cow dung, bird droppings, and pristine waters. Samples from each environment had a typical composition of streptococcus types. *Enterococcus faecalis* was present, but not as a dominating enterococcal species, in samples in which fecal contamination was probable. The use of fecal streptococci as fecal indicators requires better knowledge of the ecology of these bacteria (Niemi *et al.*, 1993)

Survival of fecal microorganisms in marine and freshwater sediments was studied by Davies *et al.*, (1995). Presence of pathogens of fecal material was reported in the aquatic environment from a number of catchment sources such as sewage outfalls, seepage from septic tanks, and urban and agricultural runoff (Geary and Davies, 2003). Fecal pollution of coastal waters from domestic sewage discharges results in mass development of indicator bacteria. Total coliform, *E.coli* and fecal streptococci in mud and waters at three stations of Dandi seacoast have been examined at bimonthly intervals for two successive years (Mogal and Dube, 1996). On the basis of study of fecal indicator bacteria, FC/FS ratio was derived to determine pollution and waters of two stations were indicative of fecal pollution of human origin (Mogal, 1997). Studies made by Qadri *et al.*, (1993) revealed a significant seasonal variations in physicochemical and bacteriological properties of Ganga river water. The remarkably high level of coliforms, fecal coliforms and fecal streptococci reflected the poor
quality of water and public health. Problem associated with drinking of such water. Bacteriological study of Lake Oswin water by Zmyslowska and Golas (2003) revealed the incidence of total coliform, fecal coliform and fecal streptococci. In 36.5% of the lake water samples, the FC: FS ratio was higher than 4 (range: 0.7 to 4). In 18% of samples, it ranged from 0.043 to 0.7 and in 9% it was lower than 0.043. This indicates the excretal contamination with excrements of human origin.

The study of bacteriological quality of run-off water from pastureland conducted by Doran and Linn (1979) revealed that rainfall run-off from the grazed area contained 5 to 10 times more fecal coliform than run-off from the fenced un-grazed area. There was little difference in total coliform counts between the two areas, but fecal streptococcal counts were higher in run-off from the ungrazed area and reflected the contributions from wild life.
2.9. Prevalence of Salmonella in aquatic environment

*Salmonella*, a name coined by Lignieres in 1900 in honour of D.E. Salmon, an American bacteriologist, is a prominent member of the family Enterobacteriaceae. *Salmonella* species are Gram-negative, flagellated, facultatively anaerobic bacilli characterized by O, H, and Vi antigens. Based on recent molecular studies all *Salmonella* belong to one species and seven subspecies. *Salmonellae* are ubiquitous human and animal pathogens, and cause a disease salmonellosis, which is common throughout the world. Salmonellosis in humans usually takes the form of a self-limiting food poisoning (gastroenteritis), but occasionally manifests as a serious systemic infection (enteric fever), which requires prompt antibiotic treatment (Giannella, 1996).

The primary habitat of *Salmonella* spp is the intestinal tract of animals, birds, reptiles, man and rarely insects (Varnam and Evans, 1991). *Salmonella* are widely distributed in the environment and their dissemination into the natural environment is mainly through human and animal excretions (Le minor, 1981). *Salmonella* is frequently isolated from water sources, which serve as bacterial reservoirs and may aid transmission between hosts. *Salmonella* is constantly released into the environment from infected humans, farm animals, pets, and wildlife. *Salmonella* appears to withstand a wider variety of stresses associated with environmental fluctuations and may persist in water environment for some time. Compared to other bacteria, *Salmonella* has high survival rates in aquatic environments (Winfield and Groisman, 2003).

*Salmonellae* have been reported from fresh water systems by several workers (Kadlecova, 1977, Alcaide and Garay, 1984, Arvanitidou *et al.*, 1997, Baudart *et al.*, 2000 and Moore *et al.*, 2003). Almost all types of fresh water bodies such as, rivers, reservoirs, lakes, natural dam water, wells, ponds, natural springs, tap water, ground water and other types found
to harbor *Salmonella*. The source of *Salmonella* to these systems is mostly from sewage discharge (Smith *et al*., 1978, Alcaide *et al*., 1983, Polo *et al*., 1998). The presence of *Salmonella* and its relationship with indicators of faecal pollution was investigated in aquatic habitats by Polo *et al*., (1998). The highest frequency was obtained in rivers (58.7% of samples) followed by freshwater reservoirs (14.8%) and sea water (5.9%). In the same way river waters contaminate estuarine and marine systems like sea, coastal belts, beaches, bays and others. Some of the estuaries have high number of *Salmonella* due to sewage contamination (Rhodes and Kator, 1989). Many workers have reported the incidence of *Salmonella* in estuaries (Rhodes and Kator, 1988; 1989, Ferguson *et al*., 1996), in estuarine organisms (Comar *et al*., 1979 and Gore *et al*., 1992), coastal waters (Venkateswaran *et al*., 1989, Sunarya *et al*., 1997 and Baudart *et al*., 2000), sea water, (Polo *et al*., 1999, Martinez-Urtaza *et al*., 2004) and in coastal bays (Majorri *et al*., 1977, Peterson *et al*., 1984).

Baudart *et al*., (2000) has investigated the diversity of *Salmonella* strains isolated from different natural aquatic systems within a Mediterranean coastal watershed (riverine, wastewater, and marine coastal areas). The ecology of *Salmonella* in Porto Novo coastal environment was studied by Ramamurthy and Natarajan (1987). The distribution of *Salmonella* from the Vellar Estuary and Pitchavaram (India) was studied for a year, followed by a survey of this pathogen in different seafoods. All water and sediment samples were positive for the pathogen and it was beyond detectable levels in freshly caught fish and crustaceans. Sediment was the most conducive for persistence of *Salmonella*, while oysters proved to be major reservoirs. Higher percentages occurred during monsoon in environmental samples (water and sediment) and in seafood samples. Martinez-Urtaza *et al*., (2004) have studied the temporal and spatial distribution of *Salmonella* contamination in the coastal waters of Glacia.
(northwestern Spain) relative to contamination events with different environmental factors (temperature, wind, and hours of sunlight, rainfall, and river flow) over a period of 4 years. *Salmonella* was isolated from seawater as well as mollusks. The incidence was found to be high in water column samples rather than marine benthos. Different serovars such as *Salmonella enterica* serovar Senftenberg, serovar Typhimurium and Agona were identified. Serovar Senftenberg was detected at specific points on the coast and could not be related to any of the environmental parameters analyzed. All serovars except *Salmonella* serovar Senftenberg were found principally in the southern coastal areas close to the mouths of rivers, and their incidence was associated with high southwestern wind and rainfall.

The presence of *Salmonella* in marine environments did not vary seasonally and was independent of water temperature. Furthermore, *Salmonella* exhibited high survival rate following mixing of sewage effluent with brackish water, a transition that caused a dramatic increase in salinity (Winfield and Groisman, 2003). Venkateswaran et al., (1989) studied seasonal variation of human pathogens such as *Vibrio cholerae* non-01 and *Salmonella* spp. in Fukuyama coastal waters and the role of zooplankton in their distribution. Better isolation of an allochthonous pathogen, viz., *Salmonella* spp., was noticed from the water samples when swabs were employed. Out of 251 isolates serotyped, 18 with 3 variants of *Salmonella* spp. were identified. A high amount of nutrients in the water column increased the survival rate of these pathogens in saline waters as evidenced by a higher incidence of various serotypes in polluted Fukuyama port than in clean marine waters. Role of zooplankton could be noticed in influencing seasonal distribution of *V. cholerae* non-01 as well as *Salmonella* spp.
The USFDA, has maintains a zero tolerance for *Salmonella* in foods, claiming that its presence is always the result of fecal contamination as *salmonella* is not indigenous to the aquatic environment. However, evidence from catfish ponds in the USA and eel ponds in Japan clearly indicate that the *salmonella* is naturally present in the environment. The presence of *salmonella* has previously been convincingly demonstrated in shrimp culture ponds in Southeast Asia and the coastal environment in India. However, most of these indigenous aquatic strains belong to the serotype *S. weltevreden*, which is not commonly associated with human infections. As further evidence to support the case for removal of the zero tolerance it would be useful to determine whether such aquatic strains possess the potential to cause disease in humans. PCR-based techniques would be helpful in such studies (James, 1999).