3. Review of literature

3.1. Diversity of actinobacteria in the marine environment

In the marine environment, two locations have been distinguished, (1) Littoral/inshore zone and (2) Deep sea sediments. It has been noted that the population density of actinomycetes as well as other microorganisms is denser in the shallow sea than in the deep sea (Weyland, 1969). Isolation of actinomycetes from the marine environment has been less when compared to the terrestrial environment. However, research has gained momentum in the last three decades and several attempts have been made to isolate the actinomycetes from the marine environment (Zobell, 1946; Weyland, 1969; Walker and Collwell, 1975; Okami and Okazaki, 1978; Weyland, 1981; Jensen et al., 1991; Imada, 2005; Imada et al., 2010).

Baam et al. (1966) initiated the study on the diversity of actinomycetes from the Indian marine environment. Chandramohan et al. (1972) isolated 15 Streptomyces spp. from the sediments of 15 fathom line in the Bay of Bengal. Okazaki and Okami (1972) isolated 136 strains of actinomycetes from 37 samples collected at three inlets of the Sagami Bay and reported the occurrence of Microbispora, Nocardia, Actinomyces, Chainia and Streptomyces. Presence of the species of Streptomycetes in the marine, estuarine and mangrove sediments of Portonovo was investigated by Samuelpaulraj (1973). He could isolate a number of Streptomyces species from all the sediment samples collected during his study. Ecology of actinomycetes in a coastal sand belt and the littoral zone, was studied by Watson and Williams (1974).
A new species designated as *Streptomyces mariensis* was isolated from the marine water sample collected from the Bay of Bengal near the Palm Beach (Sambamurthy and Ellaiah, 1974). Lakshmanaperumalsamy (1978) studied the seasonal occurrence and distribution of actinomycetes in the sediments of the coastal environment of Portonovo. Totally, 1289 Streptomyces strains were isolated along with some other genera (*Micromonospora* and *Nocardia*). Vanajakumari (1979) also studied the seasonal occurrence and distribution of actinomycetes, isolated from the estuarine, backwater and marine regions of Portonovo. Majority of the actinomycetes were the species of *Streptomyces* and a few were *Actinomyces* species.

Okami *et al.* (1979) isolated a new species, *S. tenjiamariensis* from the shallow sea mud around the Sagami Bay. Veiga *et al.* (1983) isolated 39 *Streptomyces* spp. from the depth of 10 m deep in the Lacorufia Bay (Spain). Goodfellow and Williams (1983) studied the occurrence and distribution of actinomycetes in the deep-sea sediments. Goodfellow and Haynes (1984) found actinomycetes population in both bathyal and abyssal depths and in the same year, Helmke and Weyland (1984) isolated actinomycetes forms from the marine sediments. The representative genera were *Rhodococcus*, *Nocardia* and *Mycobacterium*. They erected the new species, *Rhodococcus marinonascens*.

Pisano *et al.* (1986) isolated 120 isolates of actinomycetes from the marine sediments of the Sandy Hook Bay, New Jersey by applying different pretreatment methods. Ellaiah and Reddy (1987) isolated 141 strains of actinomycetes from the sediments of the Vishakapatnam coast which included *Streptomyces, Micromonospora, Nocardia, Streptosporangium, Micropolyspora* and *Streptoverticillium*. Approximately
400 strains of actinomycetes were isolated from the sediments of the Oyster Bay Harbour area of Long Island, New York by pretreatment methods (Pisano et al., 1988). Takahashi et al. (1989) isolated 200 strains of actinomycetes from the sea mud of Gamo, Miyagi Prefecture, Japan. Pisano et al. (1989) isolated *Streptomyces* and *Micromonospora* from the marine sediments, using rifampicin antibiotic. Jensen et al. (1991) isolated totally 289 actinomycetes strains from the near-shore marine sediments collected at 15 island locations throughout the Bahamas. They recorded bimodal distribution of actinomycetes population in relation to depth with a rapid decrease of *Streptomyces* and an increase of *Actinoplanetes*.

Balagurunathan (1992) isolated 51 strains from the Parangipettai littoral zone. Majority of the genera were *Streptomyces* and *Nocardia*. Pisano et al. (1992) isolated 116 actinomycetes from the marine sediments. Takizawa et al. (1993) obtained 298 isolates from the sediment samples at eight stations from the Chesapeake Bay. Of these, 249 isolates belonged to the genus *Actinoplanetes*. Mathew et al. (1994) isolated *Streptomyces* sp. from *Villorita cypinoides* collected from the Veli Lake. Moran et al. (1995) by using 16S rRNA, isolated actinomycetes from the salt marsh and mangrove areas of Georgia, Athens and found that *Streptomyces* populations were the indigenous components. Colquhoun et al. (1998) isolated *Rhodococcus* from deep sea. Dhevendaran and Annie (1999) isolated 16 *Streptomyces* from fish, shellfish and sediments of the Veli estuarine lake.

Ghanem et al. (2000) isolated actinomycetes from the near-shore marine sediments and waters of four different sites in Alexandria, using four different media viz. Starch nitrate agar, Starch casein agar, Chitin agar and Colloidal chitin agar. Among
them, Starch nitrate agar favoured the growth of actinomycetes. Sivakumar (2001) proposed two new species of actinomycetes, *Streptomyces kathirae* and *Actinopolyspora indiensis*, isolated from the Pitchavaram mangrove ecosystem. Patil *et al.* (2001) isolated 133 marine actinomycetes from 129 marine samples, collected along the Tuticorin coast. Most of the isolates were *Streptomyces*. Balagurunathan and Subramaniam (2001) isolated 51 *Streptomyces* from the littoral sediments of Parangipettai. Mincer *et al.* (2002) reported that the major taxa of obligate marine bacteria occurred within the order Actinomycetales and were from the ocean sediments. Dhevendaran and Anithakumari (2002) reported 240 strains of *Streptomyces* from the guts of the fish, *Therapon jarbua* and *Villorita cyprinoides*.

Ellaiah *et al.* (2004) investigated marine actinomycetes from five different marine sediment samples of the Bay of Bengal near the Kakinada coast of the Andhra Pradesh. Totally, 60 isolates were obtained by using starch casein agar medium. Sabry *et al.* (2004) isolated *Nocardiopsis aegyptia* from the marine sediments of Abu Qir Bay, on the western seashore of Alexandria, Egypt. A group of 20 *Micromonospora* isolates were recovered from the coastal sediments of Aberystyryth (Zhao *et al.*, 2004). Sahu *et al.* (2004) isolated 40 strains of actinomycetes from the gut contents of three species of fishes collected from the Vellar estuary, Bay of Bengal.

Magarvey *et al.* (2004) isolated 102 actinomycetes strains and reported two new genera of actinomycetes within the family Micromonosporaceae, from the subtidal marine sediments collected from the Bismarck Sea and the Solomon Sea of the coast of Papua New Guinea. Dhevendaran and Praseetha (2004) isolated 17 pigment producing *Streptomyces* from 14 different species of seaweeds of Cape Comorin using different
culture media *viz.* actinomycete isolation agar, Kuster’s agar and glycerol asparagine agar. Among them, more number of *Streptomyces* was isolated in glycerol asparagine agar. Sirvibool *et al.* (2004) isolated 567 thermotolerant actinomycetes strains from 64 soil samples of the coastal ecosystem of Chonburi, Rayong and Trat provinces. Kokare *et al.* (2004) isolated 80 actinomycetes strains and identified 16 species of *Streptomyces* and one each of *Streptoverticillium, Catellatospora, Nocardia* and *Actinopolyspora* from the Maharrastra and Goa coasts, using eight different selective media.

Dhanasekaran *et al.* (2005) isolated 107 actinomycetes strains from 16 marine sediments of the Tamilnadu coastal area. Imada (2005) isolated 10 actinomycetes strains from the deep sea water and sediment samples. Kathiresan *et al.* (2005) investigated on the marine actinomycetes diversity from different coastal ecosystems *viz.* mangroves, estuary and sand dune, including the industry dominated coast. From this investigation, they established that mangrove sediments serve as the rich source for actinomycetes diversity. Fiedler *et al.* (2005) isolated 600 actinomycetes from the marine sediments of the Pacific and Atlantic oceans. Among them, 25% belonged to the genus *Streptomyces*, 29% to *Micromonospora*, 15% to *Pseudonocardia* and 33% to *Rhodococcus*.

Adinarayana *et al.* (2005) isolated a new variant of *S. hawaiiensis* from the marine sediments of the Machilipatnam coast of the Bay of Bengal. Sahu *et al.* (2005a) estimated the actinomycetes population density from different samples *viz.* water, sediments, seaweeds, molluscs and finfishes of the Vellar estuary and found that the sediments harbour higher population density as compared to the water samples. Among the biological samples, molluscs recorded higher population density in shell surface region than the gut content, while the finfishes recorded higher population density in gut
contents followed by gills and skin. Sahu et al. (2005b) isolated actinomycetes from the sediments and molluscan samples of the Vellar estuary. Senthilkumar et al. (2005) isolated 41 halophilic actinomycetes strains from the salt marsh area of the Vellar estuary, using different media and reported that the starch casein agar is the best for the isolation of actinomycetes.

Maldonado et al. (2005a) reported Micromonospora, Rhodococcus and Streptomyces speari from the marine environment of Japan Trench (Pacific Ocean), Canary Basin (Atlantic Ocean) and selected fjords in Norway. Mincer et al. (2005) isolated 366 Salinospora strains from 200 marine samples collected around the islands of Bahamas. Jensen et al. (2005) observed 6425 colonies from 275 marine samples collected around the island of Guam. Sivakumar et al. (2005) isolated 91 strains of actinomycetes from different locations of the Pichavaram mangrove ecosystem using three different media viz. Starch Casein Agar (SCA), Glucose Asparagine Agar (GAA) and Kuster’s Agar (KUA). Consistently, a higher number of populations occurred in the KUA medium and the highest population density recorded was $4 \times 10^4$ CFU/g. This led them to conclude that KUA medium would be more suitable for enumerating the actinomycetes populations from the mangrove environment. Niladevi and Prema (2005) isolated 21 actinomycetes strains from seashore and 19 from saltpan environment of the Palk Bay, India. You et al. (2005) isolated a total of 94 actinomycetes strains form the nearshore marine sediments of a shrimp farm in which 87.2% belonged to the genus Streptomyces and others to Micromonospora.

Jensen and Mafnas (2006) isolated Salinospora from the marine sediments collected at six geographically distinct locations. Zhang et al. (2006) investigated on the
sponge associated actinomycetes diversity, *Hymeniacidon perleve* from the Yellow Sea, China and reported the occurrence of 106 actinomycetes strains which include *Actinoalloteichus, Micromonopora, Nocardia, Nocardiopsis, Pseudonocardia, Rhodococcus* and *Streptomyces*. Thirty eight actinomycetes were isolated from the sediments collected from the Marina Trench (10,898 m) using marine agar and media selective for actinomycetes notably Raffinose-histidine agar. Phylogenetic analysis based on 16S rRNA gene sequencing showed that the isolates belonged to the genera *Dermacoccus, Kocuria, Micromonospora, Streptomyces, Tsukamurella* and *Williamsia* (Aree *et al.*, 2006).

Jacob and Prema (2006) isolated *Streptomyces lydicus* from the mangrove environment of Cochin, India. Actinomycetes (35 strains) were also isolated from the sponge, *Craniella australians*, of which, 24 matched with *Actinomyces* and 11 belonged to *Streptomyces* (Li and Liu, 2006). Lam (2006) reported the occurrence and wide distribution of indigenous marine actinomycetes in the oceans and in different marine ecosystems. Peraud (2006) conducted microbiological analyses on a sponge *Acanthostrongylophora* sp. with a particular emphasis on the isolation of actinomycetes because of the higher number of actinomycetes sequences present in the sponge 16S rRNA gene library and their excellent track record as bioactive compound producers. Sahu *et al.* (2006) investigated on the antagonistic actinomycetes from the sediment samples of the Vellar estuary. Kundu *et al.* (2006) isolated 39 actinomycetes strains from different parts of the alimentary canal of the estuarine fishes collected from the Vellar estuary and also Muthurayar *et al.* (2006) isolated 18 actinomycetes strains from the fish,
Chanos chanos collected from the Vellar estuary. Kokare et al. (2006) isolated 80 actinomycetes strains from Alibag, Janjra and Goa coastal regions of India.

Forty actinomycetes strains were isolated from the different organs viz. skin, gills and gut in three different species of fishes viz. Mugil cephalus, Chanos chanos and Etroplus suratensis, using three different media i.e. Kuster’s agar, Glycerol aspargine agar and Starch casein agar. Among the three media, Kuster’s agar medium was found to be the suitable medium for isolating actinomycetes from fish (Sahu et al., 2007). Jiang et al. (2007) isolated 54 actinobacterial strains using different media viz. Gausa’s medium No.1, Glycerol arginine agar (GAA), Starch casein KNO₃ agar (SCKA), Streptomycete media (SM) and 2216E, from the marine sponge, Haliclona sp. collected from the shallow waters of the South China Sea. Based on the 16S rRNA gene sequencing, the isolates were found to belong to the genera, Streptomyces, Nocardiopsis, Micromonospora and Verrucosispora. Vijayakumar et al. (2007) isolated 192 actinomycetes colonies from 18 marine sediment samples of the Palk Strait region of the Bay of Bengal, India. The isolates were assigned to Streptomyces (39), Actinopolyspora (10), Saccharopolyspora (7), Actinomadura (4), Nocardiopsis (3), Micromonospora (2), Actinomyces (1), Actinoplanes (1) and Microbispora (1).

Murugan et al. (2007) isolated 35 actinomycetes strains from the gut contents of the finfish (Mugil cephalus). Esawy (2007) isolated mesophilic Streptomyces albus AZA from the mediterranean seashore, Alexandria. Baltz (2007) isolated actinomycetes strains from the deepest part of the Mariana Trench even at depths of 10, 898 m and reported the occurrence of Micromonospora isolates from the deep sea samples. Marilize et al. (2007) reported 3 genera and three species of actinomycetes from the sediments of an estuary in
Plettenberg Bay, South Africa. Raghavendrudu and Kondalarao (2007) studied the occurrence of actinobacteria from the mangrove sediments of the Gaderu river of Gautami-Godavari estuarine system. Twenty two actinobacterial strains were isolated and of these, 14 belonged to the genus *Streptomyces* represented by three species *viz.* *S. parvulus*, *S. flavoviridis* and *S. lusitanus*; three isolates belonged to *Streptoverticillium* and four, to *Micromonospora*.

Approximately 3, 200 actinomycetes were isolated using four different agar media from the samples collected at different locations of the largest Norwegian fjords, the Trondheim fjord where *Micromonospora* was dominant (Bredholt *et al.*, 2008). Remya and Vijayakumar (2008) isolated 173 actinomycetes colonies from the near shore marine environment and mangrove ecosystem at eight different locations of Kerala, West Coast of India. Majority of them was assigned to the genus, *Streptomyces*. Gunalakshmi *et al.* (2008) isolated 20 strains of actinomycetes from the sediments of a shrimp pond. The relationship between the distributions of actinomycetes and antagonistic behaviour with the physico-chemical characteristics of the Sundarbans was investigated by Mitra *et al.* (2008). Gandhimathi *et al.* (2008) isolated 26 endosymbiotic actinomycetes from the Bay of Bengal. Jiang *et al.* (2008) isolated 52 actinobacterial strains from the marine sponge *Lotrochota* sp. collected from the South China Sea. Roes *et al.* (2008) isolated *Gordonia lacunae* (BS2) from the esturine sediments of Plettenberg Bay.

belonged to diverse genera *viz.* *Gordonia, Isoptericola, Micromonospora, Nocardiopsis, Saccharopolyspora* and *Streptomyces*. Furthermore, two new species, namely, *Saccharopolyspora cebuensis* SPE-10-1^T^ and *Streptomyces axinellae* PO1001^T^ were identified as novel anti-infective agent producers. Xin *et al.* (2008) investigated the sponge (*Hymeniacidon perleve*) associated actinobacterial communities. Nearly 300 actinobacteria were isolated by using seventeen different media from six marine sediment samples collected from the Gulf of California and the Gulf of Mexico. 16S rRNA gene analysis revealed that the isolates belonged to several actinobacterial *taxa*, notably *Actinomadura, Dietzia, Gordonia, Micromonospora, Nonomuraea, Rhodococcus, Saccharomonospora, Salinispora, Streptomyces, Solwaraspora* and *Verrucosispora* (Maldonado *et al.*, 2009).

Basha *et al.* (2009) isolated ten marine actinomycetes strains from sediment samples obtained from Tamilnadu and Kerala of India. Vimal *et al.* (2009) isolated twenty five actinomycetes strains from Puducherry, southeast coast of India and designated them as VITSVK1-VITSVK25. *Streptomyces* strain AQBMM35 was isolated from the marine sponge, *Mycale mytilorum* collected from the West Coast of India, using glycerol aspergine agar medium (ISP-5) (Dharmaraj *et al.*, 2009). Zhao *et al.* (2009) isolated 239 actinobacterial strains from the sediment samples collected from the Xinghai Bay, Xiaoping Island and Changhai in Dalian, China, by employing fifteen selective media. Phylogenetic analysis of their 16S rRNA sequences showed that these strains belong to the genera, *Streptomyces* and *Micromonospora*. One of the strains was identified as a new species of *Streptomyces*. Suthindhiran and Kannabiran (2009) isolated moderately halophilic *Saccharopolyspora salina* from the sediments of Marakkanam
coast of Tamilnadu at a depth of 400 m. Manivasagan et al. (2009) isolated *Streptomyces* sp. PM-32 from the sediment samples of the Bay of Bengal. Ye et al. (2009) isolated *S. griseorubens* WBF9 from the marine sediments of Weihai, China. Selvin et al. (2009) isolated *Streptomyces* sp. (MS101), *Micromonospora* sp. (MS128) and *Saccharomonospora* sp. (MS136) along with some bacteria from sponges.

Totally, 30 marine actinomycetes strains were isolated from different locations of the Muthupet mangroves, using Starch casein agar (Vijayakumar et al., 2010). Raja et al. (2010) isolated 17 actinobacterial strains from the rhizosphere sediments of mangroves. Pugazhvendan et al. (2010) isolated 34 actinomycetes strains from Chennai (Tamil Nadu) coastal area. Schneemann et al. (2010) isolated 46 actinobacterial strains from the marine sponge, *Halichondria panicea* of the Baltic Sea and these strains were identified as belonging to the genera, *Actinoalloteichus*, *Micrococcus*, *Micromonospora*, *Nocardiopsis* and *Streptomyces* based on the 16S rRNA gene sequencing. Abdelmohsen et al. (2010) isolated 90 actinomycetes strains from 11 different species of marine sponges collected from the offshore region of Ras Mohamed (Egypt) and Rovinj (Croatia). All these isolates were phylogenetically related to 18 different actinomycetes genera belonging to five different suborders.

Gnanam (2010) isolated 61 actinobacterial strains from four different stations of the Bay of Bengal. Sabarathnam et al. (2010) isolated 11 actinomycetes colonies from the sponge, *Dendrilla nigra* and identified them as *Streptomyces* sp. and *Nocardiopsis* sp. and one remained unidentified. Similarly, Sun et al. (2010) reported six genera *viz.* *Salinispora*, *Gordonia*, *Mycobacterium*, *Nocardia*, *Rhodococcus* and *Streptomyces* associated with the marine sponge, *Hymeniacidon perleve*. 
Ogunmwonyi et al. (2010) reported 84 culturable actinomycetes, belonging to 15 genera isolated from the water and rock scrapings of Nahoon beach in the Eastern Cape Province of South Africa. The rock scrapings yielded more actinomycetes which included *Actinoplanes*, *Actinosynnema*, *Nocardia*, *Nocardiopsis*, *Streptosporangium*, *Intrasporangium* and *Kibdellosporium*. They also reported that the *Streptomyces* was most dominant. Arifuzzaman et al. (2010) isolated 55 actinomycetes strains from the sediment samples of Karanjal region in Sundrabans and identified them as belonging to *Actinomyces*, *Nocardia*, *Streptomyces* and *Micromonospora*.

Imada et al. (2010) reported the occurrence of *Streptomyces* (37%) and *Micromonospora* (26%) from the marine sediments of the neritic zone, in and around the Japan sea. Ravikumar et al. (2010) reported the occurrence of 63 sponge associated actinomycetes strains collected from the Arabian sea, South west coast of India. Manivasagan et al. (2010) isolated 125 actinobacterial strains from the sediments, collected from six different stations. Among them, 90 strains were identified as *Streptomyces* and *Actinopolyspora* (10 each), *Micromonospora* (8), *Nocardiopsis* (7), *Actinomadura* (5) and *Actinomyces* (5). Lakshmipathy et al. (2010) isolated *Streptomyces* spp. VITDDKS from the saltpan sediments of the coastal region in Tamilnadu. Deepika and Kannabiran (2010) observed 100 actinomycetes colonies on the Starch casein agar medium from Ennore saltpan sediments. Thenmozhi and Kannabiran (2010) isolated *Streptomyces* sp. from the marine sediments, collected from the Bay of Bengal coast of Puducherry.

Selvam et al. (2011) isolated 56 actinomycetes strains from the marine sediments of the South Indian coastal region, using starch casein agar. Sivakumar et al. (2011)
isolated bioactive compound producing actinobacteria from the marine sediments of Bay of Bengal at a depth of 10-40m near Pudimadaka coast of Andra Pradesh. Among the isolates, *Rhodococcus* and *Streptomyces* showed promising activities. Ravikumar *et al.* (2011) studied the biodiversity of actinomycetes in Manakkudi mangrove ecosystem, southwest coast of India. The study revealed that the diversity of actinomycetes was maximal in the rhizosphere soil than the non-rhizosphere soil. The study also emphasized that the presence of actinomycetes in the Manakkudi mangrove ecosystem could pave way for the establishment of disease free mangrove seedlings in the nursery and the field.

Sathiyaseelan and Stella (2011) isolated, identified and studied the antagonistic activity of seven actinomycetes strains from the Muthupet mangrove environment. Seven actinomycetes species showed antagonistic activity against human pathogens like, *Escherichia coli*, *Pseudomonas* sp., *Klebsiella* sp. and *Bacillus* sp. Dharmaraj (2011) isolated 94 marine actinomycetes isolated from four sponges *viz.* *Callyspongia diffusa*, *Mycale mytilorum*, *Tedania anhelans* and *Dysidea fragilis*. A novel actinomycetes strain, GW25-5\(^T\) (*Streptomyces fildesensis*) was isolated from a soil sample collected from the Fildes Peninsula, King George Island, West Antarctica (Li *et al.*, 2011). A total of 19 morphologically distinct strains of actinobacteria were isolated from the coral reef environs of the Poomarichan island, Gulf of Mannar (Karuppiah, 2011).

Jianyou *et al.* (2011) isolated two different actinomycetes strains, *Streptomyces roseobiolascens* XAS585 and *S. roseofulvus* XAS588 from the marine coastal and offshore mud, Zhuhai city, Guangdong province, China. Bai *et al.* (2011) identified the genus *Brevibacterium* within the Actinomycetales order from the water samples of Pearl
Bay of Fujian Province, China. Reddy et al. (2011) reported a marine actinobacterial strain *Streptomyces rochei* (MTCC10109) from the sea water of Vishakhapatnam coast. Nair et al. (2011) isolated 96 strains of sponge associated actinomycetes from the Bay of Bengal.

Sharma and David (2012) isolated and identified 304 actinomycetes colonies from 175 sediment samples of the Pulicat estuary, Muttukadu estuary and Ennore estuary. Among them, 162 isolates were *Streptomyces*, 104 were *Actinopolyspora* and 11 isolates were *Nocardioides*. Nearly, 87 isolates of *Streptomyces* were found to be associated with the gut of marine ornamental fishes namely *Chaetodon collare* and *Archamia fucata* (Sheeja et al., 2012). Thenmozhi and Kannabiran (2012) studied the antimicrobial and antioxidant properties of the marine *Streptomyces* sp VITSTK7 isolated from the marine sediments collected from the Bay of Bengal coast of Puducherry, India. The study revealed that the ethyl acetate extract of the isolate possessed both free-radical scavenging and antimicrobial activities. Fifty one actinobacteria strains were obtained from the salt pan sediments, along the coast of Kothapatanam, Ongole of Andhra Pradesh, using three different media viz. Actinomycetes isolation agar, Starch casein agar and Kuster’s agar. Among them, Actinomycetes isolation agar promoted more actinobacterial colonies when compared to other media. Among the 50 strains, 80% was assigned to *Streptomyces*, 10%, to *Actinomyces* 6%, to *Nocardia* and 4%, to *Micromonospora* (Kumar and rao, 2012a). Gulve and Deshmukh (2012) isolated 107 marine actinomycetes strains from the near shore sediments and seawater of the Konkan coast, Maharashtra.
Mangrove soil samples were collected from Nizampatnam situated along the south east coast of Andhra Pradesh, pre-treated and plated on asparagine-glucose agar medium. One strain isolated (VCK-10) belonged to *Pseudonocardia* (Mangamuri *et al*., 2012). *Streptomyces* species were also isolated from the marine sediment samples from different locations of the Visakhapatnam coast of India, using CaCo$_3$ pretreatment (Spandana *et al*., 2012). Similarly, Raju *et al*. (2012) isolated actinomycetes from Nizampatnam port area. Rao *et al*. (2012a) isolated 20 actinomycetes strains from Visakhapatnam and most of them were identified as *Streptomyces*. Janardhan *et al*. (2012) isolated five actinomycetes strains from the mangrove sediments of Pennar. Rao *et al*. (2012b) isolated 20 actinobacterial strains from the mangrove sediments of Visakapatnam, using ISP2 medium (International Streptomyces project) and 12 strains were identified as *Streptomyces*. Boroujeni *et al*. (2012) isolated 30 actinomycetes strains from six soil samples of Kuruva Island and Pookot lake, Wayanad district of Kerala. Based on the morphological and biochemical characteristics, the isolates were assigned to the genus, *Streptomyces*.

Kumar and Rao (2012b) isolated 55 actinobacterial colonies from the sediments of Thondi coastal area, using three different media (Actinomycetes isolation agar, Kuster’s agar and Starch casein agar). Valli *et al*. (2012) isolated 21 actinomycetes strains from the marine sediments and water samples of Royapuram, Muttukadu, Mahabalipuram sea shore and Adyar estuary, using actinomycetes isolation agar.

Rajkumar *et al*. (2012) studied the actinobacterial diversity of the Bhitherkanika mangroves, east coast of Orissa, India. A total of 116 actinobacterial colonies were recorded from 30 mangrove and marine sediment samples of the Bhitherkanika
mangrove environment. The isolates were assigned to *Streptomyces* (43), *Saccharopolyspora* (5), *Nocardiopsis* (5), *Micromonospora* (3), *Actinomadura* (5), *Actinomycetes* (1) and *Actinopolyspora* (5). Twelve different actinomycetes were isolated from mangrove sediments and identified as *Streptomyces* (Raghunathan and Umadevi, 2012). A total of 68 actinomycetes were isolated from the near shore marine environment locations of the Bigeum Island, South West coast of South Korea, using Starch casein agar. Majority of the isolates were assigned to *Streptomyces* (66%) and the remaining were identified as *Nocardiopsis* (18%), *Micromonospora* (11%) and *Actinopolyspora* (5%) (Parthasarathi et al., 2012). Kalyani et al. (2012) studied the antimicrobial activity of the marine actinomycetes isolated from the marine sediments of Konark of Orrisa.

A total of 327 strains were isolated from eight different marine sponges collected from the South China Sea and the Yellow sea and 108 representative isolates were selected for phylogenetic analysis. Ten families and 13 genera of *Actinomycetales* were detected, among which, five genera were the first records from marine sponges. Oligotrophic medium M5 (water agar) proved to be efficient for selective isolation, and “*Micromonospora–Streptomyces*” was proposed as the major distribution group of sponge-associated actinomycetes from the China Sea and ten isolates were thought to be novel species. Sponge *Hymeniacidon perleve* was found to contain the highest generic diversity (seven genera) of actinomycetes. Phylogenetic analyses of Housekeeping genes of the isolates indicated one ubiquitous *Micromonospora* species, one unique *Streptomyces* species and one unique *Verrucosispora* phylogroup (Xi et al.,
Poongodi et al. (2012) isolated *Mycobacterium* sp. from the Kurusadai island, Gulf of Mannar.

Wu et al. (2012) reported 110 culturable actinobacteria associated with the seagrass (*Thalassia hemprichii*), using six culture media viz. M1, M8, G2, HZ, G and HC. The strains belonged to *Streptomyces*, *Micromonospora*, *Saccharomonospora*, *Mycobacterium*, *Actinomycetospora*, *Nonomuraea*, *Verrucosispora*, *Nocardiopsis*, *Microbacterium* and *Glycomyces*. *S. caelestis* was isolated from the coastal waters of the Red sea (Liu et al., 2012). Seventeen isolates were obtained by Attimarad et al. (2012) from the coastal sediments, collected from Gokharna and Muradeshwara of Karnataka, using SCA medium.

Sobolevskaya et al. (2013) studied the biological activity of feigrisolides a, b and c of a marine isolate, *Streptomyces* sp. 6167. It was found that feigrisolide B induces apoptotic process in the Ehrlich carcinoma cells (IC 50 =17.4 μg/ml), possesses cytotoxic activity against the developing eggs of the sea urchin *Strongylocentrotus intermedius* and immobilizes sperm of the urchin in dose less than 1 μg/ml. Sirisha et al. (2013) studied the enzyme activities and antibacterial potential of actinomycetes isolated from the sediments obtained from different locations of the Bay of Bengal, India. The results revealed that 81%, 59%, 44%, 31% and 24% of the isolates exhibited amylase, protease, chitinase, L-asparaginase and cellulase activities respectively. Screening for antibacterial activity revealed that 10 isolates exhibited antibacterial activity. The marine actinomycetes isolates exhibited more antimicrobial activity against gram positive bacteria than the gram negative bacteria. Out of the 63 isolates, 85% (*n*=53) isolates
belonged to the genus *Streptomyces*, 7% (n=5) to *Micromonospora*, 4% (n=3) to *Nocardia* and 3% (n=2) to *Streptosporangium*.

Mohanraj and Sekar (2013) isolated *Streptomyces* sp LCJ94 from the Bay of Bengal. Mohseni *et al.* (2013) isolated 44 actinomycetes strains from the Caspian sea sediments at a depth of 5-10 cm, using different media. Palomo *et al.* (2013) isolated 44 marine actinomycetes of the family Micrococcaceae, from the sponges collected from the Florida Keys (USA). Pylogenetic analysis showed that these strains belonged to *Kocuria* and *Micrococcus*.

Sivasankar *et al.* (2013a) isolated and studied the antibacterial activity of 46 actinobacterial strains obtained from the sediments of the Uppanar estuary, Cuddalore, India against human pathogenic bacteria and brain shrimp lethality. Dastager and Damare (2013) studied the occurrence and distribution of actinobacteria in the marine environments, especially in the sediments of Chorao island, Goa and a total of 200 isolates of actinobacteria were obtained. Djinni *et al.* (2013) isolated *S. sundarbansensis* from the Algerian marine brown alga *Fucus* sp. Sivasankar *et al.* (2013b) isolated 50 actinobacterial strains from the sediments of the Bay of Bengal and evaluated them for L- asparaginase production.

### 3.2. Actinobacteria research in the Andaman and Nicobar islands

There are only few studies on the diversity of actinobacteria in various parts of the Andaman and Nicobar islands. Chandramohan and Nair (1992) isolated 69 strains of *Streptomyces* from the sediments of the Andaman and Nicobar islands. Chinnaraj and Untawale (1992) isolated 9 actinomycetes strains from the submerged parts of the
mangrove of the Andaman island. Kerkar (1994) isolated *Streptomyces* sp. from an intertidal zone of the Andaman island.

Peela *et al.* (2005) isolated 88 actinomycetes strains from 26 marine sediment samples obtained from nine islands of the Andaman coast of the Bay of Bengal. They were assigned to *Streptomyces* (64), *Micromonospora* (8), *Nocardia* (5), *Streptoverticillium* (7) and *Saccharomonospora* (4). Sahu *et al.* (2007) investigated the occurrence and the population density of actinomycetes from eight different stations of the Little Andaman and the isolates showed close similarity to *Streptomyces xantholiticus*, *S. aureofasciens*, *S. gattieri*, *S. galbus* and *S. rimosus* which possessed antagonistic activity against shrimp pathogens. Sethubathi (2009) isolated 80 actinobacterial strains and tentatively identified 22 strains at the genus level and 18 strains at the species level from the Little Andaman island.

Aarthi *et al.* (2009) screened carbohydrate degrading enzyme producing thermophilic actinobacteria from the mud volcano sediments of the Baratang Island, Andamans. Aarthi (2009) isolated 19 thermophilic actinobacterial strains from the mud volcano of the Baratang island and found that 3 strains (T1, T5 and T8) belonged to the genus *Streptomyces* which possessed cytotoxicity at a lower concentration of 31.25 µg/ml and it was non-toxic to the Vero cell (normal cell line) in the same concentration.

Murugan (2009) isolated 20 strains of marine actinobacteria from the Little Andaman island and investigated their antagonistic activity. Revathi *et al.* (2010) studied the anti-pathogenic activity of marine actinobacteria from the Rutland island of the Andamans. Chandrakumar (2010) isolated *Nocardiospsis* sp. (CN2) from the Car-
Nicobar island and screened it for anticancer activity against the Hela cell lines. Swarnakumar (2010) isolated 52 actinobacterial strains from the Nicobar group of islands, out of which, 10 strains were identified (*Streptomyces*) and studied for their anticancer properties. Karthik *et al.* (2010) stated that the Nicobar marine environment supports the existence of taxonomically diverse populations of actinomycetes. Their study revealed that the majority of the isolates (90%) required sea water for their growth which is an indication of the presence of higher degree of marine actinomycetes.

Sethubathi (2011) investigated the actinobacterial diversity of the coral reef environs of three stations namely Hut Bay jetty, Buttler Bay and Dugong creek of the Little Andaman island and recorded higher actinobacterial population diversity from the Dugong creek and the lowest from the Hut Bay jetty. He isolated 15 actinobacterial strains and noted the bioelectricity producing capacity of *Streptomyces albidoflavus*. Kamala (2011) isolated and identified 10 actinobacterial strains from the Nancowry island and screened their alkaloids for antioxidant potential. Baskaran *et al.* (2011) reported that the mangrove sediments of the Andaman and Nicobar islands could offer an opportunity for the discovery of antibiotics from the marine actinomycetes. They isolated bioactive compound producers from the mangrove sediments, using various pre-treatments, on three different media.

Poosarala *et al.* (2013) isolated six actinomycetes strains from the marine sediments of the Andaman and Nicobar islands and studied their antibiotic producing ability. The strains belonged to the genus *Streptomyces*. Abirami *et al.* (2013) isolated eight actinomycetes strains from three different sites of the Andaman and Nicobar islands. A total of 26 actinobacterial strains were isolated from the marine sediments
from various sites of Port Blair Bay (Meena et al., 2013). Aarthi (2013) isolated 13 strains of marine actinobacteria from the mud sample of Baratang island, the Andamans. Among them, nine strains were identified as *Streptomyces* and four strains were identified as *Nocardiopsis*.

### 3.3. Pyrosequencing

Based on pyrosequencing, Gaidos *et al.* (2010) showed that the microbial community of the interior flat of Checker Reef in Kane’ohe Bay was dominated by the bacterial phyla *viz.* Proteobacteria, Firmicutes and Actinobacteria, the archaeal order *Nitrosopumilales* and the uncultivated divisions of Marine Group III (*Euryarchaeota*) and Marine Benthic Group C (*Crenarchaeota*).

Kouridaki *et al.* (2010) have made a comparative analysis of five 16S rRNA gene cloning libraries from the deep-sea sediments (water column depth: 400 m) of the Northeastern Pacific Ocean and Eastern Mediterranean Sea. This is in fact the first comparison of the bacterial communities living in these deep-sea ecosystems. They also estimated chlorophyll-α, organic carbon and C/N ratio which provided with evidences for significant differences in the trophic state of the sediments between the Northeastern pacific Ocean and the much warmer Eastern Mediterranean Sea. There were 11 different taxonomic groups, with *Gammaproteobacteria* predominating in the Northeastern Pacific Ocean sediments and *Acidobacteria*, in the Eastern Mediterranean microbial community.

Qian *et al.* (2011) studied the microbial communities of the least-explored ecosystems, Atlantis II Deep and Discovery Deep in the Red Sea. Taxonomic classification of pyrosequencing reads of the 16S rRNA gene amplicons showed vertical
stratification of microbial diversity from the surface water to 1500 m below the surface. Significant differences in both the bacterial and archaeal diversity were observed in the upper layer with cyanobacterial abundance whereas the deeper layer harboured a large proportion of *Proteobacteria*. Among Archae, Euryarchaeota, especially Halobacteriaales, was found to be dominant in the upper layer but diminished drastically in the deeper layers where *Desulfurococcales* belonging to Crenarchaeota was the dominant group. Thus, this study indicated that the microbial communities observed from the various environments of the Red sea were different from those of the other parts of the world.

Jackson *et al.* (2012) elucidated the bacterial community profiles associated with the marine sponges *Raspailia ramosa* and *Stelligera stuposa* sampled from a single geographical location in Irish waters. Four bacterial phyla (Actinobacteria, Bacteroidetes, Firmicutes and Proteobacteria) were obtained. Further, bacterial OTUs (2,109 total), at 95% sequence similarity, from ten bacterial phyla were recovered from *R. ramosa*, 349 OTUs were identified in *S. stuposa* representing eight phyla, while 533 OTUs from six phyla were found in the surrounding seawater.

Sylvan *et al.* (2012) examined the deep sea vents for microbial diversity and ecology, using the tag pyrosequencing of the V6 region of the 16S rRNA and full-length 16S rRNA sequencing on inactive hydrothermal sulfide chimney samples from 9°N on the East Pacific Rise to learn their bacterial composition, metabolic potential, and succession from venting to non venting (inactive) regimes. Alpha-, beta-, delta-, and gamma proteobacteria and members of the phylum *Bacteroidetes* dominated all the inactive sulfides. Greater than 26% of the V6 tags obtained were closely related to lineages involved in sulfur, nitrogen, iron, and methane cycling. Epsilonproteobacteria
represented <4% of the V6 tags recovered from inactive sulfides and 15% of the full-length clones, despite their higher abundance in active chimneys. Members of the phylum Aquificae were common in the active vents.

Wang et al. (2012) determined the microbial community of the different wastewater treatment plants (WWTPs) and investigated the effects of waste water characteristics, operational parameters, and geographic locations. Activated sludge samples were collected from 14 waste water treatment systems located in four cities in China. High-throughput pyrosequencing was used to examine the 16S rRNA genes of bacteria in the waste water treatment systems. Results showed that there were 60 genera of bacterial populations commonly shared by all 14 samples, including Ferruginibacter, Prosthecobacter, Zoogloea etc., indicating that there was a core microbial community in the microbial populations of WWTPs at different geographic locations. Canonical Correspondence Analysis (CCA) results showed that the bacterial community variance correlated most strongly with water temperature, conductivity, pH, and dissolved oxygen (DO) content. Variance partitioning analyses suggested that waste water characteristics had the greatest contribution to the bacterial community variance, explaining 25.7% of the variance of bacterial communities independently, followed by operational parameters (23.9%) and geographic location (14.7%).

Wang et al. (2013) analyzed the bacterial community of the intertidal zones of Bohai Bay, China, adopting pyrosequencing-based approach to analyze the 16S rRNA gene of bacteria in the sediments collected from two typical intertidal zones – Qikou (Qi) and Gaoshaling (Ga). Results showed that, at a 0.03 distance, the sequences from the Qi sediment were assigned to 3252 operational taxonomic units (OTUs) belonging to 34 phyla, 69 classes and 119 general and the 3740 OTUs from the Ga sediments had 33
phyla, 66 classes and 146 genera. While comparing the bacterial communities of the two intertidal sediments, significant difference was observed in the dominant composition and distribution at phylum, class and genus levels. Canonical correspondence analysis (CCA) showed that the median grain size and DO were the most important factors regulating the bacterial abundance and diversity.

Orgiazzi et al. (2013) established the microbial consortium, which is not usually subjected to change and hence, possibly resistant/resilient to disturbances and a varying soil context. Fungi form the major part of soil biodiversity; yet the mechanisms driving their large-scale ecological ranges and distribution are poorly understood. Degree of fungal community overlapped among 16 soil samples of distinct ecosystems and distant geographic localities (truffle grounds, a Mediterranean agro-silvo-pastoral system, serpentine substrates and a contaminated industrial area) were assessed by examining the distribution of fungal ITS1 and ITS2 sequences in a dataset of 454 libraries. ITS1 and ITS2 sequences were assigned to 1,660 and 1,393 Operational Taxonomic Units (OTUs; as defined by 97% sequence similarity), respectively. Fungal beta-diversity was found to be spatially auto correlated. At the level of individual OTUs, eight ITS1 and seven ITS2 OTUs were found in all the soil sample groups.

Further the above review of literature it can be understood that detailed studies are needed on the diversity of culturable and culture-independent marine actinobacteria of the islands and hence the present study from the Neil island of the Andamans, India.