Chapter 18
Marine Enzymes from Microbial Symbionts of Sponges and Corals

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Contents

Abstract Sponges and corals are great pool of diverse microbes because they are closely associated with microorganisms that occur either extracellularly or intracellularly. The recent studies have revealed new microbial communities and novel compounds from sponges and corals. Many reports are found toward the availability of antibiotics from the sponge-/coral-associated microorganisms; very few reports are available for the enzymes, but there are no scientific research reports with the potentiality in medical and biotechnological applications. Therefore, there is an urgent need of exploration of marine enzymes from sponges and corals for human and environmental perspectives. This chapter will focus on current and future prospects of marine enzymes from microbial symbionts especially sponges/corals.

Keywords Sponges · Corals · Symbionts · Enzymes

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18.1 Introduction

Marine microorganisms have a specific association with marine invertebrates which include sponges, and corals, etc. The microorganisms from the maritime-based environment have attracted considerable attraction toward them because of huge source of natural products for biotechnological application (Fig. 18.1).

The interrelationships between the marine sponges and microorganisms which might be considered as food either permanently or temporarily were found to be incredibly complex and far being understood at the present [1, 2]. Sponges (phylum, Porifera), that are on the evolution-based scale can be termed as ancient metazoans, originated 700–800 million years ago. They are grown especially in the tropical, temperate, and also freshwater niches [3, 4]. Particularly marine sponges are populated from intertidal zones to thousands of meters deep in the ocean [5].

The sponges consist of three major lineages, which include *Calcarea* (including 5 orders and 24 families), *Demospongiae* (15 orders and 92 families), and *Hexactinellida* (which include the 6 orders and 20 families). The numbers of sponge species raise to 15,000, which might be higher [6].

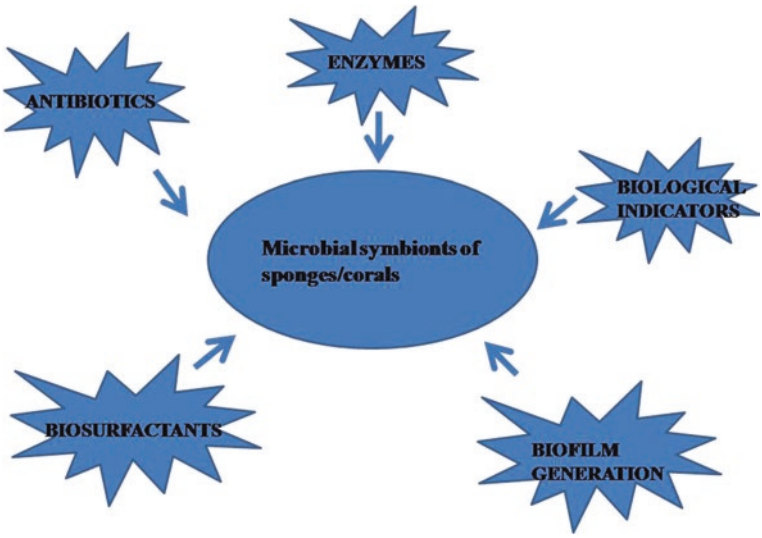

Fig. 18.1 Biotechnology potential of sponge- and coral-associated microorganisms

18.2 Sponge Microbial Association: Abundance, Diversity, and Specificity

The marine sponge mesohyl (extracellular matrix) contains a huge number of microorganisms, found in abundance surrounding the choanocyte chambers, rings of the flagellated cells that form foundation for the sponge aquiferous systems. Howbeit, the bacteriocytes of sponge species also grow, sponge species also host the microorganisms from the endosymbionts, and the pinacoderm cell also consists of increased densities of cyanobacterial species [7]. The microbial densities of the sponge are 10^9 cells/cm^3 of sponge tissue. Some sponges have high microbial abundance (HMA), whereas some species were found to have low-microbial-abundance (LMA) sponges (10^5–10^6 bacteria/cm^3 of tissue) [8].

Some genera show considerable variations which link to the total microbial abundance in certain hosts, e.g., *Chloroflexi*, *Actinobacteria*, *Cyanobacteria*, and *Poribacteria* [9–12]. The microbiomes of HMA and LMA sponges shared some functional features [13, 14].

When compared to human, sponge microbiome contains increased species diversity, whereas there is low phylum-level diversification [15]. There are about 52 different microbial phyla from which the candidate phyla were found to be associated with sponges [16–18]. The density of symbiont communities was found to be different in species ranging from a few distinct operational taxonomic units (OTU) to thousands of genetically distinct symbionts per host taxon [16, 18, 19], most of which are considered metabolically active [20]. The taxa *Gammaproteobacteria* and *Alphaproteobacteria*, *Actinobacteria*, *Chloroflexi*, *Nitrospirae*, *Cyanobacteria*, the candidate phylum *Poribacteria*, and *Thaumarchaea* were dominant in sponge [21, 22].

The marine fungal species when compared to the marine bacteria associated with the sponges were not fully explored but were found to have omnipresent relationship with sponges as reported by Namikoshi et al. [23] and Thakur and Muller [24]. There are twenty one orders from the *Ascomycota* which include the *Boliniales*, *Botryosphaeriales*, *Capnodiales*, *Chaetosphaeriales*, *Claromycetales*, *Diaporthales*, *Dothideales*, *Eurotiales*, *Helotiales*, *Hypocreales*, *Microascales*, *Moniliales*, *Mucorales*, *Onygenales*, *Phyllachorales*, *Pleosporales*, *Polyporales*, *Saccharomycetales*, *Sordariales*, *Trichosphaeriales*, and *Xylariales*, and also there are 8 orders from the *Basidiomycota* including *Agaricales*, *Agaricostilbales*, *Corticiales*, *Malasseziales*, *Polyporales*, *Sporidiobolales*, *Tremellales*, and *Wallemiales* that were reported from the marine sponges by Höller et al. [25], O'Brien et al. [26], Wang [27], Baker et al. [28], Li and Wang [29], Liu et al. [30], Paz et al. [31], Ding et al. [32], Rozas et al. [33], Wiese et al. [34], Zhou et al. [35], Suryanarayanan [36], Thirunavukkarasu et al. [37], and Yu et al. [38]. The orders *Saccharomycetales* and *Malasseziales* are not filamentous fungi. The sponge-derived fungal species have been found to be containing huge deposits of natural products, which are dealing with the enzymes isolated from the sponge-associated fungi that are very uncommon.

18.3 Enzymes from Sponge-Associated Microbes

The sponges are microbial living organisms which belong to the phylum *Porifera*. It is a multicellular organism, with pore-covered bodies and channels for circulation of water, food, and oxygen and removal of wastes. It released three times more oxygen and more organic matter than they consume when it is associated with photosynthesizing endosymbionts. Due to this, sponges have unique ecological niches. Large volumes of the seawater are consumed consisting of the organic particles by the sponge species; hence the scientific people have gathered their attention toward the microbes in sponges and the sponges itself which produce hydrolytic enzymes to convert the present organic matters into nutrients. For instance the hydrolysis of the agar can be achieved by the bacterial genus *Cytophaga* which was isolated from the sponge *Halichondria panicea* [39]. Currently more research is going on bioactive compounds from sponge-associated microbes, but only few reports are available on enzymes from sponge-associated microbes.

Marine sponges are one of the major sources producing halogenated organic compounds (bromoindoles, bromophenols, and bromopyrroles) in marine environment. The bacteria are harboring 40% of the biomass of *Aplysina aerophoba* sponges. *Desulfovibrio* bacteria (anaerobic sulfate reducers) are predominant in this sponge. Ahn et al. [40] discovered that the dehalogenation activity of *Desulfovibrio* spp. with different haloaromatics, for example, 2-bromophenol, 3-bromophenol, 4-bromophenol, 2,6-dibromophenol, 2,4,6-tribromophenol, and 3,5-dibromo-4-hydroxybenzoate, was reduced by debromination under methane-generating and sulfidogenic conditions with no activity observed in the presence of the nitrate. The increased salt tolerance of two novel esterases, namely, EstB1 and EstB2, were isolated and characterized from the genomic library *Bacillus* sp. associated with the marine sponge *Aplysina aerophoba*. The stability of the enzymes was stable in DMSO till 50% (v/v) followed by methanol, ethanol, and 2-propanol [41].

There are about 56 bacterial species which were isolated from the 6 marine sponges, namely, *Spirastrella* sp., *Phyllospongia* sp., *Ircinia* sp., *Aaptos* sp., *Azorica* sp., and *Axinella* sp. These strains are characterized and screened for amylase, carboxymethylcellulase, and proteases as reported earlier by Mohapatra et al. [42]. The screening resulted in the 44 strains to be positive for amylase, 46 for carboxymethylcellulase, and 34 for protease production, respectively. The genera belonging to *Alcaligenes*, *Alteromonas*, *Bacillus*, and *Micrococcus* were able to produce increased activity toward the amylase > 0.5 IU/ml. The genera, namely, *Alcaligenes*, *Alteromonas*, *Arthrobacter*, and *Planococcus*, and one unidentified bacterium were found to be 100% for carboxymethylcellulase activity. The protease activity was observed from the isolated bacteria. The bacterial species belonging to the genera *Alcaligenes*, *Alteromonas*, *Bacillus*, *Corynebacterium*, *Flavobacterium*, *Micrococcus*, and *Vibrio* and one of the unidentified bacterium showed protease activity ranging from 0.050 to 0.971 IU/ml. These results confirm that the enzymes producing strains are widely distributed in the bacterial genera with particular

emphasis on sponge-associated strains. Especially 10–35% strains of *Bacillus* and 50–100% strains belonging to the genera of *Alcaligenes* are able to produce large amounts of enzymes like amylase, carboxymethylcellulase, and protease.

In addition, the research carried out by Mohapatra and Bapuji [43] states that the *Arthrobacter ilicis* bacterial species and the *Mucor* sp. characterized from the sponge *Spirastrella* sp. are capable of producing acetylcholinesterase and amylase enzymes, respectively. Also, these enzymes are heat tolerant and are not affected by the cations present in the seawater which include Na^{+}, Ca^{2+}, and Mg^{2+} at the higher concentrations [44].

By using the metagenomic technology, novel enzymes with a potential in environmental biotechnology were identified like oxidoreductase and halogenases from marine sponges [27].

The bacterium, *Micrococcus* sp., showed 80% urethenase activity which was isolated from the marine sponge, *Spirastrella* sp. The EDTA did not affect the bacterial species and other major cations found in the seawater and also found to be resistant toward 20% ethanol (v/v). Therefore, the removal of urethane from the alcoholic beverages could be the possible usage [45].

The presence of the collagenolytic activity in the bacterial species isolated from the marine sponge *Cymbastela concentrica* was confirmed by polyphasic approach [46]. It was also found that the other bacterial species have genes encoding collagenolytic enzymes, while there was a low abundance of microbes isolated which included *Zobellia* sp. KMM 3665; AB084262, *Vibrio crassostreae*; AJ582809, *Bacillus pumilus*; EU236743, *Shewanella* sp. MJ5323; and DQ531951 possessing collagenolytic activities.

The thermotolerant protease was reported from the marine endosymbiotic species, *Roseobacter* sp. (MMD040), which was isolated and characterized from the marine sponge *Fasciospongia cavernosa*. In pH 9.0, it showed 92.5% activity and 89% activity at 50°C. These results indicate that it can be developed for industrial application [47]. It was also reported that the increased yields of the enzyme amylase-producing strain, *Halobacterium salinarum* MMD047, were isolated from marine sponge *Fasciospongia cavernosa* [48]. A biotechnologically important enzyme, esterase, was isolated from the bacterial species from the marine sponge *Hyrtios erecta*, that was identified by metagenomic approach. It showed activity against acetate (5.6 U/mg), butylate (5.1 U/mg), and caproate (2.8 U/mg) substrates, with thermal stability and salt tolerance property [49].

The alkaline lipase was reported from an endosymbiotic *Pseudomonas* sp. (MSI057) from the marine sponge *Dendrilla nigra* [50]. In the same sponge, extracellular cellulolytic enzyme from *Marinobacter* sp. (MSI032) was reported [51].

From the metagenomic library of the marine sponge, *Haliclona simulans*, the 58 lipase-positive isolates were reported. The sequence analysis revealed the putative lipase gene lpc53E1, which encodes 387 amino acids with a molecular mass of 41.87 kDa. The optimal activity was observed with p-nitrophenyl palmitate (C16) at 40 °C, in the presence of 5 M NaCl, pH 7. When the p-nitrophenyl palmitate (10mM)

was added as the substrate, it showed increased lipase activity of 2700 U/mg at the temperature of 40°C with the presence of 5 mM Ca^{2+} and 5 M NaCl [52].

Feby and Nair [53] screened the amylase, protease, gelatinous, lipase, deoxyribonucleic, phosphatase, and urease from bacterial species associated with two demosponges, *Dysidea granulosa* and *Sigmadocia fibulata*. *Gammaproteobacteria*, *Firmicutes*, and *Actinobacteria* were isolated from *Dysidea granulosa*, and in the case of *S. fibulata*, the *Betaproteobacteria* were isolated from the sponges. In the said scenario, sponge-associated bacteria express multiple enzymatic activities greater than four, and also they reported that *Vibrionales* was the main source for multiple enzyme production.

Dupont et al. [54] studied the prokaryotic community associated with the sponge *Asbestopluma hypogea* and its antimicrobial and antioxidant and chitinolytic activity. They found that 16 % of the bacterial isolates were positive for chitinolytic activity and they also suggested the involvement of the microbial species in the digestion processes of crustacean prey. In these, *Streptomyces* sp. S1CA strain had a potential in antimicrobial and antioxidant and chitinolytic activity.

In our lab, a significant work was carried out on enzymes from sponge-associated microorganisms.

The culture-independent metagenomic approach was taken for the screening of the complex microbiome species from the marine sponge *Ircinia* species that confirmed the presence of putative lipase gene *lipA*. The optimal activity was present at pH 9.0 with the presence of 5 mM Ca^{2+} and some of the organic solvents, like the methanol, acetone, and isopropanol at 40 °C. The SDS-PAGE confirmed 30 kDa to be the molecular weight for LipA; the main purpose can be in the detergent industry and enzyme-mediated organic synthesis. The study has widened the lipolytic gene and showed that marine sponges can be an important source for the novel enzymes [55].

The actinobacterial isolate *Streptomyces* sp. DA11, isolated from the South China Sea sponge called *Craniella australiensis*, was able to produce the chitinase enzyme which exhibited antifungal activity. The optical activity was observed at pH 8.0 at 50°C and salinity 45 g‰ psu. In comparison to the terrestrial organism-derived enzymes like the chitinase from the marine microbial sources, they have increased pH and salinity tolerance, which would contribute to the special biotechnological applications. The present study has shown the first report on the sponge-associated microbial chitinase [56]. Using Plackett-Burman design and Box-Behnken response surface methodology, the chitinase activity of 1559.2 U/g cell dry weight (36.43 U/mL) and the maximum cell dry weight of 23.3 g/L were reached after incubation of 72 h, which were 39.2-fold and 2.6-fold higher than that of the basic medium [57].

The bacterial isolate *Bacillus pumilus* B106 from the South China Sea sponge *Halichondria rugosa* was found to produce lipase enzyme, and there was an increased tolerance toward salinity, pH, and temperature. The study also extends our

understanding of possibility of sponge-associated bacteria in biotransformation of chemical compounds [58].

Currently we are working on urease from *Bacillus atrophaeus* C89 isolated from *Dysidea avara* and its role in heavy metal detection in water pollution (data not shown). No enzymes have been reported from microbes associated with sponge families such as *Agelasidae, Astroscleridae, Calthropellidae, Geodiidae, Pachastrellidae, Thrombidae, Dictyodendrillidae, Acanthochaetetidae, Alectonidae, Hemiasterellidae, Placospongiidae, Polymastiidae, Stylocordylidae, Tethyidae, Timeidae, Trachycladidae, Bubaridae, Dictyonellidae, Heteroxyidae, Halisarcidae, Calcifibrospongiidae, Phloeodictyidae, Lubomirskiidae, Malawispongiidae, Metaniidae, Metschnikowiidae, Palaeospongillidae, Potamolepiidae, Spongillidae, Spongillina incertae sedis, Plakinidae, Azoricidae, Corallistidae, Desmanthidae, Isoraphiniidae, Lithistida incertae sedis, Macandrewiidae, Phymaraphiniidae, Phymatellidae, Pleromidae, Scleritodermidae, Siphonidiidae, Vetulinidae, Latrunculiidae, Microcionidae, Rhabderemiidae, Desmacellidae, Esperiopsidae, Guitarridae, Hamacanthidae, Merliidae, Podospongiidae, Chondropsidae, Coelosphaeridae, Crambeidae, Crellidae, Dendoricellidae, Desmacididae, Hymedesmiidae, Iotrochotidae, Phellodermidae, Tedaniidae, Samidae*, and *Spirasigmidae* of the class *Demospongiae* and *Baeriidae, Lepidoleuconidae, Trichogypsiidae, Achramorphidae, Amphoriscidae, Grantiidae, Heteropiidae, Jenkinidae, Lelapiidae, Leucosoleniidae, Sycanthidae, Sycettidae, Minchinellidae, Petrobionidae, Clathrinida incertae sedis, Clathrinidae, Leucaltidae, Leucascidae, Levinellidae, Soleneiscidae, Lelapiellidae, Murrayonidae, Ancorinidae, Chondrillidae,, Suberitidae, Callyspongiidae, Niphatidae, Petrosiidae, Neopeltidae, Theonellidae, Acarnidae, Raspailiidae, Isodictyidae, Mycalidae, Myxillidae, Plysinidae, Pseudoceratinidae*, and *Paramurrayonidae* of the class *Calcarea*. There are no reports of microbially originated enzymes from the class *Hexactinellida*.

18.4 Ecology and Physiology: Urea Hydrolysis

Many of the microbial populations are able to produce urease enzyme, which hydrolyzes urea to ammonia and carbamate and therefore maintaining the nitrogen level in the atmosphere [59]. The enzyme urease is produced by diverse bacterial species at a very early stage of their growth during early lag phase. These bacterial populations enhanced the protein synthesis in host sponge by the breakage of urea to ammonia. The microorganisms could play a major role in nutritional, physiological, and ecological mode of the host sponge and its environment. Our group reported the first insight on bacterial potential in urea utilization by detecting the transcriptional activity of *ure*C gene as well as the phylogenetic diversity of bacteria with *ure*C gene [60].

18.5 Defensive Enzymes from Endosymbionts

The endosymbionts produce the enzymes which are defensive in nature, along with the industrial enzymes, like the phospholipase, as the first line of defense. In 2009, Selvin [61] reported the production of an extracellular enzyme as phospholipase A2 (PLA2) from the sponge-associated bacterial isolate *Streptomyces dendra* sp. nov. MSI051 that resulted in more or less similar phospholipase A2 activity. It was also reported that the enzyme is responsible in the host against predatory and disturbances in the habitat.

18.6 Enzymes Responsible for Secondary Metabolite Production

Polyketide synthase, non-ribosomal peptide synthetase (NRPS) [62], and FADH-dependent halogenase [63] are multifunctional enzymes which are responsible for several new antibiotics production. Using metagenomic approach, polyketide synthase [64–66], non-ribosomal peptide synthetase gene clusters [67], and functional enzymes [68, 69] were reported from marine sponge-associated microbiota (please see Chap. 12 for details).

18.7 Coral Microbial Association

The living organisms belonging to the phylum Cnidaria and class Anthozoa are termed as corals, which are immobile otherwise known as the sessile marine invertebrates and are further classified into stony corals and soft corals. The oldest recorded coral dates back to around 450–500 million years to the Ordovician Period of the Paleozoic Era as reported by Stanley [70] and Tapanila [71]. They were found to be in interrelationship with a diverse and significantly richer quantification of bacteria, archaea, and fungi, which in turn influence the anatomical and physiological functions of coral hosts as well as its ecosystem and habitat. The coral-associated microorganisms were found to be acting as key player in nutrient cycling, coral health, and coral reef resilience [72, 73].

The coral-associated microorganisms are divided into four main functional groups, namely, (a) mutualistic bacteria with possible roles in coral nutrition; (b) pathogenic bacteria; (c) bacteria which can act as a probiont, aiding the growth of beneficial bacteria but limiting the growth of pathogenic forms; and (d) purely commensal bacteria with no impact on the other three groups [74]. These microorganisms play an important role in the symbiosis relatively which play an unknown role in the coral health and disease. The *Acidobacteria*, *Actinobacteria*, *Alphaproteobacteria*, *Aquificae*, *Bacteroidetes*, *Betaproteobacteria*, *Calditrix* KSB1, *Chlamydiae*, *Chlorobi*, *Chloroflexi*, *Cyanobacteria*, *Deferribacteres*,

Deinococcus-Thermus, *Deltaproteobacteria*, *Epsilonproteobacteria*, *Firmicutes*, *Fusobacteria*, *Gammaproteobacteria*, *Gemmatimonadetes*, *Lentisphaerae*, *Nitrospirae*, OD1, *Planctomycetes*, *Spirochaetes*, *Tenericutes*, *Thermotogae*, TM7, *Verrucomicrobia*, WS3, *Zetaproteobacteria* from bacteria, *Crenarchaeota*, *Euryarchaeota* from Archaea, and *Ascomycota*, *Basidiomycota*, and *Chytridiomycota* from fungi were reported [75]. The compounds isolated from coral-associated microbes exhibited a broad spectrum of activity against pathogens, including coral pathogens [76, 77], but only few reports are only available in enzymes producing coral-associated microbes.

18.8 Enzyme from Coral-Associated Microbes

The total mean viable count of bacteria isolated from the soft coral *Lobophytum* sp. was 1.6×10^5cfu/g wet wt. Eight bacterial genera were isolated; in these genus *Pseudomonas* is dominant. It was screened for industrial enzymes such as amylase, carboxymethylcellulase, and protease. As a result, coral-associated microbes showed low to high enzyme activity [42].

The protease from *Halomonas meridiana* RA001 associated with *Acropora* sp. coral sample was reported from Palk Bay, southeast coast of India [78]. Anithajothi et al. [79] screened enzymes involved in melanin synthesis pathway (phenoloxidase (PO) and peroxidases (POD)) and free radical scavenging enzymes (super oxide dismutase (SOD), catalase (CAT)) and glutathione peroxidase (Gpx) in selected scleractinian corals such as *Acropora formosa*, *Echinopora lamellosa*, *Favia favus*, *Favites halicora*, *Porites* sp., and *Anacropora forbesi* collected from the southeast coast of India. The phenoloxidase activity was significantly lower than that of zooxanthellae except for *Favia favus*. *Favia favus* followed by *Echinopora lamellose* showed maximum antioxidant defensive enzymes. They concluded that these enzymes can be used as biomarkers for identifying the susceptibility of corals toward coral bleaching induced by pathogen.

The protease activity of three fungal isolates was reported from soft corals collected from Andaman and Nicobar marine water (lack of full information) [80]. *Bacillus aquimaris* MKSC 6.2 was isolated from a soft coral *Sinularia* sp., from Merak Kecil Island, West Java, Indonesia, which showed increased α-amylase activity, and it has the ability to degrade raw corn, rice, sago, cassava, and potato starches with the adsorption percentage in the range of 65–93% [81].

18.9 Conclusion

Sponge-associated symbionts synthesize industrially important enzymes which have been reported so far from geographically different regions such as the Bay of Bengal, India, South China Sea, France Sea, Baltic Sea, etc. (Table 18.1). This book

Table 18.1 Industrially important enzymes from sponge-associated microbes

Family	Sponge	Symbiont	Enzymes	References
Halichondriidae	*H. panacea* (Baltic Sea)	*Cytophaga* sp.	Agarase	[39]
Aplysinidae	*Aplysina aerophoba* (Marine Biological Station, Banyuls sur Mer, France)	*Desulfovibrio* spp.	Halogenase	[40]
Aplysinidae	*Aplysina aerophoba* (source not mentioned)	*Bacillus* sp.	Esterase	[41]
Spirastrellidae Spongiidae Tethyidae Siphonidiidae Axinellidae	*Spirastrella* sp., *Phyllospongia* sp., *Ircinia* sp., *Aaptos* sp., *Azorica* sp., and *Axinella* sp. (different location of Bay of Bengal, India)	*Alcaligenes*, *Alteromonas*, *Bacillus*, *Corynebacterium*, *Flavobacterium*, *Micrococcus*, *Vibrio*, and one unidentified bacterium	Amylase, carboxymethylcellulase, and proteases	[42]
Axinellidae	*Cymbastela concentrica* (Bare Island)	*Zobellia* sp. KMM 3665, *Vibrio crassostreae*, *Bacillus pumilus*, *Shewanella* sp.	Collagenase	[46]
Spirastrellidae	*Spirastrella* sp. (intertidal region of Havelock Island, Andaman Sea, India)	*Arthrobacter ilicis*	Acetylcholinesterase	[43]
Spirastrellidae	*Spirastrella* sp. (intertidal region of Havelock Island, Andaman Sea, India)	*Mucor* sp.	Amylase	[48]
Spirastrellidae	*Spirastrella* sp. (intertidal region of Havelock Island, Andaman Sea, India)	*Micrococcus* sp.	Urethanase	[45]

(continued)

Table 18.1 (continued)

Family	Sponge	Symbiont	Enzymes	References
Thorectidae	*Fasciospongia cavernosa* (peninsular coast of India)	*Roseobacter* sp.	Protease	[47]
Thorectidae	*Fasciospongia cavernosa* (peninsular coast of India)	*Halobacterium salinarum*	Amylase	[48]
Thorectidae	*Hyrtios erecta* (coast of Ishigaki Island, Okinawa, Japan)	Metagenome	Esterase	[49]
Darwinellidae	*Dendrilla nigra* (southwest coast of India)	*Pseudomonas* sp.	Lipase	[50]
Darwinellidae	*Dendrilla nigra* (peninsular coast of India)	*Marinobacter* sp.	Cellulose	[51]
Chalinidae	*Haliclona simulans* (Kilkieran Bay, off the west coast of Ireland)	Metagenome	Lipase	Selvin et al. [82]
Dysideidae *Chalinidae*	*Dysidea granulosa* and *Sigmadocia fibulata* (Kavaratti Island, Lakshadweep, west coast of India)	*Gammaproteobacteria*, *Firmicutes*, and *Actinobacteria* *Betaproteobacteria*	Amylase, protease, gelatinase, lipase, deoxyribonucleic, phosphatase, and urease	[53]
Cladorhizidae	*Asbestopluma hypogea* (coast of La Ciotat, France)	*Streptomyces* sp. S1CA	Chitinase	[54]
Irciniidae	*Ircinia* sp. (Yongxing Island, South China Sea)	Metagenome	Lipase	[55]
Tetillidae	*Craniella australiensis* (South China Sea)	*Streptomyces* sp. DA11	Chitinase	[56]
Halichondriidae	*Halichondria rugosa* (South China Sea)	*Bacillus pumilus* B106	Lipase	[58]

chapter brings out the fact that members of the class *Demospongiae* are not only the richest producer of medicinally important bioactive compounds, but it is also a good producer of industrially important enzymes in association with microbes.

From the 92 families of the class *Demospongiae*, 15 families associated microbes have been isolated and characterized to be industrially important enzymes, which include the families *Halichondriidae, Aplysinidae, Spirastrellidae, Spongiidae, Tethyidae, Siphonidiidae, Axinellidae, Spirastrellidae, Thorectidae, Darwinellidae, Chalinidae, Dysideidae, Cladorhizidae, Irciniidae*, and *Tetillidae*.

Both bacteria and fungi have been isolated from a wide range of marine sponges. The diversity and symbiotic relationship of bacteria have been studied to a greater extent than that of fungi isolated from sponges, and even the enzymes also more reported from bacteria than fungi associated with sponges. Only one report was available for fungi (*Mucor* sp. for amylase). *Axinellidae, Spirastrellidae, Chalinidae, Cladorhizidae, Irciniidae*, and *Halichondriidae* family-associated symbionts were reported for only enzymes but not for antibiotics.

The coral-associated symbionts or isolates which produce the industrially important enzymes are reported from geographically different regions from Palk Bay, southeast coast of India, Bay of Bengal, India, Andaman and Nicobar, and Indonesia. The nine families from the class Anthozoa have been identified to produce industrially important enzymes.

Sponges and corals are a pool of novel microorganisms. When compared to terrestrial microorganisms, it is capable to tolerate different temperatures, at diverse pH and saltiness. It is more suitable for industrial process. The discovery of potent microbial associates producing enzymes has opened up a new era in marine industry. So far, many studies are carried out for antibiotics, but for enzymes only few reports are available. Hence, researchers and investigators should turn their attention toward the production of such valuable industrial and pharmaceutical enzymes from sponge- and coral-associated microorganisms.

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