



# Diversity of Chitinase-Producing Bacteria and Their Possible Role in Plant Pest Control

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## Abstract

In nature, chitin is the second most plentiful and renewable polysaccharide and is present among versatile group of organisms from fungi and nematodes to arthropods and crustaceans. Enzymatic degradation is the preferable environmentally safe mode of bioprocessing of this inert biopolymer. Chitin-scavenging enzyme-producing sources are covering the living groups from prokaryotes to plants, viruses, vertebrates, and even human. Current-day biotechnologies have raised the development of bioprocesses by using microbes especially bacteria. Bacteria that produce chitinases are with varieties of habitats ranging from Antarctic soil to hot spring, crustacean waste site, animal gut, and endophytic ecosystems. Chitin metabolism is a necessary life-supporting goings-on in agronomic plant pests like fungi, insects, and parasitic nematodes which are negatively proportionate to the agricultural production systems. Placement of such potent chitinolytic bacteria for plant fortification against attacking pests is a well-practiced, biotechnologically equipped biocontrol strategy. By-products of chitin by enzymatic hydrolysis, like oligomers or monomers, have several applications in persuading the plant defense systems. Carrying the host-defensive activity to biocontrol potentiality against plant pests, bacteria with chitinolytic property also behaved as a plant growth-promoting biofertilizing employee in modern-day sustainable agricultural practices. In this context, the distribution of chitinase-producing bacteria according to their diversity of habitats is studied, and the less explored habitats can be an arsenal for biocontrolling agents against plant pests.

## Keywords

Chitinase · Bacteria · Diversity · Biocontrol · Plant pest

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## 18.1 Introduction

Chitin is the second most abundant biodegradable carbon substrate after cellulose, which exists naturally in the biosphere as a structural polysaccharide of  $\beta$ -(1,4)-linked *N*-acetyl-D-glucosamine (GlcNAc). In nature, chitin is available in two crystalline formats,  $\alpha$  and  $\beta$ . In the case of  $\alpha$ -chitin, it is the most copious crystalline form, and the linear chains of GlcNAc unit are assembled in an antiparallel fashion, commonly exemplified by the shrimps and crabs, fungi, and cysts of *Entamoeba*. On the other hand,  $\beta$ -chitin is made up of parallel chains of GlcNAc units and found in squid pens (Yan and Fong 2015; Jang et al. 2004). Overall, chitin is extensively distributed in nature, mainly as an organizational polysaccharide in fungal cell walls (predominantly in *Ascomycota*, *Basidiomycota*, and *Chytridiomycota*), exoskeletons of arthropods, external shells of crustaceans, egg shell, and gut lining of parasitic nematodes (Brzezinska et al. 2014; Lenardon et al. 2010). The applicable fields of chitin are biotechnologically noteworthy, from chemical, biochemical, food, and pharmaceutical (antimicrobial, anticholesterol, antitumor, drug delivery, dietary fiber, and wound healing) industries (Patil et al. 2000; Gooday 1999; Muzzarelli et al. 1999; Dixon 1995) to wastewater treatment and management (Flach et al. 1992).

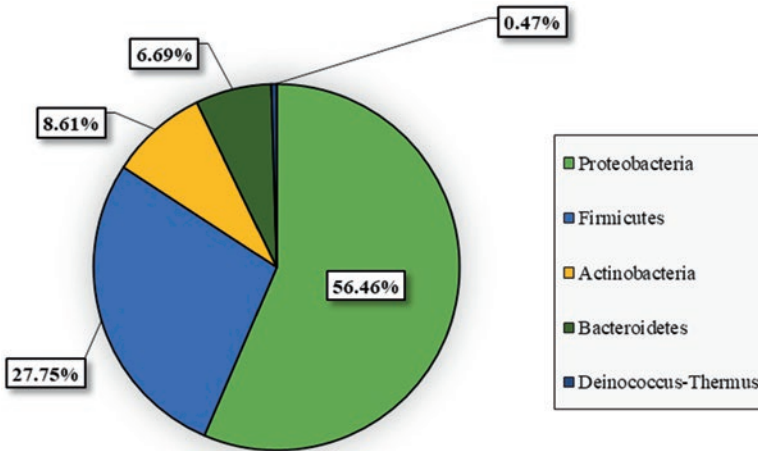
The insolubility of chitin and its inertness to chemical agents have amplified the exploration for substitute disposal methods such as biological processing. One such preferable practice is enzymatic treatment because of its uniformity toward the reaction and the products. Oligomers or monomers, by-products of chitin, have several applications in eclectic arenas (Patil et al. 2000). For such bio-based handling, chitinase comes first, and it acts to hydrolyze the  $\beta$ -1,4-glycosidic bonds between the *N*-acetyl-D-glucosamine residues that encompass a chitin chain (Henrissat 1999). Chitinases are classified into two types, exochitinases and endochitinases, based on their site and the nature of their hydrolyzed bonds (Henrissat 1999; Henrissat and Bairoch 1996). Endochitinases cleave chitin chains in random locations, generating low molecular weight oligomers, such as chitotriose, chitotetraose, and diacetylchitobiose. The exochitinases have been alienated into two subcategories: chitobiosidases which gradually release diacetylchitobiose from the non-reducing end of the chitin and  $\beta$ -*N*-acetylglucosaminidases, cleaving the oligomers of chitin (products of endochitinase), thereby producing monomers of glucosamine (Hamid et al. 2013).

Chitinases so far sequenced are also classified into glycoside hydrolase families (families 18, 19, and 20), constructed on the basis of amino acid sequence resemblance of their catalytic domains. The chitinases with different family backgrounds have dissimilar amino acid sequence and completely unlike three-dimensional (3D) structures (Perrakis et al. 1994; Henrissat 1991) and molecular mechanisms. Therefore, they are likely to have evolved from diverse lineages. The family 18 chitinases hydrolyze glycosidic bonds with the retention of anomeric configuration at C1 atom (Kramer and Koga 1986). The catalytic domains of these chitinases have a fold of barrel with a catalytic groove as demonstrated by 3D structural analysis of hevamine (Kramer and Muthukrishnan 1997). These chitinases catalyze the hydrolysis of Glc-N-Ac-Glc-N-Ac and Glc-N-Ac-Glc-N- linkages. These chitinases are inhibited by allosamidine, an isomer of *N*-acetyl glucosamine. On the other hand,

the family 19 chitinases hydrolyze glycosidic bond with an inversion of anomeric configuration at C1 atom (Stinizi et al. 1993; Broglie et al. 1991). The catalytic domain of these chitinases has a fold of high helical content and structural similarity, including conserved core of the enzyme (Grison et al. 1996). They catalyze the hydrolysis of Glu-N-Ac and Gluc-N-Ac linkages only. The activity of these chitinases is insensitive to allosamidine. They catalyze the hydrolysis of chitin similar to acid-base mechanism (Grison et al. 1996; Desouza and Murray 1995). The conserved region of the catalytic domain of this family of chitinases resembles crystal structure of lysozyme (Terwisscha et al. 1996). Family 18 (subfamilies A, B, and C) includes chitinases derived mostly from fungi but also from bacteria, viruses, animals, insects, and plants. Family 19 comprises chitinases derived from plants (classes I, II, and IV), and several are derived from bacteria, e.g., *Streptomyces griseus*. Family 20 includes *N*-acetylglucosaminidase from *Vibrio harveyi* and *N*-acetylhexosaminidase from *Dictyostelium discoideum* and human (Brzezinska et al. 2014; Dahiya et al. 2006; Duo-Chuan 2006; Patil et al. 2000; Henrissat 1999). Largely, chitinases produced by a versatile group of living systems range from microbes like bacteria, fungi, and virus to insects, plants, and animals and are also present in human blood serum (Gohel et al. 2006).

Modern biotechnology has raised the development of bioprocesses to use microbes to produce value-added bio-chemicals like enzymes (Yan and Fong 2015). Chitinolytic microorganisms play an indispensable biogeochemical role in chitin bioprocessing (Ilangumaran et al. 2017). Chitinase-producing microorganisms exhibit their wide range of distribution in the environment. Not only they are present in extreme habitat like Antarctic soil, hot spring, and soda lake, but also their attendance was observed from crustaceans' waste to gut system, rhizospheric soil, and endophytic domains. These workhorses of the chitinase production company are both the eukaryotic and prokaryotic types of microorganisms. Chitinolytic fungi comprise 25–60% of the entire mold fungi, but their figure is inferior to the digit of bacteria (Brzezinska et al. 2014). The majority of the fungi belong to *Ascomycota*, whereas in bacteria, *Proteobacteria* are dominant over *Firmicutes*, *Actinobacteria*, and *Bacteroidetes* (Fig. 18.1).

Apart from the chitinase-producing capability of fungi, it is also responsible for causing various plant diseases. Plant diseases cause massive loss to the plant population together with economically important crop plants, causing misery to human beings (late blight of potato by *Phytophthora infestans* and brown spot of rice by *Helminthosporium oryzae* lead to Irish and Bengal famines, respectively) (Agrios 2005). Fungal phytopathogens are the serious intimidations to the commercial crops like cereals, potatoes, vines, fruits, and vegetables and are orthodoxly demolished by chemical fungicides. But the extensive uses of chemical fungicides are presumed to be lethal for the beneficial insects and microorganisms in the habitat soil and invade the food chain through biomagnification, leading to metabolic disorders, massive mutation, and carcinogenic effect on human beings. But modern approaches like biological control through biomolecules like chitinases for aiding sustainable agriculture give a substitute environment-friendly policy for monitoring phytopathogens like insects, fungi, and nematodes (Gaurav et al. 2017; Brzezinska et al. 2014).



**Fig. 18.1** Abundance of chitinase-producing culturable bacteria

So, microorganisms from diversified natural resources with chitinolytic activity can open a new arena in biotechnological approaches as a “green fungicide” or “green insecticide” or as a whole “green pesticide” and also can be a treasure box for human welfare as it may replace the use of chemical fungicide and insecticide.

## 18.2 Diversity of Culturable Chitinase-Producing Bacteria

Microorganisms utilize composite chitin molecule as carbon and energy source by hydrolyzing it into simple sugars known as the chitinase producers (Gaurav et al. 2017). Several natural resources are used for isolation of chitinase-producing bacteria and fungi. Such natural resources are like soil, water, shrimp shell waste, crab cell waste, fishing fields, seafood-processing industries, plant endophytes, and gut systems. The soil resources reflect great variations like agricultural, rhizospheric, mangrove, and Antarctic soils. The water resources are like hot spring, soda lake, Lonar lake, freshwater lake, marine water, and shrimp-cultivating ponds. Among the gut systems, both the vertebrate (fish and bat) and invertebrate (insect, earthworm) are explored. Chitinolytic bacterial flora consists of both the Gram-positive and Gram-negative types with respect to all the isolated fields. Among the reported culturable bacterial diversity, *Proteobacteria* is the predominant one (56.46%) followed by *Firmicutes* (27.75%), *Actinobacteria* (8.61%), *Bacteroidetes* (6.69%), and *Deinococcus-Thermus* (0.47%) (Fig. 18.1). Culturable microorganisms possess chitinase production with habitat specificity and are listed in Table 18.1.

**Table 18.1** Chitinase-producing soil bacteria

Organism	Habitat	Phylum	References
<i>Chromobacterium</i> sp.	Cultivation soil	<i>Proteobacteria</i>	Han et al. (2018)
<i>Streptomyces samsunensis</i> UAE1	Mango rhizospheric soil	<i>Actinobacteria</i>	Kamil et al. (2018)
<i>Micromonospora tulbaghiae</i> UAE1		<i>Actinobacteria</i>	
<i>Stenotrophomonas maltophilia</i>	Agricultural rhizospheric soil	<i>Proteobacteria</i>	Shaikh et al. (2018)
<i>Pseudomonas</i> sp.		<i>Proteobacteria</i>	
<i>Alcaligenes</i> sp.		<i>Proteobacteria</i>	
<i>Bacillus</i> sp.	Saline soil	<i>Firmicutes</i>	Jafari et al. (2018)
<i>Paenibacillus</i> sp.		<i>Firmicutes</i>	
<i>Staphylococcus</i> sp.		<i>Firmicutes</i>	
<i>Bacillus</i> sp.	Tea rhizospheric soil	<i>Firmicutes</i>	Vandana et al. (2018)
<i>Pseudomonas</i> sp.		<i>Proteobacteria</i>	
<i>Bacillus pumilus</i> RST25	Shellfish-processing industrial soil	<i>Firmicutes</i>	Gaurav et al. (2017)
<i>Pseudomonas</i> sp.	Avocado field soil	<i>Proteobacteria</i>	Vida et al. (2017)
<i>Serratia</i> sp.		<i>Proteobacteria</i>	
<i>Stenotrophomonas</i> sp.		<i>Proteobacteria</i>	
<i>Bacillus</i> sp. SJ-5	Soybean rhizospheric soil	<i>Firmicutes</i>	Jain et al. (2017)
<i>Enterobacter</i> sp.	Soil sample	<i>Proteobacteria</i>	Ong et al. (2017)
<i>Zymomonas</i> sp.		<i>Proteobacteria</i>	
<i>Streptomyces mexicanus</i>	Agricultural and industrial soils	<i>Actinobacteria</i>	Das et al. (2017)
<i>S. albidoflavus</i>		<i>Actinobacteria</i>	
<i>Pedobacter</i> sp. PR-M6	Decayed mushroom soil	<i>Bacteroidetes</i>	Song et al. (2017)
<i>Streptomyces</i> sp.	Vineyard soil	<i>Actinobacteria</i>	Ilangumaran et al. (2017)
<i>Pseudomonas putida</i>	Rhizospheric soil	<i>Proteobacteria</i>	Keshavarz-Tohid et al. (2017)
<i>Pseudomonas fluorescens</i>	Soil isolate	<i>Proteobacteria</i>	Alhasawi and Appanna (2017)
<i>Loktanella fryxellensis</i>	Antarctic soil	<i>Proteobacteria</i>	Shivaji et al. (2017)
<i>L. salsilacus</i>		<i>Proteobacteria</i>	
<i>L. vestfoldensis</i>		<i>Proteobacteria</i>	
<i>Pseudorhodobacter antarcticus</i>		<i>Proteobacteria</i>	
<i>P. psychrotolerans</i>		<i>Proteobacteria</i>	
<i>Robiginitomaculum antarcticum</i>		<i>Proteobacteria</i>	
<i>Roseicetrum antarcticum</i>		<i>Proteobacteria</i>	
<i>R. antarcticus</i>		<i>Proteobacteria</i>	
<i>Sphingomonas aerolata</i>		<i>Proteobacteria</i>	
<i>S. aurantiaca</i>		<i>Proteobacteria</i>	

(continued)

**Table 18.1** (continued)

Organism	Habitat	Phylum	References
<i>S. faeni</i>		<i>Proteobacteria</i>	
<i>Alteromonas stellipolaris</i>		<i>Proteobacteria</i>	
<i>Glaciecola polaris</i>		<i>Proteobacteria</i>	
<i>Granulosicoccus antarcticus</i>		<i>Proteobacteria</i>	
<i>Lysobacter oligotrophicus</i>		<i>Proteobacteria</i>	
<i>Marinomonas polaris</i>		<i>Proteobacteria</i>	
<i>Shewanella livingstonensis</i>		<i>Proteobacteria</i>	
<i>S. vesiculosa</i>		<i>Proteobacteria</i>	
<i>Antarcticimonas flava</i>		<i>Bacteroidetes</i>	
<i>Cellulophaga algicola</i>		<i>Bacteroidetes</i>	
<i>Flavobacterium collinsense</i>	Antarctic soil	<i>Bacteroidetes</i>	Shivaji et al. (2017)
<i>Gelidibacter gilvus</i>		<i>Bacteroidetes</i>	
<i>Leeuwenhoekiella aequorea</i>		<i>Bacteroidetes</i>	
<i>Muricauda antarctica</i>		<i>Bacteroidetes</i>	
<i>Pedobacter ardleyensis</i>		<i>Bacteroidetes</i>	
<i>Polaribacter sejongensis</i>		<i>Bacteroidetes</i>	
<i>Salegentibacter salegens</i>		<i>Bacteroidetes</i>	
<i>Exiguobacterium soli</i>		<i>Firmicutes</i>	
<i>Paenibacillus cookii</i>		<i>Firmicutes</i>	
<i>Planococcus maitriensis</i>		<i>Firmicutes</i>	
<i>Psychrosinus fermentans</i>		<i>Firmicutes</i>	
<i>Leifsonia rubra</i>		<i>Actinobacteria</i>	
<i>Marisediminicola antarctica</i>		<i>Actinobacteria</i>	
<i>Pseudonocardia antarctica</i>		<i>Actinobacteria</i>	
<i>Deinococcus frigans</i>		<i>Deinococcus-Thermus</i>	
<i>Bacillus pumilus</i>		<i>Firmicutes</i>	Rishad and Jisha (2016)
<i>B. aerophilus</i>		<i>Firmicutes</i>	
<i>Pseudomonas plecoglossicida</i>	Mangrove soil	<i>Proteobacteria</i>	
<i>Achromobacter insolitus</i>		<i>Proteobacteria</i>	
<i>Lysinibacillus fusiformis</i>		<i>Firmicutes</i>	
<i>Bacillus</i> sp.	Rhizospheric soil	<i>Firmicutes</i>	Thakkar et al. (2016)
<i>Aeromonas hydrophila</i>	Rhizospheric soil	<i>Proteobacteria</i>	Kuddus and Ahmad (2013)
<i>A. punctata</i>	Fish processing effluent	<i>Proteobacteria</i>	
<i>Streptomyces rimosus</i>	Agricultural soil	<i>Actinobacteria</i>	Brzezinska et al. (2013)

(continued)

**Table 18.1** (continued)

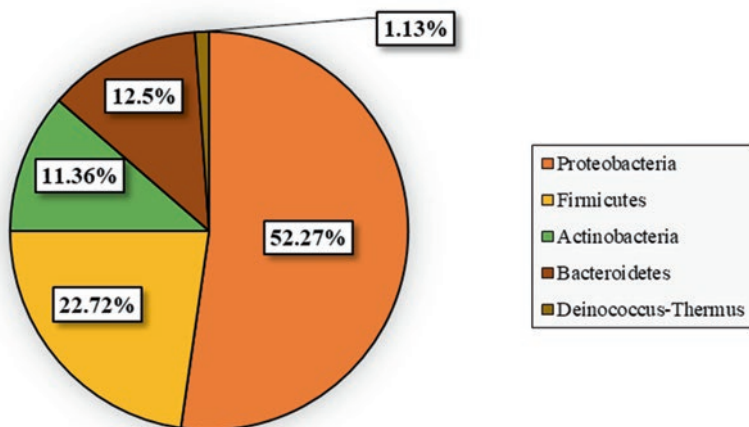
Organism	Habitat	Phylum	References
<i>Stenotrophomonas maltophilia</i>	Rhizospheric soil	<i>Proteobacteria</i>	Jankiewicz et al. (2012)
<i>Serratia</i> sp.	Rhizosphere of agronomic plant	<i>Proteobacteria</i>	Someya et al. (2011)
<i>Stenotrophomonas</i> sp.		<i>Proteobacteria</i>	
<i>Lysobacter</i> sp.		<i>Proteobacteria</i>	
<i>Mitsuaria</i> sp.		<i>Proteobacteria</i>	
<i>Paenibacillus</i> sp.		<i>Firmicutes</i>	
<i>Bacillus</i> sp.		<i>Firmicutes</i>	
<i>Erwinia</i> sp.		<i>Proteobacteria</i>	
<i>Aeromonas</i> sp.		<i>Proteobacteria</i>	
<i>Pseudomonas</i> sp.		<i>Proteobacteria</i>	
<i>Achromobacter</i> sp.		<i>Proteobacteria</i>	
<i>Flavobacterium</i> sp.		<i>Bacteroidetes</i>	
<i>Microbacterium</i> sp.		<i>Actinobacteria</i>	
<i>Bacillus pumilus</i>		Soil sample from various locations in Iran	
<i>Serratia</i> sp.	Rhizospheric soil of rice fields	<i>Proteobacteria</i>	Amin et al. (2011)
<i>Pseudomonas</i> sp.		<i>Proteobacteria</i>	
<i>Bacillus cereus</i>	Rhizospheric soil of pepper	<i>Firmicutes</i>	Mubarik et al. (2010)
<i>Bacillus licheniformis</i>	Rhizospheric soil of maize, wheat, and rice	<i>Firmicutes</i>	Kamil et al. (2007)
<i>B. thuringiensis</i>		<i>Firmicutes</i>	
<i>Stenotrophomonas maltophilia</i>		<i>Proteobacteria</i>	
<i>Bacillus</i> sp.	Soil samples from Youngduck, South Korea	<i>Firmicutes</i>	Joo et al. (1996)

### 18.2.1 Chitinase-Producing Bacteria Isolated from Soil

Reports regarding chitinase-producing soil bacteria are studied in detail so far. A list of soil bacteria with chitinolytic activity are given in Table 18.1. Among the reported bacterial diversity, *Proteobacteria* is the dominant group (52.27%) over the *Firmicutes* (22.72%), *Bacteroidetes* (12.5%), *Actinobacteria* (11.36%), and *Deinococcus-Thermus* (1.13%) (Fig. 18.2).

### 18.2.2 Chitinase-Producing Bacteria Isolated from Different Water Bodies

Chitinase-producing bacteria are also reported from various water bodies such as shrimp ponds, marine water, Lonar lake, hot spring, and moat water. Among them, shrimp-cultivating ponds are the potent container of the chitinolytic bacteria. The



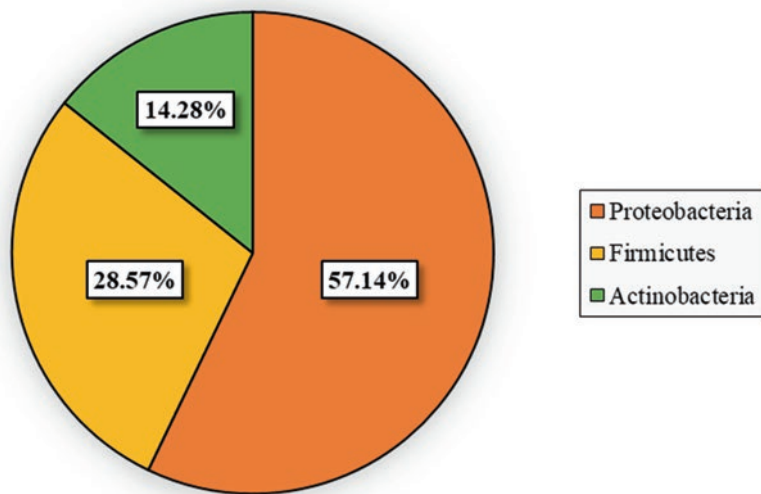
**Fig. 18.2** Diversity of chitinase-producing soil bacteria

**Table 18.2** Waterborne chitinolytic bacteria

Water body	Organism	Phylum	References
Marine water	<i>Paenibacillus</i> sp. AD	<i>Firmicutes</i>	Kumar et al. (2018)
Freshwater lake	<i>Andreprevotia lacus</i>	<i>Proteobacteria</i>	Tran et al. (2018)
	<i>Brevibacillus brevis</i>	<i>Firmicutes</i>	
	<i>Aeromonas hydrophila</i>	<i>Proteobacteria</i>	
	<i>A. salmonicida</i>	<i>Proteobacteria</i>	
	<i>Serratia plymuthica</i>	<i>Proteobacteria</i>	
Irrigation well water	<i>Pseudomonas</i> sp.	<i>Proteobacteria</i>	Tabli et al. (2018)
	<i>Serratia</i> sp.	<i>Proteobacteria</i>	
Marine water	<i>Bacillus cereus</i>	<i>Firmicutes</i>	Ravikumar and Perinbam (2016)
Hot spring	<i>Paenibacillus</i> sp.	<i>Firmicutes</i>	Chrisnasari et al. (2016)
Shrimp pond	<i>Vibrio alginolyticus</i>	<i>Proteobacteria</i>	Vincy et al. (2014)
Moat water	<i>Chitiniphilus shinanonensis</i>	<i>Proteobacteria</i>	Huang et al. (2012)
Lonar lake	<i>Streptomyces</i> sp.	<i>Actinobacteria</i>	Bansode and Bajekal (2006)
	<i>Nocardia</i> sp.	<i>Actinobacteria</i>	
	<i>Bacillus</i> sp.	<i>Firmicutes</i>	

list of chitinase-producing bacteria isolated from different water bodies are presented in Table 18.2. In the middle of all reported bacterial variations from the different water bodies, *Proteobacteria* is the mostly rich group of bacteria (57.14%) followed by *Firmicutes* (28.57%) and *Actinobacteria* (14.28%) (Fig. 18.3).





**Fig. 18.3** Chitinase-producing bacteria isolated from water bodies

**Table 18.3** Chitinolytic bacteria isolated from crab cell waste

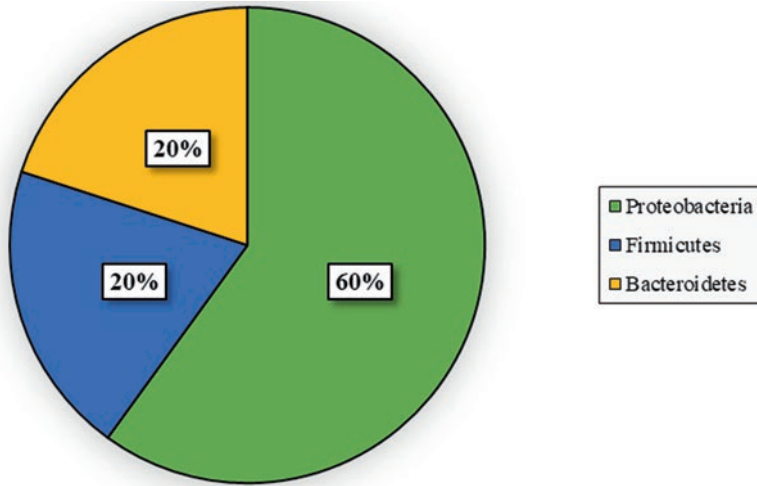
Organism	Phylum	References
<i>Vibrio aestuarianus</i>	<i>Proteobacteria</i>	Anuradha and Revathi (2013)
<i>Flavobacterium</i> sp.	<i>Bacteroidetes</i>	
<i>Shewanella</i> sp.	<i>Proteobacteria</i>	
<i>Exiguobacterium</i> sp.	<i>Firmicutes</i>	
<i>Aeromonas</i> sp.	<i>Proteobacteria</i>	Ahmadi et al. (2008)

### 18.2.3 Chitinase-Producing Bacteria Isolated from Crab Shell Waste

Crab cells are made up of chitin. Therefore, promising chitinase-producing bacteria can be isolated from these wastes. Reports regarding the chitinolytic bacteria from crab cell wastes are recorded in Table 18.3. Bacterial diversity in this area is commanded by *Proteobacteria* (60%), and the rest of the representatives are from *Firmicutes* (20%) and *Bacteroidetes* (20%) (Fig. 18.4).

### 18.2.4 Chitinase-Producing Bacteria Isolated from Shrimp Shell Waste

Shrimp shell wastes are the major sources of chitin as they are made up of chitinous exoskeleton. Reports regarding the bacteria isolated from the shrimp shell waste are enlisted in Table 18.4. Data regarding the bacterial diversity from the shrimp shell



**Fig. 18.4** Chitinase-producing bacteria isolated from crab cell waste

waste are dominated by *Proteobacteria* (66.66%) over the *Actinobacteria* (16.66%) and *Firmicutes* (16.66%), as shown in Fig. 18.5.

### 18.2.5 Chitinase-Producing Endophytic Bacteria

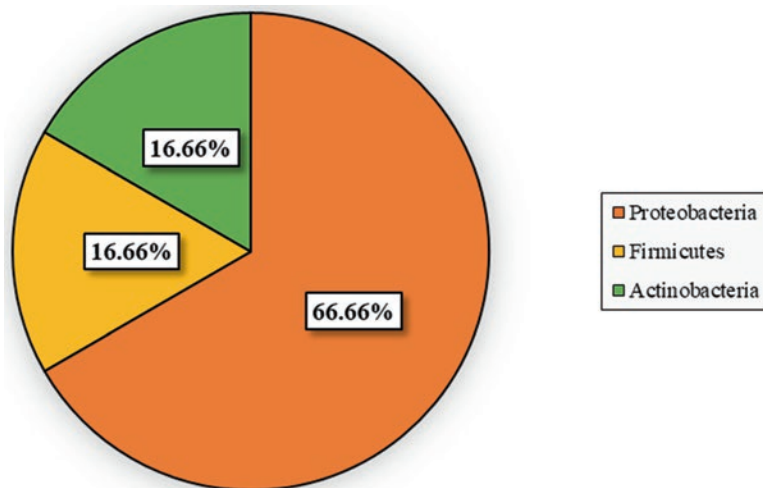
Endophytic bacteria with chitinase production ability are reported from economically important crop plants like potato, maize, and brassica. A list is given in the Table 18.5. In this area, most of the chitinolytic bacteria are from the *Proteobacteria* (40%), *Firmicutes* (40%), and *Actinobacteria* (20%) (Fig. 18.6).

### 18.2.6 Chitinase-Producing Gut Bacteria

Chitinase production by the gut bacteria is reported among the invertebrates and vertebrates. Among the invertebrates, insect and earthworm are the only reports where chitinolytic symbiotic gut microbes are observed (Tables 18.7 and 18.8). Fish and bat are the two vertebrates where chitinase-producing gut bacteria (Tables 18.6 and 18.9) are studied so far. Here, the reported gut bacteria are listed in Table 18.6.

**Table 18.4** Chitinolytic bacteria isolated from shrimp shell waste

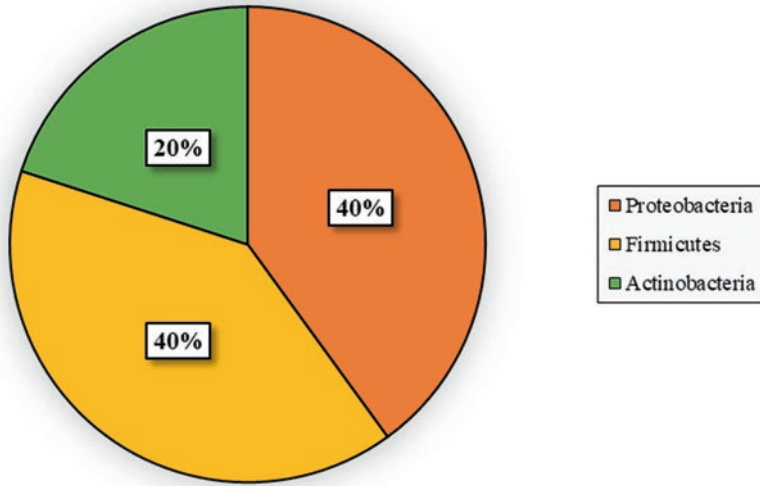
Organism	Phylum	References
<i>Paenibacillus elgii</i> TS 33	Firmicutes	Tariq et al. (2017)
<i>Acinetobacter johnsonii</i>	Proteobacteria	Setia and Suharjono (2015)
<i>Bacillus amyloliquefaciens</i>	Proteobacteria	
<i>Aeromonas hydrophila</i>	Proteobacteria	Halder et al. (2013)
<i>Streptomyces</i> sp.	Actinobacteria	Thiagarajan et al. (2011)
<i>Aeromonas</i> sp.	Proteobacteria	Ahmadi et al. (2008)



**Fig. 18.5** Chitinolytic bacteria from shrimp cell waste

**Table 18.5** Endophytic chitinolytic bacteria

Organism	Phylum	Plant	References
<i>Rhizobium</i> sp.	Proteobacteria	<i>Zea mays</i>	Patel and Archana (2017)
<i>Arthrobacter</i> sp.	Actinobacteria	Roots of <i>Brassica rapa</i>	Padder et al. (2017)
<i>Rhizobium</i> sp.	Proteobacteria		
<i>Bacillus</i> sp.	Firmicutes		
<i>Bacillus licheniformis</i>	Firmicutes	Stem tissue of <i>Solanum tuberosum</i>	Aounallah et al. (2017)



**Fig. 18.6** Chitinolytic endophytic bacteria

### 18.2.6.1 Chitinase-Producing Fish Gut Bacteria (Table 18.6)

**Table 18.6** Chitinolytic fish gut bacteria

Organism	Phylum	Fish	References
<i>Pseudomonas</i> sp. SSPZ11	<i>Proteobacteria</i>	<i>Rastrelliger kanagurt</i>	Thomas et al. (2018)
<i>Exiguobacterium</i> sp. SSPZ15	<i>Firmicutes</i>	<i>Catla catla</i>	
<i>Vibrio</i> sp.	<i>Proteobacteria</i>	<i>Paralichthys adspersus</i>	Leiva et al. (2017)
<i>Bacillus</i> sp.	<i>Firmicutes</i>		
<i>Photobacterium</i> sp.	<i>Proteobacteria</i>		
<i>Staphylococcus</i> sp.	<i>Firmicutes</i>		
<i>Carnobacterium</i> sp.	<i>Firmicutes</i>		
<i>Exiguobacterium</i> sp.	<i>Firmicutes</i>		
<i>Klebsiella</i> sp.	<i>Proteobacteria</i>		
<i>Arthrobacter</i> sp.	<i>Actinobacteria</i>		
<i>Raoultella</i> sp.	<i>Proteobacteria</i>		
<i>Kluyvera</i> sp.	<i>Proteobacteria</i>		
<i>Myroides</i> sp.	<i>Bacteroidetes</i>		
<i>Streptococcus</i> sp.	<i>Firmicutes</i>		
<i>Vagococcus</i> sp.	<i>Firmicutes</i>		
<i>Staphylococcus</i> sp.	<i>Firmicutes</i>		
<i>Acinetobacter</i> sp.	<i>Proteobacteria</i>		
<i>Psychrobacter</i> sp.	<i>Proteobacteria</i>		
<i>Lactobacillus</i> sp.	<i>Firmicutes</i>		
<i>Weissella</i> sp.	<i>Firmicutes</i>		
<i>Lactococcus</i> sp.	<i>Firmicutes</i>		
<i>Bacillus cereus</i>	<i>Firmicutes</i>	<i>Clarias gariepinus</i>	Ajayi et al. (2016)
<i>Bacillus aryabhatai</i>	<i>Firmicutes</i>	<i>Clarias batrachus</i>	Dey et al. (2016)
<i>B. flexus</i>	<i>Firmicutes</i>		
<i>B. cereus</i>	<i>Firmicutes</i>		

(continued)

**Table 18.6** (continued)

Organism	Phylum	Fish	References		
<i>Bacillus pumilus</i>	<i>Firmicutes</i>	<i>Labeo rohita</i>	Banerjee et al. (2015)		
<i>B. flexus</i>	<i>Firmicutes</i>	<i>Catla catla</i>			
		<i>Cirrhinus mrigala</i>			
<i>Pseudomonas</i> sp.	<i>Proteobacteria</i>	<i>Gadus morhua</i>	Lazado et al. (2012)		
<i>Psychrobacter</i> sp.	<i>Proteobacteria</i>				
<i>Acinetobacter johnsonii</i>	<i>Proteobacteria</i>	<i>Salmo salar</i>	Askarian et al. (2012)		
<i>Acinetobacter</i> sp.	<i>Proteobacteria</i>				
<i>Agrococcus baldri</i>	<i>Actinobacteria</i>				
<i>Bacillus cereus</i>	<i>Firmicutes</i>				
<i>B. thuringiensis</i>	<i>Firmicutes</i>				
<i>B. subtilis</i>	<i>Firmicutes</i>				
<i>Bacillus</i> sp.	<i>Firmicutes</i>				
<i>Carnobacterium</i> sp.	<i>Firmicutes</i>				
<i>Staphylococcus equorum</i>	<i>Firmicutes</i>				
<i>Staphylococcus</i> sp.	<i>Firmicutes</i>				
<i>Vibrio fischeri</i>	<i>Proteobacteria</i>			<i>Paralichthys olivaceus</i>	Sugita and Ito (2006)
<i>V. scophthalmi</i>	<i>Proteobacteria</i>				
<i>V. ichthyenteri</i>	<i>Proteobacteria</i>				
<i>V. carchariae</i>	<i>Proteobacteria</i>				
<i>V. harveyi</i>	<i>Proteobacteria</i>				
<i>V. scophthalmi</i>	<i>Proteobacteria</i>				
<i>Ferrimonas balearica</i>	<i>Proteobacteria</i>	<i>Canthigaster rivulata</i>	Itoi et al. (2006)		
<i>Pseudoalteromonas piscicida</i>	<i>Proteobacteria</i>			<i>Ditrema temmincki</i>	
<i>Grimontia hollisae</i>	<i>Proteobacteria</i>	<i>G. punctate</i>			
<i>Photobacterium damsela</i>	<i>Proteobacteria</i>	<i>Gonnistius zonatus</i>			
<i>P. leiognathi</i>	<i>Proteobacteria</i>				
<i>P. lipolyticum</i>	<i>Proteobacteria</i>				
<i>P. phosphoreum</i>	<i>Proteobacteria</i>	<i>Gymnothorax kidako</i>			
<i>P. rosenbergii</i>	<i>Proteobacteria</i>				
<i>Vibrio chagasii</i>	<i>Proteobacteria</i>	<i>Microcanthus strigatus</i>			
<i>V. fischeri</i>	<i>Proteobacteria</i>				
<i>V. fortis</i>	<i>Proteobacteria</i>				
<i>V. gallicus</i>	<i>Proteobacteria</i>				
<i>V. harveyi</i>	<i>Proteobacteria</i>				
<i>V. natrigens</i>	<i>Proteobacteria</i>				
<i>V. nigripulchritudo</i>	<i>Proteobacteria</i>		<i>Parajulis poecilepterus</i>		
<i>V. ordalii</i>	<i>Proteobacteria</i>				
<i>V. parahaemolyticus</i>	<i>Proteobacteria</i>				
<i>V. pomeroyi</i>	<i>Proteobacteria</i>				
<i>V. ponticus</i>	<i>Proteobacteria</i>	<i>Pseudocaranx dentex</i>			
<i>V. proteolyticus</i>	<i>Proteobacteria</i>				
<i>V. rumoiensis</i>	<i>Proteobacteria</i>				
<i>V. shilonii</i>	<i>Proteobacteria</i>		<i>Girella leonina</i>		
<i>V. tasmaniensis</i>	<i>Proteobacteria</i>				
<i>V. tubiashii</i>	<i>Proteobacteria</i>				

### 18.2.6.2 Chitinase-Producing Insect Gut Bacteria (Table 18.7)

**Table 18.7** Chitinolytic insect gut bacteria

Organism	Phylum	Insect	References
<i>Cellulomonas macrotermidis</i>	Actinobacteria	<i>Macrotermes barneyi</i>	Sun et al. (2018)
<i>Pseudomonas</i> sp.	Proteobacteria	<i>Plutella xylostella</i>	Indiragandhi et al. (2007)
<i>Stenotrophomonas</i> sp.	Proteobacteria		
<i>Acinetobacter</i> sp.	Proteobacteria		
<i>Serratia marcescens</i>	Proteobacteria		

### 18.2.6.3 Chitinase-Producing Earthworm Gut Bacteria (Table 18.8)

**Table 18.8** Chitinolytic earthworm bacteria

Organism	Phylum	Earthworm	Reference
<i>Pseudomonas stutzeri</i> EGB3	Proteobacteria	<i>Eisenia foetida</i>	Prasanna et al. (2014)

### 18.2.6.4 Chitinase-Producing Gut Bacteria of Bat (Table 18.9)

**Table 18.9** Chitinolytic bat gut bacteria

Organism	Phylum	Bat	References
<i>Serratia liquefaciens</i>	Proteobacteria	<i>Myotis lucifugus</i>	Whitaker et al. (2004)
<i>S. marcescens</i>	Proteobacteria	<i>M. septentrionalis</i>	
<i>Bacillus coagulans</i>	Firmicutes		
<i>B. thuringiensis</i>	Firmicutes		
<i>B. cereus</i>	Firmicutes		
<i>Enterobacter agglomerans</i>	Proteobacteria		
<i>E. aerogenes</i>	Proteobacteria		
<i>E. cloacae</i>	Proteobacteria		
<i>Hafnia alvei</i>	Proteobacteria		
<i>Citrobacter amelonaticus</i>	Proteobacteria		

Chitinase-producing bacteria from different natural resources are stated in this chapter. There are many reports available in regard to soil and water. Reports in relation to shrimp shell waste and crab cell waste are plenty, but gut bacterial reports for chitinase production are limited only in two groups, i.e., insect and earthworm

(invertebrates) and fish and bat members (vertebrates). There are vast resources of unexplored fields in relation to chitinase-producing gut microbes. Therefore, gut microorganisms possessing chitinolytic activity can be a hidden tool toward the biotechnological approaches (Figs. 18.7, 18.8, 18.9 and 18.10).

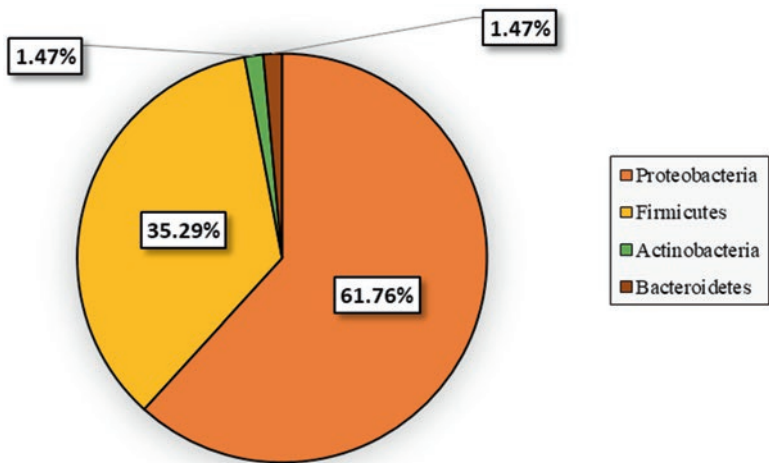


Fig. 18.7 Chitinolytic fish gut bacteria

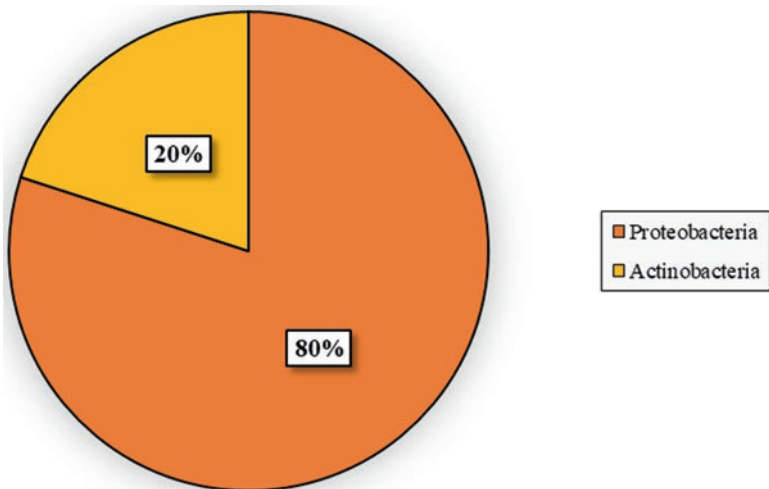
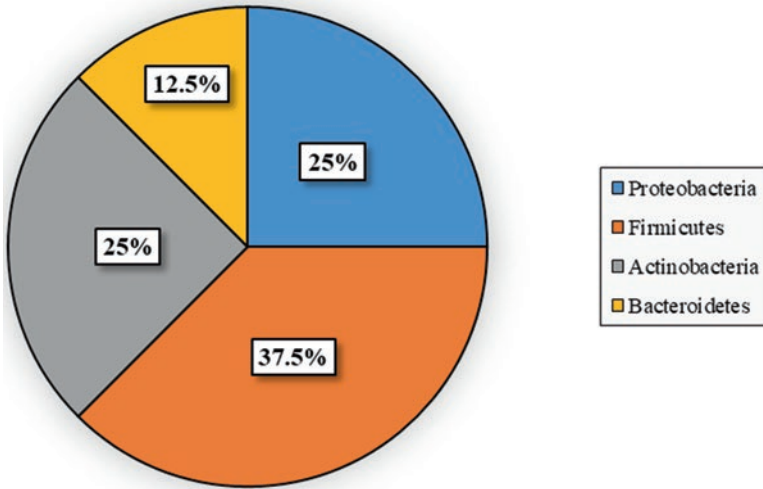
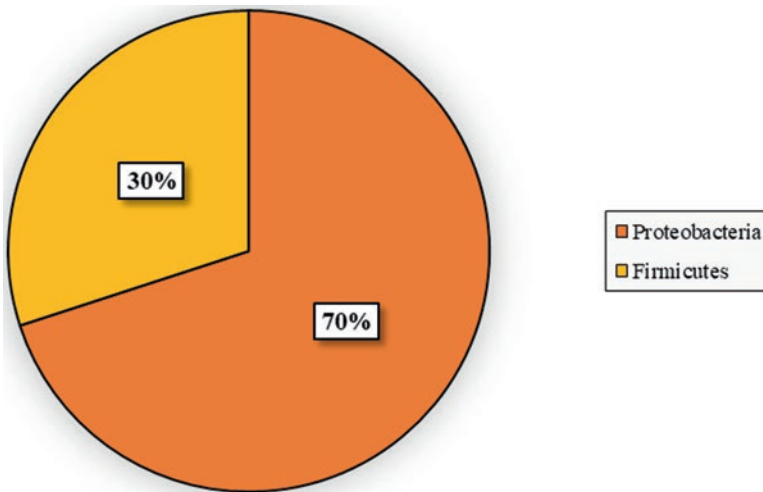


Fig. 18.8 Chitinolytic insect gut bacteria



**Fig. 18.9** Chitinolytic earthworm gut bacteria



**Fig. 18.10** Chitinolytic bat gut bacteria

### 18.3 Their Role in the Habitat

Microorganisms which utilize merged chitin molecule as carbon and energy source by hydrolyzing it into simple sugars are known as the chitinase producers (Gaurav et al. 2017). Their wide-ranging abundance has already been stated earlier. Chitinolytic microbes can be isolated from the habitats on the basis of availability of their food material like chitin. Such habitats cover from shrimp shell waste area and crab shell dumping zone to soil, water, gut environments, and so on. Microbial



residency on these types of locale plays an indispensable role to simplify the rigid chitin which subsequently produces oligomers and monomers, and these products cause several beneficial benefits toward the residing environment, chiefly as the biofertilizing, biocontrolling, and biowaste managing agents.

Among the natural resources, crustacean biowastes exclusively shrimp and crab shells have the maximum chitin content up to 60% (Chakrabarti 2002; Wang et al. 2006; Kandra et al. 2012). Annually, around  $10^{11}$  tons of chitinous ingredients are produced in the aquatic environment, but there is no considerable addition of chitin in the ocean sediments as the chitinolytic microorganisms in the aquatic ecosystem basically degrade them (Ghorbel-Bellaaj et al. 2012; Halder et al. 2012). So, the microbial population belonging to these habitats like marine water, shrimp shell waste, and crab shell waste exhibits a significant chitin-reducing activity as they utilize these biowastes as nutritional resources. Evidences are also available in support of the bacterial type isolated from these habitats (Tables 18.2, 18.3, and 18.4). Microbial residents in such type of habitats are also serving as an environmentally autoregulated biowaste management agent. Marine microorganisms have established inimitable metabolic and physiological abilities to harvest novel metabolites which are not often existing in microbes of terrestrial origin. Away from their bio-recycling capability, some marine bacteria have a good potential for the control of fungal phytopathogens and mycotoxins (Kong 2018).

Reports concerning the chitinase-producing microorganisms isolated from the variable soil environments are numerous and listed in Table 18.1. The presence of such kind of microbes plays several advantageous characters in that type of soil atmosphere. From antifungal assets are through chitinase production to plant growth-promoting properties like phosphate and zinc solubilization ability, indole 3-acetic acid and siderophore production, seed germination enhancing ability, etc. (Sarbadhikary and Mandal 2017; Kejela et al. 2017; Patel and Archana 2017; Adhikari et al. 2017). In the current scenario, the participation of microbial inoculants as biofertilizers and biocontrol agents in the agriculture industry has been growing noticeably. Microbial inoculants are favored to reduce environmental toxicity instigated by chemicals and pesticides.

In the case of gut ambience, the presence of such type of microorganisms strictly depends upon the food habit of the host because they take part in the host's digestion and nutritive processes. Microbes that degrade the dietary compounds can retain, proliferate, and establish symbiosis, and the others that are unable to degrade are washed out (Banerjee et al. 2017). In the later part of this endeavor, it can be observed that several reports are available related to gut microbes of insect, earthworm, fish, and bat that can hydrolyze chitin. These hosts are the consumers of chitinous materials, and it can be assumed that these gut microbes play a role in their digestion, vitamin synthesis, and antifungal activity with their chitinolytic efficiency (Dillon and Dillon 2004; Genta et al. 2006).

So, in this framework, the role of the chitinase producers in their habitats stands with a great biotechnological importance for modern-day sustainable agriculture, which leads to a pronounced human welfare phenomenon by replacing ecotoxic chemical fertilizers, fungicides, and pesticides.

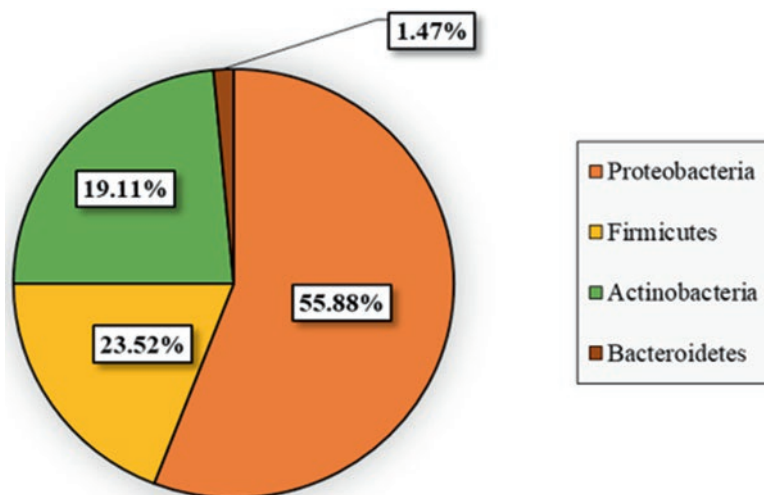
## 18.4 Potential Applications

Microbial enzymes are relatively more stable than corresponding enzymes derived from plants or animals (Wiseman 1995). Enzymes of microbial origin have been used in various industries for many centuries. Enzymes from microbial sources are widely used in industrial processes mainly because of their low cost, large productivity, vast availability, chemical stability, and flexibility (Banerjee et al. 2016), and bacterial chitinases are such kind of biomolecules. Chitinase enzyme has received increased attention due to its wide range of biotechnological applications, especially in agriculture for biocontrol of phytopathogenic fungi and harmful insects (Kuddus and Ahmad 2013). Chitinases are with immense importance in the biotechnology and bioprocessing ranges; because of their versatile potentiality as pesticide (against fungi, insects, and nematodes), they induce plant disease resistance, alternative petroleum feedstock, waste water management, marine by-products treatment (shrimp shell waste and sea food degradation), pharmaceutical industry activities (chitosaccharides), protoplast isolation from fungi and yeast, and preparation of single-cell protein (Kumar et al. 2018; Mao et al. 2017; Ilangumaran et al. 2017; Honda et al. 2017; Wang and Liang 2017; Aggarwal et al. 2015; Brzezinska et al. 2014; Halder et al. 2013; Mubarik et al. 2010).

### 18.4.1 Induce Plant Defense System

Biocontrol activities and plant growth-promoting potentialities are not only synchronized by the bacterial chitinolytic property but also obtained by the derivatives of chitin molecules. Their operational machineries are the outcome in direct antimicrobial responsibilities, stimulation of plant defense responses, and plant metabolic activity (El Hadrami et al. 2010; Ramírez et al. 2010). Chitosan has the capability to prevent the growth of a variety of bacteria and fungi (Rabea et al. 2003; El Hadrami et al. 2010; Xia et al. 2011; Sharp 2013). The antimicrobial potentiality of chitosan is known for its cationic features, which disrupt potassium signaling cascade in pathogens. Furthermore, chitosan interrupts membrane integrity of vacuoles and endomembrane organelles in fungal pathogens (Rabea et al. 2003; Sharp 2013). One such example was investigated by O'Herlihy et al. (2003) where chitosan exhibits the inhibitory activity against *Phytophthora capsici* and *P. infestans*. Another improvised nanotechnology-based work has been revealed by Chandra et al. (2015) where the chitosan nanoparticles (CNP) are capable of inducing and augmenting immune response in plants. CNP-treated leaves of *Camellia sinensis* produced substantial progress in the plant's innate immune response by the induction of defense enzyme activity, upregulation of defense-related genes including that of several antioxidant enzymes, and elevation of the levels of total phenolics (Fig. 18.11).

Chitin oligosaccharides perform as pathogen-associated molecular patterns (PAMPs) due to their structural resemblance to the ingredients of pathogen cell wall in various plant pathosystems. PAMPs are accepted by host transmembrane pattern recognition receptors (PRRs), which signal defense corridors of induced systemic

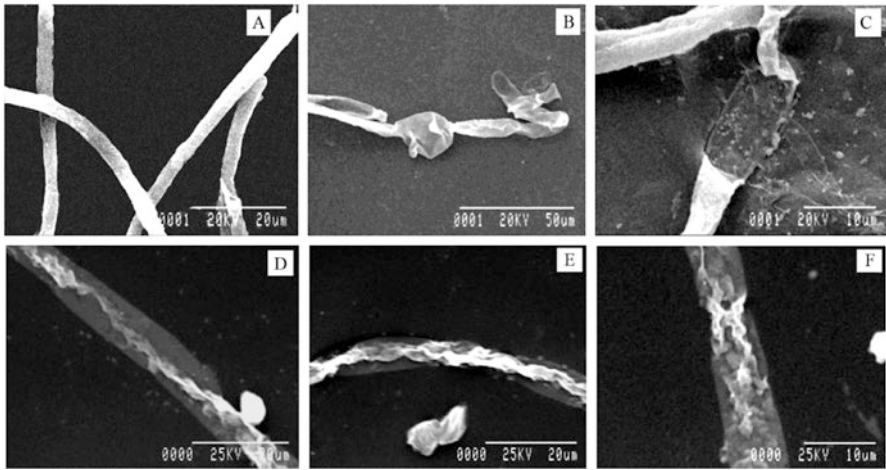


**Fig. 18.11** Antifungal bacterial diversity

resistance (ISR) and systemic acquired resistance (SAR) (Eckardt 2008; Zipfel 2009). As a result, when real pathogen occurrence happens, the plant disease resistance mechanisms deliberately boosted protection against it. Thus, chitin derivatives attained from microbial degradation of crustaceans shells can be applied as elicitors of innate and systemic immune responses in plants (Benhamou 1996; Jones and Dangl 2006). The chitinous extracts assembled from microbial degradation were applied to induce disease resistance in *Arabidopsis thaliana* against *Pseudomonas syringae* pv. tomato DC3000 and *Botrytis cinerea* (Ilangumaran et al. 2017).

#### 18.4.2 Antifungal Activity of Bacterial Chitinase

Awareness in biological control has amplified over the past decades. The necessity for the replacements of chemical fungicides arises because of their penetration into the food chain which leads to the human health hazard and establishes resistant phytopathogens and also accelerates environmental contamination in parallel. Recently, biological control has been dedicated on bacteria-producing mycolytic enzymes, exclusively chitinases, recognized to hydrolyze chitin, a key element of fungal cell walls. In this context, antagonistic bacterial chitinases provide an environmentally sound substitute to synthetic chemicals because of their perceived safety and inferior environmental impact. Biological control policies have turned into an imperative attitude for aiding sustainable agriculture (Brzezinska et al. 2014; Berg and Hallmann 2006). Commercial biocontrol representatives mainly belong to the spore-forming bacteria because of their durability in a diversity of formulations and field environments for an extended period even under adverse situations (Subbanna et al. 2018).



**Fig. 18.12** Degradation of fungal (*Rhizopus stolonifer*) cell wall by chitinase-producing bacterial strains (Ghosh et al. 2015)

The mainstream of pathogenic fungi comprises chitin and  $\beta$ -(1,3) glucan in their cell walls (Bartnicki-Garcia 1968), and disbanding or disruption of these organizational polymers has negative consequences over the growth and differentiation of fungi (Poulose 1992). One of the key antagonist apparatuses used by the biocontrol agents for these types of phytopathogens is the enzymatic disintegration of cell walls heading to leakage of fungal protoplasm (Lim et al. 1991; Kim and Chung 2004). Cell wall-degrading enzymes, especially chitinolytic enzyme-producing biocontrolling bacteria, are able to effectively control plant pathogenic fungi in this way (Broglie et al. 1991; Ordentlich et al. 1988) (Fig. 18.12). Abilities of bacteria to produce antifungal chitinase are widely known (Table 18.10), and the majority of biocontrolling bacteria belong to *Proteobacteria* (55.88%), *Firmicutes* (23.52%), *Actinobacteria* (19.11%), and *Bacteroidetes* (1.47%).

### 18.4.3 Insecticidal Activity of Bacterial Chitinase

Insect infestation is a major issue of many agronomic crops. Insects attack more than 500 plant species belonging to 63 plant families. Insects are the vector of plant virus member especially of the geminivirus group. Some diseases associated with the whitefly are lettuce necrotic yellows, irregular ripening of tomato, silver leaf of squash, cotton leaf curl, tobacco leaf curl, and cassava mosaic. Meanwhile, chitin-scavenging enzymes are applied to renovate chitin-holding raw material into biotechnologically serviceable apparatuses; they are a significant concern of chemical and pharmaceutical activities (Aggarwal et al. 2015).

In insects, the dynamic configurations such as exoskeleton, appendages, peritrophic membrane, etc. are made up of chitin as a chief structural element. Therefore, the growth and development are intensely administrated by building and

**Table 18.10** Antifungal activity of bacterial chitinases

Bacteria	Phylum	Antagonistic against	References
<i>Chromobacterium</i> sp.	<i>Proteobacteria</i>	<i>Cylindrocarpon destructans</i>	Han et al. (2018)
<i>Streptomyces samsunensis</i> UAE1	<i>Actinobacteria</i>	<i>Lasiodiplodia theobromae</i>	Kamil et al. (2018)
<i>Micromonospora tulbaghia</i> UAE1	<i>Actinobacteria</i>		
<i>Bacillus</i> sp.	<i>Firmicutes</i>	<i>Rhizoctonia solani</i>	Vandana et al. (2018)
<i>Pseudomonas</i> sp.	<i>Proteobacteria</i>	<i>Corticium invisum</i> <i>Fomes lamanensis</i>	
<i>Aeromonas salmonicida</i> SWSY-1.411	<i>Proteobacteria</i>	<i>Trichoderma reesei</i>	Tran et al. (2018)
<i>A. salmonicida</i> SWSY-1.31	<i>Proteobacteria</i>		
<i>Serratia plymuthica</i> SWSY3.47	<i>Proteobacteria</i>		
<i>Pseudomonas</i> sp.	<i>Proteobacteria</i>	<i>Aspergillus niger</i>	Tabli et al. (2018)
<i>Serratia</i> sp.	<i>Proteobacteria</i>	<i>Botrytis cinerea</i> <i>Pythium aphanidermatum</i>	
<i>Coralloccoccus</i> sp. EGB	<i>Proteobacteria</i>	<i>Verticillium dahliae</i>	Li et al. (2017)
		<i>Fusarium oxysporum</i>	
		<i>Ustilagoidea vires</i>	
<i>Pseudomonas</i> sp.	<i>Proteobacteria</i>	<i>Rosellinia necatrix</i>	Vida et al. (2017)
<i>Serratia</i> sp.	<i>Proteobacteria</i>		
<i>Stenotrophomonas</i> sp.	<i>Proteobacteria</i>		
<i>Bacillus</i> sp. SJ-5	<i>Firmicutes</i>	<i>Rhizoctonia solani</i>	Jain et al. (2017)
		<i>Fusarium oxysporum</i>	
<i>Bacillus pumilus</i> RST25	<i>Firmicutes</i>	<i>Fusarium solani</i>	Gaurav et al. (2017)
		<i>Aspergillus niger</i>	
		<i>Fusarium solani</i>	
<i>Paenibacillus elgii</i> .	<i>Firmicutes</i>	<i>Fusarium solani</i>	Tariq et al. (2017)
		<i>Aspergillus parasiticus</i>	
		<i>A. fumigates</i>	
<i>Pedobacter</i> sp. PR-M6	<i>Bacteroidetes</i>	<i>Rhizoctonia solani</i>	Song et al. (2017)
		<i>Botrytis cinerea</i>	
<i>Pseudomonas</i> sp.	<i>Proteobacteria</i>	<i>Colletotrichum gloeosporioids</i>	Kejela et al. (2017)
		<i>Fusarium oxysporum</i>	
<i>Bacillus</i> sp.	<i>Firmicutes</i>	<i>Fusarium oxysporum</i>	Abdallah et al. (2017)
<i>Paenibacillus ehimensis</i> MA2012	<i>Firmicutes</i>	<i>Colletotrichum gloeosporioides</i>	Seo et al. (2016)
<i>Pseudoalteromonas piscicida</i>	<i>Proteobacteria</i>	<i>Aspergillus niger</i>	Paulsen et al. (2016)
		<i>Botrytis cinerea</i>	
<i>Burkholderia cenocepacia</i> VBC7	<i>Proteobacteria</i>	<i>Rhizopus stolonifer</i>	Ghosh et al. (2015)
<i>Pseudomonas poae</i> VBK1	<i>Proteobacteria</i>		

(continued)

**Table 18.10** (continued)

Bacteria	Phylum	Antagonistic against	References
<i>Streptomyces vinaceusdrappus</i> S5MW2	Actinobacteria	<i>Rhizoctonia solani</i>	Yandigeri et al. (2015)
<i>Streptomyces scabrisporus</i>	Actinobacteria	<i>Bipolaris sorokiniana</i>	Wang et al. (2015)
		<i>Fusarium oxysporum</i>	
		<i>Rhizoctonia solani</i>	
		<i>Phytophthora capsici</i>	
<i>Streptomyces sporovirgulis</i> <i>S. rimosus</i>	Actinobacteria	<i>Alternaria alternata</i>	Brzezinska et al. (2014)
		<i>Fusarium solani</i>	
<i>Brevibacillus laterosporus</i>	Firmicutes	<i>Fusarium equiseti</i>	Prasanna et al. (2013)
<i>Aeromonas hydrophila</i> SBK1	Proteobacteria	<i>Aspergillus flavus</i>	Halder et al. (2013)
		<i>Fusarium oxysporum</i>	
<i>Stenotrophomonas maltophilia</i>	Proteobacteria	<i>Fusarium solani</i>	Suma and Podile (2013)
		<i>F. oxysporum</i>	
		<i>Rhizoctonia solani</i>	
		<i>Alternaria alternata</i>	
<i>Bacillus cereus</i> IO8	Firmicutes	<i>Botrytis cinerea</i>	Hammami et al. (2013)
<i>Stenotrophomonas maltophilia</i>	Proteobacteria	<i>Fusarium solani</i>	Jankiewicz et al. (2012)
		<i>F. oxysporum</i>	
		<i>Rhizoctonia solani</i>	
		<i>Alternaria alternata</i>	
<i>Streptomyces roseolus</i> DH	Actinobacteria	<i>Aspergillus</i> sp.	Jiang et al. (2012)
		<i>Rhizopus chinensis</i>	
		<i>Penicillium</i> sp.	
		<i>Mucor</i> sp.	
<i>Serratia marcescens</i> B4A	Proteobacteria	<i>Rhizoctonia solani</i>	Zarei et al. (2011)
		<i>Bipolaris</i> sp.	
		<i>Alternaria raphani</i>	
		<i>A. brassicicola</i>	
<i>Serratia</i> sp. CN-01	Proteobacteria	<i>Fusarium oxysporum</i>	Amin et al. (2011)
<i>Serratia</i> sp. CN-07	Proteobacteria		
<i>Pseudomonas</i> sp. CN-05	Proteobacteria		
<i>Pseudomonas fluorescens</i>	Proteobacteria	<i>Rhizoctonia solani</i>	El-Mougy et al. (2011)
		<i>Fusarium solani</i>	
<i>Streptomyces tendae</i> TK-VL_333	Actinobacteria	<i>Aspergillus niger</i>	Kavitha and Vijayalakshmi (2011)
		<i>Fusarium oxysporum</i>	
<i>Bacillus thuringiensis</i> subsp. <i>colmeri</i> 15A3	Firmicutes	<i>Rhizoctonia solani</i>	Liu et al. (2010)
		<i>Botrytis cinerea</i>	
		<i>Penicillium chrysogenum</i>	
		<i>P. piricola</i>	
		<i>P. glaucum</i>	
		<i>Sclerotinia fuckeliana</i>	

(continued)

**Table 18.10** (continued)

Bacteria	Phylum	Antagonistic against	References
<i>Bacillus pumilus</i> SG2	Firmicutes	<i>Fusarium graminearum</i>	Ghasemi et al. (2010)
		<i>Rhizoctonia solani</i>	
		<i>Magnaporthe grisea</i>	
		<i>Sclerotinia sclerotiorum</i>	
		<i>Trichoderma reesei</i>	
		<i>Botrytis cinerea</i>	
		<i>Bipolaris</i> sp.	
<i>Streptomyces</i> sp. DA11	Actinobacteria	<i>Aspergillus niger</i>	Han et al. (2009)
		<i>Candida albicans</i>	
<i>Rhizobium</i> sp.	Proteobacteria	<i>Aspergillus flavus</i>	Sridevi and Mallaiah (2008)
		<i>A. niger</i>	
		<i>Curvularia lunata</i>	
		<i>Fusarium udum</i>	
<i>Streptomyces hygroscopicus</i>	Actinobacteria	<i>Colletotrichum gloeosporioides</i>	Prapagdee et al. (2008)
		<i>Sclerotium rolfsii</i>	
<i>Bacillus cereus</i> YQQ 308	Firmicutes	<i>Fusarium oxysporum</i>	Chang et al. (2007)
		<i>F. solani</i>	
		<i>Pythium ultimum</i>	
<i>Serratia plymuthica</i> C-1	Proteobacteria	<i>Phytophthora capsici</i>	Kim et al. (2007)
<i>Chromobacterium</i> sp. C-61	Proteobacteria	<i>Rhizoctonia solani</i>	
<i>Lysobacter enzymogenes</i> C-3	Proteobacteria	<i>Fusarium oxysporum</i>	
		<i>F. solani</i>	
<i>Bacillus licheniformis</i>	Firmicutes	<i>Rhizoctonia solani</i>	Kamil et al. (2007)
<i>B. licheniformis</i>	Firmicutes	<i>Macrophomina phaseolina</i>	
<i>B. thuringiensis</i>	Firmicutes	<i>Fusarium culmorum</i>	
<i>Stenotrophomonas maltophilia</i>	Proteobacteria	<i>Pythium</i> sp.	
		<i>Alternaria alternata</i>	
		<i>Sclerotium rolfsii</i>	
<i>Streptomyces halstedii</i> AJ-7	Actinobacteria	<i>Alternaria alternata</i>	Joo (2005)
		<i>Botrytis cinerea</i>	
		<i>Fusarium oxysporum</i>	
<i>Enterobacter</i> sp. NRG4	Proteobacteria	<i>Fusarium moniliforme</i>	Dahiya et al. (2005)
		<i>Aspergillus niger</i>	
		<i>Mucor rouxii</i>	
		<i>Rhizopus nigricans</i>	
<i>Vibrio pacini</i>	Proteobacteria	<i>Mucor racemosus</i>	Bao-qin et al. (2004)
		<i>Trichoderma viride</i>	
		<i>Zygorhynchus heterognmus</i>	

(continued)

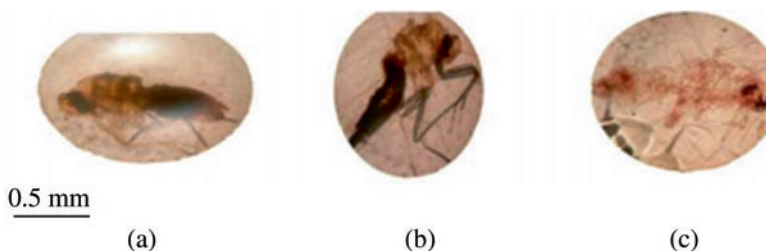
**Table 18.10** (continued)

Bacteria	Phylum	Antagonistic against	References
<i>Pseudomonas</i> sp.	<i>Proteobacteria</i>	<i>Macrophomina phaseolina</i>	Gohel et al. (2004)
<i>Pantoea dispersa</i>	<i>Proteobacteria</i>	<i>Fusarium</i> sp.	
<i>Enterobacter amnigenus</i>	<i>Proteobacteria</i>		
<i>Serratia plymuthica</i> HRO-C48	<i>Proteobacteria</i>	<i>Botrytis cinerea</i>	Frankowski et al. (2001)
<i>Serratia marcescens</i> strain B2	<i>Proteobacteria</i>	<i>Botrytis cinerea</i>	Someya et al. (2001)
<i>Alcaligenes xylosoxydans</i>	<i>Proteobacteria</i>	<i>Fusarium</i> sp.	Vaidya et al. (2001)
		<i>Rhizoctonia bataticola</i>	
<i>Bacillus</i> sp. 739	<i>Firmicutes</i>	<i>Fusarium oxysporum</i>	Melent'ev et al. (2001)
		<i>F. culmorum</i>	
		<i>Helminthosporium sativum</i>	
<i>Serratia marcescens</i>	<i>Proteobacteria</i>	<i>Sclerotinia minor</i>	Tarabily et al. (2000)
<i>Streptomyces viridodlasticus</i>	<i>Actinobacteria</i>		
<i>Micromonospora carbonacea</i>	<i>Actinobacteria</i>		
<i>Paenibacillus</i> sp. 300	<i>Firmicutes</i>		
<i>Streptomyces</i> sp. 385	<i>Actinobacteria</i>	<i>Fusarium oxysporum</i>	Singh et al. (1999)
<i>Bacillus</i> sp. BG-11	<i>Firmicutes</i>	<i>Rhizopus arrhizus</i>	Bhushan (1998)
		<i>Rhizoctonia solani</i>	
		<i>Sclerotium rolfsii</i>	
		<i>Phytophthora infestans</i>	
		<i>Fusarium oxysporum</i>	
		<i>Phanerochaete chrysosporium</i>	
<i>Serratia marcescens</i>	<i>Proteobacteria</i>	<i>Sclerotium rolfsii</i>	Ordentlich et al. (1988)

transformation of these chitinous assemblies (Merzendorfer and Zimoch 2003). Thus, addition of chitinolytic enzymes can interrupt in the basic functional progressions similar to ecdysis and redevelopment of peritrophic membrane. Reports suggest chitinase enhanced destruction to the peritrophic membrane of the insect gut (Subbanna et al. 2018). In that way, the creation of a less operative barricade results in appreciable decline in feeding and reduction in the proficiency of digestive procedure, nutritional consumption, and growth. Apart from the straight destruction of peritrophic membrane, chitinases can also perform physical malformations in midgut epithelial cells, like bloating, elongations, and creations of several vacuoles (Terra and Ferreira 2005; Otsu et al. 2003; Gongora et al. 2001; Wiwat et al. 2000).

As the exo-skeletal and other portions of the insects are made up of chitin, prospective chitinolytic bacterial isolates are taking place as a promising biopesticide in the field of improvised biotechnology (Singh et al. 2016). Biocontrol of such insects through potent chitinolytic bacteria is reported so far and can be applied as





**Fig. 18.13** Degradation of whitefly (*Bemisia tabaci*) exoskeleton with *Bacillus cereus* chitinase [(a) Control whitefly; (b) day 1, treatment with bacterial chitinase; (c) day 3, degradation of insect exoskeleton] (Mubarik et al. 2010)

insecticides to control these plant pests (Merzendorfer and Zimoch 2003). According to Aggarwal et al. (2015), a potent chitinase producer, *Serratia marcescens*, demonstrates the highest mortality range of *Spodoptera litura* larvae up to the level 70.8%. Another evidence shows the efficiency of *Bacillus cereus* as a biocontrol agent upon agronomic pest like *Bemisia tabaci* (Mubarik et al. 2010). The potentiality of exoskeleton degradation of the whitefly treated with chitinase isolated from *B. cereus* is given in Fig. 18.13. Keeping the evidences alive, Otsu et al. (2003) exhibit that chitinase-secreting *Alcaligenes paradoxus* KPM-012A was exploited as a biocontrol agent of phytophagous ladybird beetles *Epilachna vigintioctopunctata*. The use of biocontrol agent *Bacillus thuringiensis* H1 has a promising effect on different stages of *Musca domestica* lifecycles (Salama et al. 2016).

Reports regarding the significant plant pest control by the chitinolytic bacteria are reported in such forms like larval developmental control of pests and can be exemplified by *Trichoplusia ni* (Broadway et al. 1998), *Helicoverpa armigera* (Chandrasekaran et al. 2012; Singh et al. 2016), and *Malacosoma neustria* (Danismazoglu et al. 2015) and sucking pests like *Myzus persicae* (Broadway et al. 1998; Rahbe and Febvay 1993), *Bemisia argentifolii*, *Hypothenemus hampei* (Broadway et al. 1998), and *Hypothenemus hampei* (Martínez et al. 2012).

#### 18.4.4 Antagonistic Effect Against Nematodes

Apart from the antifungal and insecticidal fitness, the chitinolytic bacteria also exhibit their nematocidal property against the plant parasites. Nematodes are key agricultural pests of potatoes and in some other crops. Economic crop miscarriage can happen when the nematode population in soil is extraordinarily high. Chemical nematicides are operative but are very toxic to humans and are environmentally hurtful. In search of such alternative, certain bacteria can diminish nematode mobility (Stirling 1984), while other bacteria are on the right path and can produce combinations lethal to plant-parasitic nematodes (Sikora 1991; Spiegel et al. 1991; Oostendorp and Sikora 1990). One such investigation is chitinase-producing soil isolates like *Chromobacterium* sp. UP1 and *Stenotrophomonas maltophilia* MI-12, which inhibited egg hatch of the potato cyst nematode, *Globodera rostochiensis*, up

to 70% as the main constituent of the eggshell of *G. rostochiensis* is chitin (Cronin et al. 1997; Clarke and Hennessy 1976).

Nematode eggs are mainly composed of chitin as the chief structural ingredient. This chitinous facility offers resistance counter to chemical and biological nematocides (Wharton 1980). Chitinases are known to affect egg hatching of many parasitic nematodes like *Meloidogyne hapla* (Mercer et al. 1992), *M. incognita* (Lee and Kim 2015; Nguyen et al. 2007; Jung et al. 2002), *M. javanica* (Spiegel et al. 1991), and *M. arenaria* (Kalaiarasan et al. 2006) by disfiguring and vandalizing the egg shells, leading to either suppression of hatching (Cronin et al. 1997; Lee and Kim 2015) or premature exposure of juveniles which are ineffectual to persist in soil environment (Jung et al. 2002). However, some studies reported discrepancy in susceptibility of eggs and juvenile to chitinases.

In connection with antifungal, insecticidal, and nematicidal properties, there is an upsurge of attention to evolve environment-friendly plant pest-controlling substitutions like chitinase-producing bacteria. This investigation was conducted to travel the unexplored areas of chitinolytic microbes' hub and their possible application as a green pesticide.

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## 18.5 Conclusions

Chitin in the environment is both abundant and prevalent at the same time. Actually, it is the second most abundant biodegradable biopolymer on earth, next to cellulose. Chitin is found in many lifeforms, such as shells (shrimps and crabs), exoskeletons and gut linings of arthropods (crustaceans and insects), and cell walls of several fungi, including some yeasts and structural framework unit of some protista as well as of nematode eggs. The biomolecules that can solubilize that inflexible chitin are known as chitinases. Chitinase can be produced from bacteria, fungi, viruses, plants, and human also. Plant chitinase is produced as a PR protein in response to its defense mechanisms. Bacterial chitinases are recorded from different natural resources like diverse soil and water habitats and shrimp and crab shell waste and also from altered gut systems. Numerous varieties of soil environments are the residence of so many types of chitinolytic bacterial groups. The variants of soil backgrounds are ranging from Antarctic to mangrove, vineyard, agricultural field, and rhizospheric soils of several categories like tea, mango, wheat, maize, rice, and pepper plants. Chitinase-producing bacteria are the resident among the wide range of water bodies from marine to freshwater, hot spring, irrigation well, Lonar lake, shrimp pond, and moat water. These chitinolytic bacteria are the dwellers not only of soil and water but also of shrimp and crab waste dumping area. Interestingly, they are also reported as plant endophytes of agronomic plant parts like root, stem, and leaves. Apart from the rhizospheric soil appearance to endophytic residence, chitinase producers are also present in both the vertebrate and invertebrate gut environments such as fish, bat, insect, and earthworm.

In connection with the abundance of the chitinolytic bacteria in both the endophytic and the endozoic manner, it can be stated that these chitinase-producing

bacteria can deliver metabolic competences, necessary nutrients, and protection against pathogens through enzymatic performances which seem to share evolutionary trends. Many microbial genomes possess different genes encoding chitinolytic enzymes, which have been extensively investigated, but studies regarding the use of microorganisms that utilize insoluble chitin as a carbon source in the area of gut system are sparse. Study of chitinolytic gut microflora is in its infancy; only a few have been studied in adequate detail. As there is versatility within the animal population in terms of population size, habitat, feeding habit, etc., it may be expected that gut microflora can be a gem container consisting of several chitinase producers.

Reported investigations regarding the uses of chitinases and potent chitinolytic microorganisms especially bacteria in the biotechnologically advanced sustainable agriculture are receiving immense attention. From the biocontrol potentiality to biofertilizing ability, these microorganisms approach a new bio-based concept that can reduce the use of chemical fungicides, pesticides, and fertilizers with the assistance of such natural chitinase producers. These chitinolytic bacteria can, therefore, be used as a raw material in biotechnology for environmentally safe and affordable agriculture that leads to human welfare.

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## 18.6 Future Perspectives

- Fungicidal and insecticidal activity of bacterial chitinase may supplement the use of chemical fungicides and insecticides.
- Bioaccumulation of fungicide and insecticide in agronomic crop fields leads to human health risk by biomagnification.
- Inductive plant defense mechanism through the by-products of microbial chitinases like chitooligomers and monomers will secure more pest control potentiality.
- Formulation of microbes as biofertilizers with capabilities like plant growth-promoting traits can create a novel biotechnologically advanced agronomic tool.

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