Gut Microbiota from Lower Groups of Animals: An Upcoming Source for Cellulolytic Enzymes with Industrial Potentials

Gargi Nandy 1,†, Modhurima Chakraborti 2,†, Arnab Shee 1,†, Gautam Aditya 1,†, Krishnendu Acharya 2,*

1 Department of Zoology, University of Calcutta, 35, Ballygunge Circular Road, Kolkata-700 019, India
2 Molecular and Applied Mycology and Plant Pathology Laboratory, Centre of Advanced Study, Department of Botany, University of Calcutta, 35, Ballygunge Circular Road, Kolkata-700 019, India
* Correspondence: krish_paper@yahoo.com;
† These authors contributed equally to this work.

Abstract: Cellulosic plant materials are a reliable source of renewable energy. Cellulose-based plant materials are now being used for bioenergy production as alternatives to fossil fuels. The traditional way of converting lignocellulosic materials to ethanol and other bioenergy is an expensive and environmentally unsafe process. Several research works have been conducted to find outsource of low-cost cellulolytic enzymes. Initially, fungal species were considered as sources of cellulolytic enzymes. Later on, several studies showed that bacterial species are a more potent source of cellulose-degrading enzymes. Phytophagous lower invertebrates are a good source of cellulolytic gut bacteria. They utilize a wide variety of plant materials as their food source. In this review, thorough literature studies have been made to explore the invertebrate groups that are novel sources of cellulolytic gut bacteria with high efficacy for enzyme production. This study also encompasses a brief description of cellulose, the activity, and cellulase enzyme application in industrial aspects.

Keywords: renewable energy; cellulose; cellulase; lower invertebrates; cellulolytic gut bacteria; microorganisms.

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1. Introduction

Lignocellulosic biomass is the most abundant biological macromolecules in nature. It can be a promising source of renewable raw materials for the production of biofuels and various chemicals[1-12]. The plant cell wall comprises 35-50% cellulose and 20-35% hemicellulose with 5-30% lignin that together provides 90% of the dry weight of plant materials[2]. These huge amounts of biomasses are ultimately disposed of as waste materials in nature. But proper processing of these lignocellulosic wastes can mitigate the environmental and energetic demand for sustainable and renewable bioenergy [3,13-16]. Recent trends have adopted cellulosic raw materials over fossil fuels [10,13,17,18] because of their several drawbacks. Brazil is the pioneered country in utilizing renewable energy and produces ethanol from sugarcane since the 1970s [13]. But the processing of these energy resources through instrument intensive, the thermochemical treatment process is very expensive [19] and needs an alternative one. The traditional way of converting lignocellulosic materials to ethanol requires acid-reliant hydrolysis and fermentation steps, which ended up with the formation of
a large amount of calcium sulfate deposited as waste materials with some adverse effects on the environment [13]. The development of environmentally safe and economically feasible technologies for cellulase production is the key requirement for successfully utilizing plant biomass as a viable and foreseeable carbon source. Enzymatic degradation by cellulase or hemicellulase is the cost-effective way to saccharify cellulose and hemicellulose, respectively [20,21] to its monomer [22] hexose and pentose residues. Other hydrolytic enzymes such as pectinase, xylanase, and ligninase also ensure a high rate of degradation of the cellulose to its monomer and a high yield of biofuels lignocellulosic plant biomass [23]. The rate and efficacy of ethanol production from these monomers solely depend on the fermentation efficiency and enzymatic activity of microorganisms. These enzymes have potential application in food processing, winery, textile and laundry industry, paper and pulp preparation, animal feed, agricultural industry, and waste management process [1,24-28]. In bioethanol's industrial production, basic yeast *Saccharomyces cerevisiae* is used as it has some unique features, including high productivity of ethanol and alcohol tolerance [6,29-32]. But the activity of *Saccharomyces cerevisiae* gradually decreases due to byproduct inhibition and thus restricts its application for industrial use [33,34]. Thus identification and isolation of impeccable microorganisms with high production efficacy, high yield of several biofuels, and resistances to inhibitors are the necessary steps for industrial production of biofuels from cellulosic raw materials[30,35]. Initially, several cellulose digestive enzymes have been isolated from several fungal species, but they have some limitations, including low specific activity, low thermal stability, and narrow pH range tolerance. That is why several bacterial species are being explored later on for isolation and screening of cellulase production [2]. Herbivorous animals and wood-feeders cannot synthesize cellulase within their body but rely on their gut bacterial community [14], which possess a repertoire for cellulase synthesis [36]. Some cellulolytic bacteria strains have also been identified from environmental sources such as agricultural wastes, composts, woody wastes etc. [37-41]. Recently isolation and identification of gut microbiota from the phytophagous animals have gained momentum due to the diverse availability of several phytophagous insects, beetles, termites that thrive through several ecological niches and feed on several leafy and woody materials. In this review, an in-depth literature study has been conducted to enlist the lower invertebrates recognized so far to harbor cellulolytic bacterial populations within their gut. The lower invertebrates with endogenous cellulolytic systems are also discussed here - this review also encloses a brief description of cellulase and its mode of action. Furthermore, biotechnological approaches for improving its activity and application in several industrial aspects have also been discussed.

2. Structure of Cellulose and Cellulase

Cellulose is a fibrous, tough, and water-insoluble substance, which gives rigidity to plant cell walls and is found in stalks, stems, trunk, and all the woody portions of the plant body. It is a tasteless, odorless, and hydrophilic substance. It is a linear and unbranched homopolysaccharide made of D-glucose unit with the chemical formula (C₆H₁₂O₆)n. The number of D-glucose units can range from 10,000 – 15,000. In cellulose, glucose residues are linked by β 1-4 glycosidic bond. In nature, cellulose molecules exist in four crystalline forms (Ia, Ib, II, and III), which vary in physicochemical properties. The crystalline structure of cellulose comprises several cellulose fiber chains, which are interlinked by hydrogen bonds between hydroxyl groups of adjacent molecules. These hydrogen bonds and Vander Wall
forces together make robust and stable cellulose crystals. At ambient temperature, these hydrogen bonds of cellulose molecules can only be hydrolyzed by the cellulase enzyme system's synergistic action. Cellulase is a multienzyme system, which consists of three major components: 1. 4-β-endoglucanase (EC 3.2.1.4), 1,4-β-exoglucanase (EC 3.2.1.91) and β-glucosidase (EC.3.2.1.21) (β-D-glucoside glucohydrolase or cellobiase) [42]. Endoglucanase causes random cleavage of β-1,4-glycosidic bonds along a cellulose chain, liberating a new end. Exoglucanase imparts an exo-attack at the reducing or non-reducing end of microcrystalline cellulose and produces glucose or cellobiose as the end product. β-glucosidase is responsible for cellobiose hydrolysis, producing glucose as the end product [43](Figure.1). The synergistic and sequential action of all these three enzymes facilitates the complete hydrolysis of cellulose to glucose.

Symbiotic microorganisms within the insect gut have a significant contributions to the nutritional ecology of insects [44]. The persistent association of microorganisms in the insect digestive tract provides nutritional advantage through several physiological activities, including digestion and detoxification of specific foodstuffs, synthesis of essential amino acids, vitamins, sterol, and nitrogen fixation, and production of pheromone [2,44,45]. Woodborer and plant-eating insects cannot digest their foodstuffs easily as cellulosic plant materials are very stable polymer and require enzymatic attack for degradation [44]. Partial degradation during insect chewing makes some cellulose of foodstuffs available for cellulase enzyme. Endoglucanases or CMCases from different microbial sources consist of catalytic modules of glycosyl hydrolase families (GH) 5–9, 12, 44, 48, 51, and 74. Bacterial endoglucanases possess multiple catalytic modules, carbohydrate-binding modules (CBMs), and other modules, while fungal endoglucanases possess a catalytic module with or without a CBM [43]. Most of the exoglucanases are cellobiohydrolases (CBHs), which are produced in different forms by bacteria and fungi. The catalytic modules of CBHs belong to the glycosyl hydrolase family of 5, 6, 7, 9, 48, and 74 [43].

Figure 1. Cellulose hydrolysis: Activity site of endoglucanase, exoglucanase and beta-glucosidase on cellulose molecule.

The glycoside hydrolase family's exoglucanases 48 mainly act on crystalline cellulose and induce its hydrolysis, which is mediated by bacterial cellulase systems. β-glucosidase (BGs) does not possess CBM in catalytic modules and hydrolyze soluble cellooligosaccharides and cellobiose to glucose. Cellobiose is an inhibitor of endoglucanase and CBH. Different
microorganisms produce various BGs with catalytic modules belonging to families 1, 3, and 9. Generally, aerobic fungi produce BGs extracellularly, but BGs of anaerobic bacteria remain within their cytoplasm [43]. Microbial cellulase within the anaerobic insect gut is associated with the large enzyme integrating protein scaffoldin, which contains multiple copies of cohesin modules to integrate the different enzymes and other components. These entire components together form a multi-enzyme cellulose complex [46]. Cellulase and other enzymes contain a complementary cohesin-docking domain that specifically binds to the cohesin modules of scaffoldin. Scaffoldin modules also have carbohydrate-binding domains that facilitate the cellulose complex (Figure. 2) to bind with cellulosic substrates for degradation [46]. Cellulose complex in association with several cellulases promotes the degradation of most recalcitrant cellulose molecules into monomeric glucose molecules utilized by insects and herbivorous animals as an energy source.

Figure 2. Mode of action of cellulase enzyme-Cellulosome structure.

3. Sources of Cellulolytic Bacteria

In recent years, an increasing trend in the search for newer sources of cellulose-degrading microorganisms is observed, keeping in view the diverse application of the cellulase in industrial sectors [1,11,24-26,28,47,48]. The fungus *Trichoderma reesei* was the most potential cellulase-producing microorganism [49] over the years. Nowadays, several studies have been aimed in search of newer microorganisms, including bacteria from several environmental sources, including municipal solid wastes [49], compost [37], agro-industrial wastes [7,35,38], soil [50-52], palm wastes (fiber and palm leaves), woody wastes, manure, straw and sugarcane molasses [53-55], mangrove soil sediment [56,57]. The aquatic environment such as moist peat and water of freshwater wetland reserve [58], lake sediments [59], water-sludge mixtures of hot-springs [16,60], and marine environment [61,62] also harbor a widespread spectrum of cellulose-degrading microorganisms.

Besides these environmental sources, many phytophagous lower invertebrates’ gut microbiota has been empirically studied to obtain microorganisms with cellulolytic potential. Cellulase activity within the invertebrate digestive tract has been determined in the long past [63]. Literature reflects that the following invertebrate groups have been studied previously for cellulolytic gut bacterial source:
3.1. Arthropods-insects.

Diversified habitat and plant fiber-based diet make Arthropods a potent reservoir of several gut microbial communities. Literature survey depicts that various Arthropoda species have been explored thoroughly in search of gut microbiota with cellulolytic potential [2,64]. Among Arthropods, insects are the most studied group regarding obtaining novel gut bacterial strain, which can synthesize cellulase enzyme with industrial potential [20,44,65]. Due to the wide range of diversity and multitrophic relationships between insect groups and plant hosts, insect species harbor symbiotic bacterial communities within their digestive tract [44,66,67]. Diverse ecological niches and the phytophagous nature of insects have raised interest in studying the digestion mechanism of insect species involving microbial and endogenous cellulase [20,68]. Insect group, termites have evolved with symbiotic systems [69] that efficiently degrade lignocellulosic foodstuffs [70,71,72] and thus make the termite group a promising source of cellulolytic enzymes. Termite consists of 2000 described species that are subdivided into two groups, namely ‘higher’ and ‘lower’ group [70,73,74]. Both groups are involved in symbiotic relationships with prokaryotes, but lower groups are also the protists' host [70,73,74]. As most of the termites are wood and soil dwellers, symbiotic relationships with protozoan and prokaryotic fauna within their gut help them turn over the complex biopolymer of wood and other cellulosic and lignocellulosic foodstuffs [73,75]. Termites are more potent in cellulose degradation and assimilation than other cellulose utilizing invertebrates [69]. Termites are also found to utilize fungus derived cellulolytic enzyme by making an intriguing symbiotic relationship with fungal species [76]. Cellulolytic gut bacteria have been screened in many species of termites, including Zootermopsis angusticollis [75], Nasutitermes lujae [77], Macrotermes gilvus [78], Coptotermes gestroi [79], Cryptotermes sp. [80], Coptotermes formosanus [81], Coptotermes heimi [82], Cryptotermes brevis [83], Psammotermes hypostoma Desneux [84], Amitermes evuncifer [85], Macrotermes gilvus [86], Coptotermes curvignathus [87].

The gut of Scarabaedae beetle larvae is considered a potent bioreactor for the conversion of lignocellulosic materials to biofuels [88]. Scarabaeids larvae are humivorous feeding on soil organic matter, decaying plant roots, and woods, which are digested by the enzyme-producing microorganisms inhabiting within their digestive tract. The cellulolytic bacterial community has been screened within the larval gut of several Scarabaedae beetle larvae, including Pachnoda marginata [89], Holotrichia parallela [30,90], Oryctes rhinoceros [91-93], Lepidiota mansueta [94], Euoniticellus intermedius [95], Anamola dimidiata [96]. Apart from Scarabaedae, other insect larvae such as Dendroctonus armandi (Curculionidae) [97], Osphranteria coerulescens (Cerambycidae) [98], banana pseudostem weevil Odoiporus longicollis (Coleoptera) [99] are also the host of the cellulose-degrading gut microbiome. Cellulolytic bacteria of five genera have been isolated from the larval gut of the moth Diatraea saccharalis [100,101]. The larvae of silkworm Bombyx mori feed on mulberry leaves composed of pectin, xylan, cellulose, and starch. And thus, Bombyx mori larvae also depend on gut bacteria for their dietary cellulose degradation [102,103]. Honey bees (Apis mellifera) are also considered as model organisms for the study of saccharide digestive gut microbiota [104]. Worker honey bees produce honey and bee bread by processing nectar and pollen, respectively. The honey and bee bread production mechanism depends on saccharide digestive enzymes produced by the gut microbiome of honey bees [104]. Other insects like silver crickets Lepisma sp. [105], mole crickets Gryllotalpa africana [106], rice weevil Sitophilus oryzae [107], coffee
berry borer *Hypothenemus hampei* [108], desert locust *Schistocerca gregaria* [109] also host gut microbes that degrade cellulosic foodstuffs.

Most of the termite species utilize microbial cellulase for degradation of the cellulosic foodstuffs, but the existence of endogenous cellulase has been reported within the gut of subterranean termite *Reticulitermes speratus* [110]. Apart from termite, endogenous cellulase activity has been found in other insect order also [19]. Most of the study has prioritized isolation and quantification of cellulytic bacteria from different insect gut regions; some work has been focused on metagenomic and pyrosequencing approaches to identify cellulase-encoding genes. Termites are the insects in which cellulase genes have been first discovered [111], followed by other insect species belonging to the order Coleoptera [112,113], Hymenoptera [114], Orthoptera [115], and Hemiptera. β-glucosidase and endo–β-1,4 glucanase activities have been estimated in the gut of *Nasutitermes takasagoensis* [116]. Moreover, through the metagenomic approach, 45 different glycoside hydrolases (GH family) genes have been reported in higher termite *Nasutitermes takasagoensis* [117]. Researchers have identified endogenous cellulytic systems within the beetle larvae also. With the aid of transcriptomic technology, one cellulase of glycoside hydrolase family 45 (GH45) and seven GH5 cellulases have been identified from the beetle larvae of *Mesosa myops* [118]. Two β-glycosidases (βGly1 and βGly2) have been purified from the midgut lumen of beetle *Tenebrio molitor* larvae [119]. Endogenous cellulase activities have also been detected in the gut homogenate of several cockroach species [64,120]. Cellulose digesting activity has also been determined in the digestive fluids of some other insects, including grasshopper *Dissosteira carolina* [121] and *Schistocerca gregaria* [64], longhorn beetle *Hylotrupes bajulus*, Crickets *Acheata domesticus*, Stick insects *Eurycanita calcarata* [64], and locusts species [122].

### 3.2. Annelids.

Soil and plant litter dwelling earthworms are also known to possess glucose degrading enzymatic machinery within their gut. Microbial assemblages within the earthworm gut and casts facilitate enzymatic processing and mineralization of organic polymer of soil and plant biomass [123]. Cellulose degrading microbial community has been isolated from several species of earthworm, which include *Eudrilus eugeniae* [124-126], *Amynthas heteropoda* [127], *Eisenia fetida* [127-129], *Perionyx excavatus*, and * Glyphidrilus spelaeotes* [130]. Earthworms also rely on dual digestive mechanisms involving both endogenous and microbial cellulase for lignocellulose degradation. Few reports demonstrate that earthworms possess complete enzymatic machinery for glycosidic enzymes [131-134]. Glycolytic activities in the gut have been detected in the earthworm species *Pontoscolex corethrums*[118], *Millsonia anomala* [132], *Polypheretima elongata* [133], *Hormogaster elisae* [134, 135], *Hyperodrilus africainus*, *Dichogaster terrae nigrae* [135], *Pheretima hilgendorfi* [136]. N-acetylglucosaminase, laminarinase, laminaribiase activities are found to be most potent within the gut of these earthworm species except *Pheretima hilgendorfi*. These enzymes induce degradation of β-1, 3 glucan, and chitin sub-units, which are characteristic components of fungal cell walls [131,134]. Higher activities of these enzymes corroborate that these earthworm species feed on fungus and decaying root exudates. Week activities of other glycolytic enzymes within the gut of earthworms reflect their dependency on microbial cellulases for degradation of substrates like mannan and cellulose [134]. In the case of *Pheretima hilgendorfi*, endo-β-1, 4-glucanase contributes to the degradation of cellulose, and a novel cellulase gene (phhEg) has been detected from this species [136].
3.3. Molluscs.

Apart from insects, some empirical studies have also been conducted to determine cellulolytic bacteria in snail species. Land snails (Gastropoda: Pulmonata) include several distinct lineages of terrestrial gastropods, which utilize various resources of the terrestrial ecosystem that make them efficient in exploiting the available niches, which is why the realized diversity is quite high. They are generally herbivorous, feed upon a wide range of plant materials, and many of them are the pests of agricultural and horticultural plants [137]. As most land snail species consume cellulosic and lignocellulosic materials, they can be a viable and potential source of cellulolytic gut microbe fauna. Pioneered study on bacterial cellulase in the animal gut has been conducted on land snail *Helix pomatia* [138,139], which has been followed by Florkin and Lozet 1949 [140]and Jeuniaux 1950, 1955 [141,142], who worked on the contribution of microbial cellulase and chitinase respectively in the degradation of plant material in the gut of *H. pomatia*. The African giant snail *Achatina fulica* (Gastropoda–Gastropoda) is the most studied snail species in this respect. The existence of endogenous cellulase within the gut of *A. fulica* is evident from the work of Soedigdo et al. 1970 [143] and Dar et al. 2020 [144]. Microbial communities with cellulolytic potential have been isolated from *Achatina fulica* [7,145-147] and *Arachatina marginata* [148,149]. Few works have been aimed to investigate the physiochemical environment of the gut of helicid snails[150], the occurrence of fermentative bacteria in edible snail *Helix pomatia* and *Cornu aspersum* (Gastropoda: Pulmonata) [151], and homolactic intestinal bacteria of *Helix aspersa* [152], but the detailed works emphasizing microbial contribution in the digestion of cellulose biopolymer in several other gastropod snail guts are yet to be deciphered. Other molluscan species such as marine turban shell *Batillus cornutus* has been found to possess polysaccharide digesting gut bacteria [153] and wood-boring bivalvia *Bankia setacea* also depends on nitrogen-fixing cellulolytic endosymbionts for wood degradation in the marine environment [154-157].The cellulolytic activity within the different areas of the gut of the land slug *Arionater* had been detected through the CMC zymography and esculin hydrate activity gel assays, which revealed the existence of endoglucanase and β-glucosidase enzymes [158] within their gut. Further study was carried out to isolate and identify cellulolytic bacterial colony within the Arion gut, which was the main source of enzyme activity within the gut [158]. Four endo- β-1,4-glucanases (21 K, 45 K, 65 K, and 95 K cellulase) and 2 β-glucosidases (110 K and 210 K) were purified from the digestive fluid of sea hare *Aplysia kurodai* [159]. These enzymes were able to hydrolyze CMC, filter papers, and lichenan, and these all cellulase were able to digest seaweeds, mainly sea lettuce *Undaria pinnatifida* [159].

Literature survey reflects that insect species are prioritized for the investigation of the gut bacterial community. Other phytophagous species such as terrestrial snails or algae or seaweed consuming aquatic snails and geophagous earthworms can also be efficient model species. Exploration of more invertebrate species may be helpful for the discovery of novel microorganisms with cellulolytic potentials. Lists of lower invertebrates and their gut bacterial strains with cellulolytic potentials (Table 1) and the specific activity of gut bacterial cellulolytic enzymes (Table 2) are presented in this review.

4. Biotenchnology and Industrial Application of Cellulase

Biotechnological approaches have been adopted in the long past since the 1980s to apply cellulase in the food industry, followed by several other commercial and industrial parts.
Commercially available cellulolytic enzymes are usually extracted from *Trichoderma reesei* and *Aspergillus niger* [1].

| Species name | Systematic position | Bacterial strains identified | Cellulolytic enzyme activity of the culture Supernatant of the isolated bacterial strains | Reference |
|--------------|---------------------|-------------------------------|------------------------------------------------------------------------------------------------|-----------|
| Termite      | (Odontotermes hiansensis), pill-bugs (Armadillidium sp), yellow stem borers (Scirrophaga incertulas) | Bacterial families isolated belong to Bacillaceae, Enterobacteriaceae, Microbacteriaceae, Paenibacillaceae and Promicromonosporaceae | endoglucanase, exoglucanase, β-glucosidase, xylanase, β-xylosidase, mannanase and b-D-glucanase. | [2]       |
| Termite      | (Zootermopsis angusticollis) | Among several isolates, *Cellulomonas sp.*, *Bacillus* (e.g. *B. cereus* and *B. megaterium*), and *Paenibacillus sp.* were with highest CMC degrading capability | enzyme assay was not performed, Cellulolytic bacterial strains were isolated based on the clear zone diameter of degraded CMC area around the colony in plate assay method. | [75]      |
| Wood-feeding Termite, *Nasutitermes lujae* | Arthropoda-Insecta-Blattodea-Termictidae | *Clostridium termiditis sp.* | enzyme assay was not performed, Cellulolytic bacterial strains were isolated based on the clear zone diameter of degraded CMC area around the colony in the plate assay method. | [77]      |
| Termite worker *Macrotermes gilvus* | Arthropoda-Insecta-Blattodea-Termictidae | *Bacillus megaterium* and *Paracoccus yeei* | enzyme assay was not performed, Cellulolytic bacterial strains were isolated based on the clear zone diameter of degraded CMC area around the colony in the plate assay method. | [78]      |
| Milk termite *Coptotermes gestroi* | Arthropoda-Insecta-Blattodea-Rhinotermitidae | *Bacillus sp.*, *Enterobacter sp.*, *Bacillus megaterium*, *Pseudomonas aeruginosa* and *Bacillus cereus* | enzyme assay was not performed, Cellulolytic bacterial strains were isolated based on the clear zone diameter of degraded CMC area around the colony in the plate assay method. | [79]      |
| *Cryptoterms sp.* | Arthropoda-Insecta-Blattodea-Rhinotermitidae | Three isolates of genus *Clostridium*, one isolate of group *Mycobacteriaceae*, *Lactobacillaceae* or *Coryneform* and the last one in the genus *Proteus* | enzyme assay was not performed, Cellulolytic enzyme activities had been screened based on the clear zone diameter of degraded CMC area around the colony in the plate assay method. | [80]      |
| Termite       | *Coptotermes formosanus* | *Pseudomonas mendocina*, *Barkholderia pseudomallei*, *Chryseobacterium luteola*, *Klebsiella oxytoca* and *Klebsiella terrigena* | filter paperase (The cellulolytic enzyme activity of the microbe was examined in a broth culture using filter paper as carbon source). | [81]      |
| Termite       | *Coptotermes heini* | *Bacillus sp.*, *Proteus sp.*, *Ochrobactrum sp.*, *Erwinia sp.*, *Aeromonas sp.* and *Citrobacter sp.* | enzyme assay was not performed, Cellulolytic enzyme activities had been screened based on the clear zone diameter of degraded CMC area around the colony in the plate assay method. | [82]      |
| Termite       | *Cryptoterms brevis* | *Bacillus sp.* and *Ochrobactrum eryzae* | xylanase, CMCase, lignin peroxidase, laccase | [83]      |
| Species name | Systematic position | Bacterial strains identified | Cellulolytic enzyme activity of the culture Supernatant of the isolated bacterial strains | Reference |
|--------------|---------------------|-----------------------------|----------------------------------------------------------------------------------|-----------|
| Termite Psammotermes hypostoma Desneux | Arthropoda-Insecta-Blattodea-Rhinotermitidae | *Paenibacillus lactis*, *Lysinibacillus macrolides*, *Stenotrophomonas maltophilia*, *Lysinibacillus fueliformis* and *Bacillus cereus* | cellulase (endoglucanase) | [84] |
| Termite Anitermes evanifier | Arthropoda-Insecta-Blattodea-Termitidae | *Bacillus cereus*, *Bacillus mycoides* and *Pseudomonas aeruginosa* | endoglucanase (CMCase) and exoglucanase (FPase) | [85] |
| Termite Macrotermes gilvus | Arthropoda-Insecta-Blattodea-Termitidae | *Provedencia sp.*, *Bacillus sp.* and *Staphylococcus sp.* | cellulase (on newsprint paper substrate) | [86] |
| Termite Coptotermes curvignathus | Arthropoda-Insecta-Blattodea-Termitidae | Bacterial strains isolated were mainly *Bacillus spp.* | enzyme assay was not performed, Cellulolytic enzyme activities had been screened based on the clear zone diameter of degraded CMC area around the colony in the plate assay method | [87] |
| Termite | Arthropoda-Insecta | *Diplococcus sp.*, *Diplobacillus sp.*, *Streptobacillus sp.* and *Staphylococcus sp.* | enzyme assay was not performed, Cellulolytic enzyme activities had been screened based on the clear zone diameter of degraded CMC area around the colony in the plate assay method | [160] |
| Holotrichia parallela larvae | Arthropoda-Insecta-Coleoptera-Scarabaeidae | Among many isolates *Siphonobacter aqua eclarae*, *Cellulosi microbium junkei*, *Paracoccus sulfuroxidans*, *Ochrobactrum cytisi*, *Ochrobactrum haematophilum*, *Kaistia adipata*, *Devosia riboflava*, *Labrys neptuniae*, *Ensifer adhaerens*, *Shinella zoogloeoides*, *Cortobacter freundi* and *Pseudomonas nitroreducens* were reported for the first time as cellulolytic bacteria | enzyme assay was not performed, Cellulolytic bacterial strains were isolated based on the clear zone diameter of degraded CMC area around the colony in the plate assay method | [30] |
| Long horn beetle Hylotrupes bajulus | Arthropoda-Insecta-Coleoptera-Cerambycidae | Not identified | β-glycosidase, CMC-ase, xylanase | [64] |
| Larvae of the scarab beetle Pachnoda marginata | Arthropoda-Insecta-Coleoptera-Scarabaeidae | *Promicromonospora pachnodae* sp. | CMC-ase and xylanase | [89] |
| Holotrichia parallela larvae | Arthropoda-Insecta-Coleoptera-Scarabaeidae | *Pseudomonas sp.* | endoglucanase | [90] |
| Larvae of Oryctes rhinoceros | Arthropoda-Insecta-Coleoptera-Scarabaeidae | Genus *Bacillus* and *Citrobacter* | enzyme assay was not performed, Cellulolytic, Xylanolytic, and Mannanolytic enzyme activities had been screened based on the clear zone diameter of degraded CMC area around the colony in the plate assay method | [91] |
| Larvae of Oryctes rhinoceros | Arthropoda-Insecta-Coleoptera-Scarabaeidae | *Bacillus sp.*, *Proteus sp.*, *Ochrobactrum sp.*, *Erwinia sp.*, *Aeromonas sp.*, *Citrobacter sp.* and *Pseudomonas sp.* | enzyme assay was not performed, Cellulolytic and ligninolytic enzyme activities had been screened based on the clear zone diameter area around the colony in the plate assay method | [92] |
| Larvae of grub beetle Lepidiota mansueta | Arthropoda-Insecta-Coleoptera-Scarabaeidae | *Citrobacter sp.* | enzyme assay was not performed, Cellulolytic bacterial strains were isolated based on the clear zone diameter area around the colony | [94] |
| Species name                  | Systematic position                  | Bacterial strains identified                                                                 | Cellulolytic enzyme activity of the culture Supernatant of the isolated bacterial strains | Reference |
|------------------------------|--------------------------------------|------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------|-----------|
| **Dung beetle** Euoniticellus intermedius** | Arthropoda-Insecta-Coleoptera-Scarabaeidae | Not identified                                                                                           | zone diameter of degraded CMC area around the colony in the plate assay method.                       | [95]      |
| **Larvae of Anamola dimidiata** | Arthropoda-Insecta-Coleoptera-Scarabaeidae | The majority of the isolated strain belonged to Firmicutes and Proteobacteria                           | enzyme assay was not performed, Cellulolytic bacterial strains were isolated based on the clear zone diameter of degraded CMC area around the colony in the plate assay method.        | [96]      |
| **Larvae of Dendroctonus armandi** | Arthropoda-Insecta-Coleoptera-Curculionidae-Scolytinae | Serratia sp., Pseudomonas sp., Bacillus sp., Paenibacillus sp., Sphingomonas, Brevundimonas sp., kwangchunensis sp., Brevundimonas vesicularis, Pseudoxanthomonas mexicana and Methylobacterium populi | enzyme assay was not performed, Cellulolytic bacterial strains were isolated based on the clear zone diameter of degraded CMC area around the colony in the plate assay method. | [97]      |
| **Larvae of Osmphrateria coeulescens** | Arthropoda-Insecta-Coleoptera-Cerambycidae | Bacillus sp.                                                                                              | CMC-ase                                                                                           | [98]      |
| **Banana pseudostem weevil Odoiporus longicollis** | Arthropoda-Insecta-Coleoptera-Curculionidae | Not identified                                                                                           | CMCase                                                                                           | [99]      |
| **Larvae of moth Diatraea saccharalis** | Arthropoda-Insecta-Lepidoptera-Crambidae | Klebsiella oxytoca, Klebsiella pneumonia, Klebsiella variicola, Stenotrophomonas maltophilia, Stenotrophomonas rhizophila, Bacillus pumilus, Enterococcus casselilavus, Microbacterium hominis and Microbacterium schleferi, | CMC-ase                                                                                           | [100]     |
| **Larvae of moth Diatraea saccharalis** | Arthropoda-Insecta-Lepidoptera-Crambidae | Klebsiella pneumoniae, Klebsiella sp. and Bacillus sp.                                                   | CMC-ase                                                                                           | [101]     |
| **Larvae of Bombyx mori** | Arthropoda-Insecta-Lepidoptera-Bombycidae | Bacillus circulans, Proteus vulgaris, Klebsiella pneumonia, Enterobacter sp., Citrobacter freundii and Serratia liquefaciens | cellulase, xylanase, amylase, pectinase                                                                 | [102]     |
| **Bombyx mori** | Arthropoda-Insecta-Lepidoptera-Bombycidae | Solibacillus silvestris, Bacillus aryabhattai, Lysinibacillus sp., Bacillus sp., Bacillus thuringiensis, Paenibacillus sp., Serratia marcescens, Klebsiella pneumonia and Enterobacter hormaechei | CMC-ase                                                                                           | [103]     |
| **Silver cricket Lepisma sp.** | Arthropoda-Insecta-Zygentoma-Lepismatidae | Not identified                                                                                         | filter paperase (The cellulolytic enzyme activity of the microbe was examined in a broth culture using Whatman 42 filter as carbon source) | [105]     |
| **Mole crickets Gryllotalpa africana** | Arthropoda-Insecta-Orthoptera-Gryllotalpidae | Acinetobacter junii                                                                                      | CMC-ase                                                                                           | [106]     |
| **Rice weevil Sitophilus oryzae** | Arthropoda-Insecta-Coleoptera-Curculionidae | Bacterial strains isolated belong to Bacillus and γ-Proteobacteria                                      | endoglucanase (CMCase)                                                                            | [107]     |

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| Species name               | Systematic position                              | Bacterial strains identified                                                                 | Cellulolytic enzyme activity of the culture Supernatant of the isolated bacterial strains                       | Reference |
|---------------------------|--------------------------------------------------|------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------|-----------|
| Coffee berry borer        | Hypothenemus hampei                              | Based on morphological and biochemical characteristics, isolated strain was similar to genus Brochothrix | cellulase (CMCase)                                                                                            | [108]     |
| Desert locust             | Schistocerca gregaria                            | Bacillus safensis                                                                               | enzyme assay was not performed, Cellulolytic bacterial strains were isolated based on the clear zone diameter of degraded CMC area around the colony in the plate assay method. | [109]     |
| Termite, caterpillar,     | Termite, caterpillar,                            | Not identified                                                                                  | filter paperase and endoglucanase                                                                            | [161]     |
| bookworm and snail        | bookworm and snail                               |                                                                                                |                                                                                                              |           |
| Oxya velox, Aspidimorpha  | Arthropoda-Insecta-Orthoptera-Acrididae:         | Bacterial species isolated from O. velox were Photobacter luminescens, Enterococcus faecalis,   | enzyme assay was not performed, Cellulolytic bacterial strains were isolated based on the clear zone diameter of degraded CMC area around the colony in the plate assay method. | [162]     |
| miliaris and Propylea     | Oxya velox, Arthropoda-Insecta-Orthoptera-      | Enterococcus durans, Flavobacterium odoratum, Serretia marcescens and Serretia entomaphila.     |                                                                                                              |           |
| quatrodecimpunctata       | Chrysomelidae: Propylea miliaris, Arthropoda-    | Isolates identified from P. quatrodecimpunctata were Erwinia ananans, Aeromonas salmonicidica, Enterococcus casseliflavus and Acinetobacter calcoaceticus |                                                                                                              |           |
|                           | Insecta-Orthoptera-Coccinellidae: Propylea      | Isolates identified from A. miliaris were Klebsiella oxytoca, Microbacterium imperiale, Yersinia pestis, Xenorhabdus poiani and Pseudomonas saccharophila |                                                                                                              |           |
|                           | quatrodecimpunctata                              |                                                                                                |                                                                                                              |           |
| Endogeic earthworms       | Annelida-Citellata-Haplotaixida-Megascolecidae: | Dominant bacterial and fungal genus was Burkholderia and Chaetomium respectively | exoglucanase, endoglucanase, xylanase, laccase                                                              | [123]     |
| Annythas heteropoda and   | Annelida-Citellata-Haplotaixida-Lumbriciidae:   |                                                                                                |                                                                                                              |           |
| Eisenia fetida            | Eisenia fetida                                   | **Bacillus pumilus**                                                                             | endoglucanase                                                                                                | [124]     |
| Earthworms *Eudrilus      | Annelida-Citellata-Haplotaixida-Eudrilidae       | **Bacillus sp.**                                                                                 | amyrase, nitrate reductase, cellulase, xynylase, and protease                                              | [125]     |
| eugeniæ                   |                                                                                                |                                                                                                |                                                                                                              |           |
| Earthworm *Eudrilus       | Annelida-Citellata-Haplotaixida-Eudrilidae       | **Bacillus** sp.                                                                                |                                                                                                              |           |
| eugeniæ                   |                                                                                                |                                                                                                |                                                                                                              |           |
| Earthworm *Eisenia        | Annelida-Citellata-Haplotaixida-Lumbriciidae     | **Lysinibacillus sphaericus**                                                                    | filter paperase                                                                                               | [128]     |
| foetida                   |                                                                                                |                                                                                                |                                                                                                              |           |
| Earthworm *Eisenia        | Annelida-Citellata-Haplotaixida-Lumbriciida     | **Colony of Streptococcus, Staphylococcus and Diplococcus**                                       | **CMC -ase**                                                                                                 | [129]     |
| femida                    |                                                                                                |                                                                                                |                                                                                                              |           |
| Epigeic earthworm,        | Annelida-Citellata-Haplotaixida-Megascolecidae: | **Mycobacterium sp., Stenotrophomonas sp., Acinetobacter sp., Alcaligenes sp., Chryseobacterium sp., Pseudomonas sp., Bacillus sp. and Sphingomonas sp.** | Filter paperase                                                                                               | [130]     |
| Perionyx excavatus and an  | Annelida-Citellata-Haplotaixida-Almidae:         | **Bacillus subtilis, Achromobacter sp., Ochrobactrum sp. and Klebsiella sp.**                   |                                                                                                              |           |
| endogeic, Glyphidrilus     | Glyphidrilus spelaeotes                           |                                                                                                |                                                                                                              |           |
| spelaeotes                |                                                                                                |                                                                                                |                                                                                                              |           |
| Giant African land snail  | Mollusca-Gastropoda-Stylostomatophora-Achatinida |                                                                                                 | endoglucanase, exoglucanase, xylanase                                                                         | [14]      |
| Achatina fulica           |                                                                                                |                                                                                                |                                                                                                              |           |
Table 2. Specific activity of several cellulolytic enzymes obtained from gut microbial flora of several lower invertebrate species.

| Invertebrate species | Gut microbial flora | Specific activity of enzyme obtained from gut microbial flora (maximum activities showed within the incubation period of bacteria culture, are mentioned here) | Reference |
|----------------------|---------------------|--------------------------------------------------------------------------------|-----------|
| Termite Cryptotermes brevis | *Bacillus* sp. | xylanase activity: 0.21 U/mL CMCCase activity: 0.25 U/mL | [83] |
| Termite *Psammotermes hypostoma* | *Pseudobacillus lactis* | endoglucanase activity: 1.47 U/ml | [84] |
| Termite *Psammotermes hypostoma* | *Lysinibacillus fusiformis* | endoglucanase activity: 0.22 U/ml | [84] |
| Termite *Anietermes evaniger* | *Stenotrophomonas maltophilia* | endoglucanase activity: 2.28 U/ml | [84] |
| Termite *Nonietermes bogut* | *Lysinibacillus macrolides* | endoglucanase activity: 1.93 U/ml | [84] |
| Termite *Macrotermes duwara* | *Bacillus cereus* | endoglucanase activity: 0.23 U/ml | [84] |
| Termite *Macrotermes duwara* | *Bacillus mycoides* | endoglucanase activity: 5.96 U/ml | [84] |
| Termite *Macrotermes duwara* | *PSuedomonas aeruginosa* | endoglucanase activity: 4.89 U/ml | [84] |
| Termite *Macrotermes duwara* | *Pseudomonas aeruginosa* | endoglucanase activity: 1.47 U/ml | [84] |
| Termite *Macrotermes duwara* | *Bacillus sp.* | cellulase activity: 15.7 mU/mL | [86] |
| Termite *Macrotermes duwara* | *Bacillus sp.* | cellulase activity: 2.33 U/mL | [86] |
| Termite *Macrotermes duwara* | *Bacillus sp.* | cellulase activity: 0.40 U/mL | [86] |
| Termite *Macrotermes duwara* | *Bacillus sp.* | cellulase activity: 0.19 U/mL | [86] |
| Termite *Macrotermes duwara* | *Bacillus sp.* | cellulase activity: 0.0155 U/mL | [86] |
| *Holotrichia parallela* larva | *Pseudomonas sp.* | endoglucanase activity: 0.825 U/mL | [90] |
| Species | Microorganism | Activity | Reference |
|---------|---------------|----------|-----------|
| Beetle Osphranteria coerulescens larvae | Bacillus sp. | CMC-ase activity: 4.99 U/mL | [14] |
| Moth Diatraea saccharalis larvae | Bacillus pumilus | CMC-ase activity: 0.32 U/mL | [100] |
| Moth Diatraea saccharalis larvae | Klebsiella oxytoca | CMC-ase activity: 0.22 U/mL | [100] |
| Sikworm Bombbyx mori larvae | Bacillus aryabhattai | Cellulase activity: 0.4 U/mL | [103] |
| Mole Gryllotalpa africana | Acinetobacter junii | CMCase activity: 0.35 U/ml | [106] |
| Rice weevil Sitophilus oryzae | Bacillus subtilis | Cellulase (endoglucanase activity): 132.069 ± 0.993 U/mL | [107] |
| Earthworm Eisenia fetida | Eisenia fetida | Cellulase (endoglucanase) activity: 0.1271 IU/mL | [124] |
| Earthworm Eisenia fetida | Not identified | CMC-ase activity: 26.041 IU/mL and 47.80 IU/mL produced by two different culture | [128] |
| Epigeic earthworm, Perionyx excavatus and an endogeic, Glyphidrilus spelaequetes | Mycobacterium sp. | Endoglucanase activity: 230.86 IU/mL gut extract for CMC substrate | [14] |
| | Stenotrophomonas sp. | Endoglucanase activity: 502.75 IU/mL gut extract for grass straw as substrate | [14] |
| | Alcaligenes sp. | Endoglucanase activity: 347.65 IU/mL gut extract for wheat husk as a substrate | [14] |
| | Chryseobacterium sp. | Endoglucanase activity: 122.68 IU/mL gut extract for filter paper as a substrate | [14] |
| | Acinetobacter sp. | Endoglucanase activity: 3777.61 IU/mL extract for wheat husk as a substrate | [14] |
| Achatina fulica | Bacillus subtilis | Exoglucanase activity: 24.23 IU/mL sec for filter paper as a substrate | [14] |
| | Ochrobactrum sp. | Exoglucanase activity: 82.03 IU/mL extract for CMC as a substrate | [14] |
| Achatina fulica | Bacillus subtilis | Xylanase activity: 60.221 IU/mL extract (on wheat husk as a substrate) | [14] |
| Achatina fulica | Ochrobactrum sp. | Xylanase activity: 24.23 IU/mL extract for filter paper as a substrate | [14] |
| Achatina fulica | Enterobacter sp. | Filter paperase activity: 5 U/ml | [147] |
| | Yokenella sp. | Filter paperase activity: 3 U/ml | [147] |
| Achatina fulica | Bacillus subtilis | Cellulase (CMCase) activity from fungal isolates 14.46 mg/ml sec^{-4} | [148] |
| Archachatina marginata | Bacillus subtilis | Cellulase (CMCase) activity: 2.2 mg/mL sec^{-4} | [148] |
| Streptococcus faecalis | Cellulase (CMCase) activity: 1.4 mg/mL sec^{-4} | [148] |
| Staphylococcus aureus | Cellulase (CMCase) activity: 0.2 mg/mL sec^{-4} | [148] |
| Achatina marginata | Bacillus subtilis | Cellulase activity: 1.7 mg/mL sec^{-4} | [148] |
| Streptococcus faecalis | Amylase activity: 18.40 mg/g | [149] |
| | Cellulase activity: 13.20 mg/g | [149] |
| | Protease activity: 13 mg/g | [149] |
| | α-glucosidase activity: 8.30 mg/g | [149] |
Sea snail Batillus cornutus

| Bacillus sp. | CM-cellulase activity: 22.76 U/mg protein |
|             | α-cellulase activity: 27.10 U/mg protein |
|             | laminarinase activity: 66.59 U/mg protein |
|             | kelp-lyase activity: 64.36 U/mg protein |

To obtain efficient hydrolytic potential, cellulase enzymes should possess some desired attributes, including high specific activity, high catalytic activity against crystalline cellulose, high thermostability, resistance to end-product inhibition, and stability against shear force [164]. Various genetic tools are being used for microbial strain improvement to achieve these attributes and enhance enzyme production. Several industrially used fungal strains such as A. niger, T. reesei, Saccharomyces cerevisae, Pichia pastoris, and bacterial strains like Escherichia coli, Bacillus subtilis [164] have subjected to genetic engineering for the production of a recombinant enzyme with high potential for industrial application. Homologous and heterologous expression techniques have been adopted in the recent era to overexpress microbial cellulase and other hydrolytic enzymes [164]. Owing to the genetic engineering of the cellulolytic microbial strain, cellulose-degrading enzymes' efficient production has enhanced its biotechnological potential in various industrial fields. A brief account of the application of cellulase and allied enzymes have been discussed here.

4.1. Food processing industry.

The application of enzymes in the extraction of fruit juices and pulps mitigates the problem of low yield, stability, and clarity of product, which are the main difficulties faced by the food industries in the early 1930s. Later on, progressive research on enzyme technology leads to the production of cellulase, hemicellulase, and pectinase from the food-grade microorganisms A. niger and T. reesei. A combination of these enzymes (pectinase, cellulase, hemicellulase), also called macerating enzymes, plays an important role in the extraction and clarification of vegetable and fruit juices [1] also improves the stability and textures of the purees and pulp. A mixture of pectinase and a low level of hemicellulase and cellulase, commercially known as Olivex is used to extract olive oil from olive seeds. The use of Olivex improves the quality of olive oil extract by enriching extra virgin olive oil with vitamin E and antioxidants, reducing the induction of rancidity and lowering oil content in the wastewater [165]. Infusion of pectinase enzyme helps in peeling of citrus food by reducing its bitterness. Application of β-glucosidase and pectinase ameliorate the texture, aroma, flavor, and volatiles compounds of specific fruits and vegetables [166]. Microbial enzymes are long being used in the quality improvement of bakery products also. Amylases and proteases are mainly used in the bakery industry [167], but recently the use of hemicellulase and endo-xylanase helps in equal distribution of water in dough and bread by hydrolyzing arabinoxylan present in dough [168]. This redistribution of water facilitates the enhancement of flavor, volume, softness, texture, and bakery products' stability.

4.2. Brewery and winery industry.

The application of exogenous enzymes in wine and beer biotechnology plays a key role in quality control and production rate. α and β-amylase, carboxypeptidase, and β-glucanase are endogenously synthesized during the germination of barley before malting and synergistically act hydrolyze seed reserves during the malting process. But their improper activities often result in un-malted and poor quality barley. Application of microbial β-glucanase facilitates
hydrolysis of β-glucan and reduces the wort viscosity during the maceration and fermentation process of barley. In the winery, exogenous enzymes hemicellulase, pectinase, β-glucanase are used for better maceration, improved color extraction, filtration and clarification, and wine stability and quality [165]. Furthermore, the β-glucosidase enzyme application modifies glycosylated precursors that enhance the aroma of wine [169].

4.3. Paper and pulp industry.

Application of biomechanical pulping process using enzymes instead of the only mechanical process reduces the energy expenditure during grinding and refining of the woody material in pulps. Mixtures of endoglucanase I and II and hemicellulase have been used to better drainage and beat ability in the paper mills before or after beating pulp, which in turn increases the overall production rate [1]. Cellulase and xylanase enhance the bleaching and de-inking of several types of paper wastes [170]. Overall addition of several hydrolytic enzymes ameliorates fiber brightness, strength properties, pulp freeness, and cleanliness.

4.4. Textile and laundry industry.

The application of cellulase in the bio-stoning process of denim and jeans products has achieved great success. Usage of cellulase in bio polishing of cotton fabric also has an advantage as an enzyme can readily remove surface fibers and fuzz, resulting in the glossy, smooth, and brighter appearance of cotton garments [1,165]. Cotton garments usually become fluffy and dull after repeated wash. The addition of cellulase enzyme in household detergents helps remove fluffy fibrils from cotton, boosting the appearance and brightness of the garments [1].

4.5. Animal feed.

In the animal feed industry, cellulase plays a key role in removing Anti-nutritional Factors (ANF) from the cereals, grains, and vegetables used for animal feed in poultry, cattle, and fish farming. Pretreatment with cellulase and hemicellulase induces partial digestion of lignocellulosic materials and β-glucans, dehulling cereal grains, which improves the cereal quality and ensures a high yield of milk and meat production [165].

4.6. Research development and agriculture.

A combination of hydrolytic enzymes, including cellulase, hemicellulase, ligninase, have an immense effect on plant growth and plant disease control [1]. Cellulases and β-glucanases can degrade the cell wall and inhibit the germination of spores of some phytopathogens. Mixtures of different hydrolytic enzymes facilitate the digestion of desired plant or fungal cell walls to produce protoplast, which can be used to make hybrid strains of desired properties for research purposes [23].

4.7. Waste management.

As cellulose is the most abundant biomolecules in the plant, a large number of wastes of leaf litter and other lignocellulosic materials are generated from forests, agricultural fields, and agro-industries. These wastes containing a large amount of raw cellulose may cause environmental pollution. But nowadays, with the help of enzyme technology, these unutilized
or underutilized cellulosic sources are being converted to produce several biofuels and bio commodities, sugars, and alcohol [1,171,172]. Application of garden snail (Cornu aspersum) cellulase in paper waste saccharification is empirical evidence of cellulase activity in waste management [173].

5. Conclusion and Future Prospect

Cellulase and allied enzymes are getting attraction worldwide due to their wide range of applications in vast areas of industries. Although in the past, fungal-based enzymatic systems have been used for cellulytic enzyme production, later many research works have been carried out in search of more efficient microbial enzymatic systems as a source of cellulytic enzymes. Bacterial enzymatic systems are more promising due to enzyme complexity, extreme habitat variability, and low production cost. Researchers are focusing on bacterial strain improvement to obtain tailor-made cellulytic enzymes with high specific activity and catalytic efficiency with the aid of biotechnology and enzymology. Moreover, identifying newer sources of cellulose-degrading microorganisms is essential for the isolation of novel cellulytic genes. Previous studies assert that the gut of phytophagous and herbivorous invertebrates is the host of the cellulytic bacterial niche. In the future, further exploration of such invertebrates is necessary for the isolation of novel bacteria, which will bring great prospects in the industrial application of cellulytic enzymes.

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Conflicts of Interest

The authors declare no conflict of interest.

References

1. Bhat, M.K. Cellulases and related enzymes in biotechnology. Biotechnol. Adv. 2000, 18, 355–383, https://doi.org/10.1016/S0734-9750(00)00041-0.
2. Bashir, Z.; Kondapalli, V.K.; Adlakha, N.; Sharma, A.; Bhatnagar, R.K.; Chandel, G.; Yazdani, S.S. Diversity and functional significance of cellulytic microbes living in termite, pill-bug and stem-borer guts. Sci. Rep. 2013, 2558, https://doi.org/10.1038/srep02558.
3. Snáchez, O.J.; Cardona, C.A. Trends in biotechnological production of fuel ethanol from different feedstocks. Biomass and Bioenergy. 2008, 99, 5270–5295, https://doi.org/10.1016/j.biortech.2007.11.013.
4. Himmel, M.E.; Bayer, E.A. Lignocellulose conversion to biofuels: current challenges, global perspectives. Curr. Opin. Biotechnol. 2009, 20, 316-317, https://doi.org/10.1016/j.copbio.2009.05.005.
5. Jäger, G.; Büchs, J. Biocatalytic conversion of lignocellulose to platform chemicals. Biotechnol. J. 2012, 7, 1122–1136, https://doi.org/10.1002/biot.201200033.
6. Anu; Kumar, A.; Rapoport, A.; Kunze, G.; Kumar, S.; Singh, D.; Singh, B. Multifarious pretreatment strategies for the lignocellulosic substrates for the generation of renewable and sustainable biofuels: a review. Renew. Energy. 2020, 160, 1228-1252, https://doi.org/10.1016/j.renene.2020.07.031.
7. Chakraborti, M.; Acharya, K. Agrowaste to ethanol: orchestrated by enzymes from microbes. In: Microbial Fermentation and Enzyme Technology. CRC Press, 2020.
8. Kaur, P.; Taggar, M.S.; Kaur, J. Cellulolytic microorganisms: diversity and role in conversion of rice straw to bioethanol. *Cell. Chem. Technol.* 2020, 54, 613–634, https://doi.org/10.35812/CelluloseChemTechnol.2020.54.61.
9. Khandaker, M.M.; Abdullahi, U.A.; Abdulrahman, M.D.; Badaluddin, N.A.; Mohd, K.S. Bio-ethanol production from fruit and vegetable waste by using *Saccharomyces cerevisiae*. In: *Bioethanol*. IntechOpen, 2020, https://doi.org/10.5772/intechopen.49358.
10. Rajeswari, K.; Rekha, B.; Saravanathamizhan, R. Promotion of enzymatic hydrolysis of lignocellulosic biomass using natural additives for bioethanol production. *Environ. Qual. Manage.* 2020, 1–7, https://doi.org/10.1002/tqem.21705.
11. Singh, V.P.; Sharma, D.; Prajapati, S.; Bamal, A.; Tyagi, S. A comparative study of cellulase production: minireview. *J. Sci. Innov. Res.* 2020, 9, 69–73.
12. Tsegaye, B.; Balomajumder, C.; Roy, P. Organosolv pretreatments of rice straw followed by microbial hydrolysis for efficient biofuel production. *Renew. Energy* 2020, 148,923-934, https://doi.org/10.1016/j.renene.2019.10.176.
13. Cardoso, A.M.; Cavalcante, J.J.; Cantão, M.E.; Thompson, C.E.; Flatschart, R.B.; Glogauer, A.; Scapin, S.M.; Sade, Y.B.; Beltrão, P.J.; Gerber, A.L.; Martins, O.B. Metagenomic analysis of the microbiota from the crop of an invasive snail reveals a rich reservoir of novel genes. *PLoS One* 2012, 7, https://doi.org/10.1371/journal.pone.0048505.
14. Dar, M.A.; Pawar, K.D.; Jadhav, J.P.; Pandit, R.S. Isolation of cellulolytic bacteria from the gastro-intestinal tract of *Achatina fulica* (Gastropoda: Pulmonata) and their evaluation for cellulose biodegradation. *Int. Biodeterior. Biodegrad.* 2015, 98, 73–80, https://doi.org/10.1016/j.ibiod.2014.11.016.
15. Badger, P.C. Ethanol from cellulose: a general review. *Trends in New Crops and New Uses* 2002, 1, 17–21.
16. Liu, L.; Jiao, J.Y.; Fang, B.Z.; Lv, A.P.; Ming, Y.Z.; Li, M.M.; S. https://doi.org/10.1016/j.syapm.2020.126104.
17. Goldberg, J. The Brazilian biofuels industry. *Biotechnol. Biofuels*. 2008, 1, 6–13, https://doi.org/10.1186/1756-6843-1-6.
18. Somerville, C.; Youngs, H.; Taylor, C.; Davis, S.C.; Long, S.P. Feedstocks for lignocellulosic biofuels. *Science* 2010, 329, 790–792, https://doi.org/10.1126/science.1189268.
19. Vandenbossche, V.; Brautl, J.; Vilarem, G.; Hernández-Meléndez, O.; Vivaldo-Lima, E.; Hernández-Luna, M.; Barzana, E.; Duque, A.; Manzanares, P.; Ballesteros, M.; Mata, J. A new lignocellulosic biomass deconstruction process combining thermo-mechano chemical action and bio-catalytic enzymatic hydrolysis in a twin-screw extruder. *Ind. Crops. Prod.* 2014, 55, 258–266, https://doi.org/10.1016/j.indcrops.2014.02.022.
20. Prasad, R.K.; Chatterjee, S.; Sharma, S.; Mazumder, P.B.; Vairale, M.G.; Raju, P.S. Insect gut bacteria and their potential application in degradation of lignocellulosic biomass: a review. In: *Bioremediation: applications for environmental protection and management*. Varjani, S.J.; Agarwal, A.K.; Gnansounou, E.; Gurunathan, B. (eds.). Springer, Singapore, 2018; pp. 277–299, https://doi.org/10.1007/978-981-10-7485-1_14.
21. Houfani, A.A.; Anders, N.; Spiess, A.C.; Baldrian, P.; Benalloua, S. Insights from enzymatic degradation of cellulose and hemicellulose to fermentable sugars–a review. *Biomass Bioenergy* 2020, 134, https://doi.org/10.1016/j.biombioe.2020.105481.
22. Phan, P.T.; Nguyen, B.S.; Nguyen, T.A.; Kumar, A.; Nguyen, V.H. Lignocellulose-derived monosugars: a review of biomass pre-treating techniques and post-methods to produce sustainable biohydrogen. *Biomass. Convers. Bioen. 2020*, 1–15, https://doi.org/10.1007/s13399-020-01161-7.
23. Béguin, P.; Aubert, J.P. The biological degradation of cellulose. *FEBS Microbiol. Rev.* 1994, 13, 25–58, https://doi.org/10.1111/j.1574-6976.1994.tb00333.x.
24. Kuhad, R.C.; Gupta, R.; Singh, A. Microbial cellulases and their industrial applications. *Enzyme Res.* 2011, 2011, 1–10, http://dx.doi.org/10.4061/2011/280696.
25. Karmakar, M.; Ray, R.R. Current trends in research and application of microbial cellulases. *Res. J. Microbiol.* 2011, 6, 41–53, https://doi.org/10.3923/jm.2011.41.53.
26. Menéndez, E.; Ramírez-Bahena, M.H.; Fabryová, A.; Igual, J.M.; Benada, O.; Mateos, P.F.; Peix, A.; Kolarik, M.; García-Fraile, P.*Pseudomonas celluloperorum* sp. nov., a cellulase-producing bacterium isolated from the bark beetle *Hylesinus fraxini*. *Int. J. Syst. Evol. Microbiol.* 2015, 65, 2852–2858, https://doi.org/10.1099/ijis.0.000344.
27. Bajaj, P.; Mahajan, R. Cellulase and xylanase synergism in industrial biotechnology. *Appl. Microbiol. Biotechnol.* 2019, 103, 8711–8724, https://doi.org/10.1007/s00253-019-10146-0.
28. Chakraborty, D.; Sarkar, N.; Biswas, I.; Jacob, S. Molecular aspects of prokaryotic and eukaryotic cellulases and their modulation for potential application in biofuel production. In: *Genetic and Metabolic Engineering for Improved Biofuel Production from Lignocellulosic Biomass*. Elsevier, 2020, pp. 81–95, https://doi.org/10.1016/B978-0-12-817953-6.00006-3.
29. Piskur, J.; Rozpedowska, E.; Polakova, S.; Merico, A.; Compagno, C. How did *Saccharomyces* evolve to become a good brewer? *TrendsGenet.* 2006, 22, 183–186, https://doi.org/10.1016/j.tig.2006.02.002.
Huang, S.; Sheng, P.; Zhang, H. Isolation and identification of cellulolytic bacteria from the gut of Holotrichia parallela larvae (Coleoptera: Scarabaeidae). *Int. J. Mol. Sci.* **2012**, *13*, 2563–2577, [https://doi.org/10.3390/ijms13032563](https://doi.org/10.3390/ijms13032563).

Oh, E.J.; Jin, Y.S. Engineering of *Saccharomyces cerevisiae* for efficient fermentation of cellulose. *FEMS Yeast Res.* **2020**, *20*, [https://doi.org/10.1093/femsyr/foz89](https://doi.org/10.1093/femsyr/foz89).

Walker, G.M.; Basso, T.O. Mitigating stress in industrial yeasts. *Fungal Biol.* **2020**, *124*, 387–97, [https://doi.org/10.1016/j.fungi.2019.10.010](https://doi.org/10.1016/j.fungi.2019.10.010).

Claes, A.; Deparis, Q.; Foulquié-Moreno, M.R.; Thevelein, J.M. Simultaneous secretion of seven lignocellulolytic enzymes by an industrial second-generation yeast strain enables efficient ethanol production from multiple polymeric substrates. *Metab. Eng.* **2020**, *59*, 131–141, [https://doi.org/10.1016/j.ymben.2020.02.004](https://doi.org/10.1016/j.ymben.2020.02.004).

Eardley, J.; Timson, D.J. Yeast cellular stress: impacts on bioethanol production. *Ferment.* **2020**, *6*, [https://doi.org/10.3390/fermentation6040109](https://doi.org/10.3390/fermentation6040109).

Mihajlovski, K.; Buntić, A.; Milić, M.; Rajilić-Stojanović, M.; Dimitrijević-Branković, S. From agricultural waste to biofuel: enzymatic potential of a bacterial isolate *Streptomyces fulvisimus* CKS7 for bioethanol production. *Waste Biomass Valorization* **2020**, *12*, 165–174, [https://doi.org/10.1007/s12649-020-00960-3](https://doi.org/10.1007/s12649-020-00960-3).

Thapa, S.; Mishra, J.; Arora, N.; Mishra, P.; Li, H.; O’Hair, J.; Bhatti, S.; Zhou, S. Microbial lignocellulolytic enzymes: diversity and biotechnology with reference to lignocellulosic biomass degradation. *Rev. Environ. Sci. Biotechnol.* **2020**, *19*, 621–648, [https://doi.org/10.1007/s11157-020-09536-y](https://doi.org/10.1007/s11157-020-09536-y).

Amore, A.; Pepe, O.; Ventorino, V.; Aliberti, A.; Faraco, V. Cellulolytic *Bacillus* strains from natural habitats - a review. *Chimica Oggi/Chemistry Today* **2013**, *31*, 49–52.

Amore, A.; Pepe, O.; Ventorino, V.; Birolo, L.; Giangrande, C.; Faraco, V. Industrial waste based compost as a source of novel cellulolytic strains and enzymes. *FEMS. Microbiol. Lett.* **2013**, *339*, 93–101, [https://doi.org/10.1016/j.femsle.2013.04.011](https://doi.org/10.1016/j.femsle.2013.04.011).

Saffari, H.; Pourbabaei, A.A.; Asgharzadeh, A.; Besharati, H. Isolation and identification of effective cellulolytic bacteria in composting process from different sources. *Arch. Agron. Soil. Sci.* **2017**, *63*, 297–307, [https://doi.org/10.1007/s00130-016-11980-6](https://doi.org/10.1007/s00130-016-11980-6).

Harindintwali, J.D.; Zhou, J.; Yu, X. Lignocellulosic crop residue composting by cellulolytic nitrogen-fixing bacteria: a novel tool for environmental sustainability. *Sci. Total Environ.* **2020**, *715*, [https://doi.org/10.1016/j.scitotenv.2020.136912](https://doi.org/10.1016/j.scitotenv.2020.136912).

Mahmood, R.; Afrin, N.; Jolly, S.N.; Shilpi, R.Y. Isolation and identification of cellulose-degrading bacteria from different types of samples. *World J. Environ. Biosci.* **2020**, *9*, 8–13.

Watanabe, H.; Tokuda, G. Cellulolytic systems in insects. *Annu. Rev. Entomol.* **2010**, *55*, 609–632, [https://doi.org/10.1146/annurev-ento-112408-085319](https://doi.org/10.1146/annurev-ento-112408-085319).

Zhang, X.Z.; Zhang, Y.H. Cellulases: characteristics, sources, production, and applications. *Bioprocessing Technologies in Biorefinery for Sustainable Production of Fuels, Chemicals, and Polymers* **2013**, *1*, 131–146, [https://doi.org/10.1002/9781118642047.ch8](https://doi.org/10.1002/9781118642047.ch8).

Douglas, A.E. The microbial dimension in insect nutritional ecology. *Funct. Ecol.* **2009**, *23*, 38–47, [https://doi.org/10.1111/j.1365-2435.2008.01442.x](https://doi.org/10.1111/j.1365-2435.2008.01442.x).

Jing, T.Z.; Qi, F.H.; Wang, Z.Y. Most dominant roles of insect gut bacteria: digestion, detoxification, or essential nutrient provision? *Microbiome* **2020**, *8*, 1–20, [https://doi.org/10.1186/s40168-020-00823-y](https://doi.org/10.1186/s40168-020-00823-y).

Bayer, E.A.; Belaich, J.P.; Shoham, Y.; Lamed, R. The cellulosomes: multienzyme machines for degradation of plant cell wall polysaccharides. *Annu. Rev. Microbiol.* **2004**, *58*, 521–554, [https://doi.org/10.1146/annurev.micro.57.030502.091022](https://doi.org/10.1146/annurev.micro.57.030502.091022).

Jayasekara, S.; Ratnayake, R. Microbial cellulases: an overview and applications. In: *Cellulose*. Intechopen, **2019**, pp. 1–21, [https://doi.org/10.5772/intechopen.84531](https://doi.org/10.5772/intechopen.84531).

Leo, V.V.; Ramesh, N.; Singh, B.P. Microorganisms as an efficient tool for cellulase production: availability, diversity, and efficiency. In: *New and Future Developments in Microbial Biotechnology and Bioengineering*. Elsevier, **2019**, pp. 45–61, [https://doi.org/10.1016/B978-0-444-64223-3.00004-7](https://doi.org/10.1016/B978-0-444-64223-3.00004-7).

Nitisinprasert, S.; Temmes, A. The characteristics of a new non-spore-forming cellulosomal mesophilic anaerobe strain CM126 isolated from municipal sewage sludge. *J. Appl. Bacteriol.* **1991**, *71*, 154–161, [https://doi.org/10.1111/j.1365-2672.1991.tb02972.x](https://doi.org/10.1111/j.1365-2672.1991.tb02972.x).

Ram, L.; Kaur, K.; Sharme, S. Screening, isolation and characterization of cellulase producing microorganisms from soil. *Int. J. Pharm. Sci. Invent.* **2014**, *3*, 12–18.

Magotra, S.; Magotra, M. S. Isolation of cellulose degrading bacteria from soil sample. *PalArch's Journal of Archaeology of Egypt/Egyptology* **2019**, *17*, 6099–6110.

Maravi, P.; Kumar, A. Isolation, screening and identification of cellulolytic bacteria from soil. *Biotechnol. J.* **2020**, *24*, 1–8, [https://doi.org/10.1002/bjt3.21300092](https://doi.org/10.1002/bjt3.21300092).

Alavijeh, R.S.; Karimi, K.; van den Berg, C. An integrated and optimized process for cleaner production of ethanol and biodiesel from corn stover by *Mucor indicus*. *J. Clean. Prod.* **2019**, *249*, [https://doi.org/10.1016/j.jclepro.2019.119321](https://doi.org/10.1016/j.jclepro.2019.119321).

Coniglio, R.O.; Diaz, G.V.; Fonseca, M.I.; Castrillo, M.L.; Piccinni, F.E.; Villalba, L.L.; Campos, E.; Zapata, P.D. Enzymatic hydrolysis of barley straw for biofuel industry using a novel strain of *Trametes villosa* from...
Appl. Microbiol. Biotechnol. 2020, 1–10, https://doi.org/10.1007/s00253-020-09629-9
55. Ma, L.; Lu, Y.; Yan, H.; Wang, X.; Yi, Y.; Shan, Y.; Liu, B.; Zhou, Y.; Lü, X. Screening of cellulolytic bacteria from rotten wood of Qinling (China) for biomass degradation and cloning of cellulates from Bacillus methylotrophicus. BMC Biotechnol. 2020, 20, 1–13, https://doi.org/10.1186/s12896-019-0593-8.
56. Naresh, S.; Kunasundari, B.; Gunni, A.A.N.; Teoh, Y.P.; Shuit, S.H.; Ng, Q. H.; Hoo, P.Y. Isolation and partial characterisation of thermophilic cellulolytic bacteria from north Malaysian tropical mangrove soil. Trop. Life Sci. Research 2019, 30, 123–147, https://doi.org/10.21315/tlsr-2019.30.1.8.
57. Biswas, S.; Al Saber, M.; Tripty, I.A.; Karim, M.A.; Islam, M.A.; Hasan, M.S.; Alam, A.R.U.; Jahid, M.I.K.; Hasan, M.N. Molecular characterization of cellulolytic and endo-and exoglucanase bacteria from the largest mangrove forest (Sundarbans). Ann. Microbiol. 2020, 70, 1–11, https://doi.org/10.1186/s13213-020-01606-4.
58. Chantarasiri, A. Diversity of cellulolytic bacteria isolated from a freshwater wetland reserve in Thailand and their cellulolytic activity. Appl. Ecol. Environ. Res. 2020, 18, 5965–5983, http://dx.doi.org/10.15666/aee/1804_59655983.
59. Zhang, H.; Li, Q.; Zhao, Y.; Zhang, M.; Xu, D.; Wu, Z.; Zhou, Q. Endoglucanase activity of cellulolytic bacteria from lake sediments and its application in hydrophate degradation. FEMS Microbiol. Lett. 2020, 367, https://doi.org/10.1093/femsle/fnaa200.
60. Hajiabadi, S.; Mashreghi, M.; Bahrami, A.R.; Ghazvini, K.; Matin, M.M. Isolation and molecular identification of cellulolytic bacteria from Dig Rostam hot spring and study of their cellulase activity. Biocell 2020, 44, 63–71, https://doi.org/10.32604/biocell.2020.08171.
61. Barzkar, N.; Sohail, M. An overview on marine cellulolytic enzymes and their potential applications. Appl. Microbiol. Biotechnol. 2020, 104, 6873–6892, https://doi.org/10.1007/s00253-020-10692-y.
62. Ren, W.; Xu, X.; Long, H.; Cai, X.; Huang, A.; Xie, Z. Isolation and characterization of cellulolytic marine bacteria for Litopenaeus Vannamei aquaculture using sugarcane bagasse as carbon source. Research Square 2020, https://doi.org/10.21203/rs.3.rs-67558/v1.
63. Yokoe, Y.; Yasumasu, I. The distribution of cellulase in invertebrates. Comp. Biochem.Physiol. 1964, 13, 323–338, https://doi.org/10.1016/0106-046X(64)90027-1.
64. Cazemier, A.E.; den Camp, H.J.; Hackstein, J.H.; Vogels, G.D. Fibre digestion in arthropods. Comp. Biochem.Physiol. 1997, 118, 101–109, https://doi.org/10.1016/S0300-9629(96)00443-4.
65. Pothula, R.; Shirley, D.; Perera, O.; Chantarasiri, A. Diversity of cellulolytic bacteria isolated from a freshwater wetland reserve in Thailand and identification of cellulolytic bacterium from the gu. Appl. Ecol. Environ. Res. 2017, 13, 69–80, https://doi.org/10.15666/aeer/1804_59655983.
66. Scharf, M.E.; Tartar, A. Termite digestomes as sources for novel lignocellulases. Biotechnol. Biofuel. Bioprod. Biob. 2020, 2, 540–552, https://doi.org/10.1007/s13213-016-0107-y.
67. Kumar, A.; Poonia, A.; Sharma, R.; Jangra, M.; Sehrawat, R.; Sansanwal, R. Termite gut: home to microbiome. UTFR Journal of Grassland and Wildlife Management 2020, 11, 9–23.
68. Willis, J.D.; Oppert, C.; Jurat-Fuentes, J.L. Methods for discovery and characterization of cellulolytic enzymes from insects. Insect Sci. 2010, 17, 184–198, https://doi.org/10.1111/j.1744-7917.2010.01322.x.
69. Brune, A.; Dietrich, C. The gut microbiota of termites: digesting the diversity in the light of ecology and evolution. FEMS Microbiol. Lett. 2015, 69, 145–166, https://doi.org/10.1111/1574-6941.12575.
70. Ohkuma, M. Termite symbiotic systems: efficient bio-recycling of lignocellulose. Appl. Microbiol. Biotechnol. 2003, 61, 1–9, https://doi.org/10.1007/s00253-002-1189-z.
71. Scharf, M.E.; Tartar, A. Termite digestomes as sources for novel lignocellulases. Biofuel. Bioprod. Biob. 2008, 2, 540–552, https://doi.org/10.1007/s13213-016-0107-y.
72. Brune, A.; Poonia, A.; Sharma, R.; Jangra, M.; Sehrawat, R.; Sansanwal, R. Termite gut: home to microbiome. Bull. Environ. Contam. Toxicol. 2021, 106, 994–1008, https://doi.org/10.1007/s00234-020-09154-1.
73. Upadhyaya, S.K.; Manandhar, A.; Mainali, H.; Pokhrel, A.R.R.; Rijal, A.; Pradhan, B.; Koirala, B. Isolation and characterization of cellulolytic bacteria from gut of termite. Rentech Symposium Compendium 2012, 1, 14–18.
74. Wenzel, M.; Schöning, I.; Berchtold, M.; Köpfmüller, P.; König, H. Aerobic and facultatively anaerobic cellulolytic bacteria from the gut of the termite Zootermopsis angusticollis. J. Appl. Microbiol. 2002, 92, 32–40, https://doi.org/10.1046/j.1365-2672.2002.01502.x.
75. Sibanda, A.; Ruzvidzo, O.; Ncube, I.; Ncube, T. Diversity of cellulase and xylanase-producing filamentous fungi from termite mounds. J. Yeast and Fungal Res. 2019, 10, 15–29, https://doi.org/10.5897/JYFR2019.0189.
76. Hethener, P.; Brauman, A.; Garcia, J.L. Clostridium termiditis sp. nov., a cellulolytic bacterium from the gut of the wood-feeding termite, Nasutitermes lujae. Syst. Appl. Microbiol. 1992, 15, 52–58, https://doi.org/10.1016/S0723-2020(11)80138-4.
78. Ferbiyanto, A.; Rusmana, I.; Raffiudin, R. Characterization and identification of cellulolytic bacteria from gut of worker Macrotermes gilvus. *HAYATI J. Biosci.* 2015, 22, 197–200, https://doi.org/10.1016/j.hjb.2015.07.001.

79. Tarun, L.J.R. Molecular characterization of cellulose-hydrolyzing bacteria isolates from the gut of Philippine milktermite (*Coptotermes gestroi*). *Asia Pac. J. Res.* 2016, 1, 136–143.

80. Peristiwati; Natamihardja, Y.S.; Herlini, H. Isolation and identification of cellulolytic bacteria from termite gut (*Cryptotermes sp.*). *J. Phys. Conf. Ser.* 2018, 1013, https://doi.org/10.1088/1742-6596/1013/1/012173.

81. Egwuatu, T.F.; Apphe, O.G. Isolation and characterization of filter paper degrading bacteria from the guts of *Coptotermes formosanus*. *J. Bioremed. Biodegrad.* 2018, 9, https://doi.org/10.4172/2155-6199.1000440.

82. Nidhi, K.; Gupta, S.K.; Bura, A.; Gandhi, A. Diversity of cellulose hydrolyzing bacteria from the gut of *Coptotermes heimi* (Rhinotermitidae). *Asian J. Biol. Life Sci.* 2018, 7, 28–32.

83. Tsegaye, B.; Balomajumder, C.; Roy, P. Isolation and characterization of novel lignolytic, cellulolytic, and hemicellulolytic bacteria from wood-decomposing termite *Coptotermes brevis*. *Int. Microbiol.* 2019, 22, 29–39, https://doi.org/10.1007/s10123-018-0024-z.

84. Ali, H.R.; Hemeda, N.F.; Abdelaliem, Y.F. Symbiotic cellulolytic bacteria from the gut of the subterranean termite *Psammotermes hypostoma* Desneux and their role in cellulose digestion. *AMB Express* 2019, 9, https://doi.org/10.1186/s13568-019-0830-5.

85. Femi-Ola, T.O.; Oyebamiji, B.A. Molecular characterization and cellulolytic activities of bacterial isolates from the hindgut of wood-decomposing termites *Amitermes evaniger* Silvestri. *J. Adv. Microbiol.* 2019, 1–10, https://doi.org/10.9734/JAMB/2019/45732.

86. Afraf, R.A.; Natsir, H.; Atifah, N.; Zarkoni, T.R.; Mahmud, M. Isolation and characterization of soil termites (*Macrotelitus gilvus*) cellulolytic bacteria and activity determination of cellulase enzyme on newsprint substrates. *J. Phys. Conf. Ser.* 2019, 1341, https://doi.org/10.1088/1742-6596/1341/3/032037.

87. Lang, S.S.; Hung, K.J.; Huat, O.K.P.; Samsi, I.H.; Sarbini, S.R.B. Digestive system of worker termite *Coptotermes curvignathus* Holmgren and its chemical and cellulolytic microbial properties. *Serangga* 2020, 25, 45–64.

88. Huang, S.W.; Zhang, H.Y.; Marshall, S.; Jackson, T.A. The scarab gut: a potential bioreactor for bio-fuel production. *Insect Sci.* 2010, 17, 175–183, https://doi.org/10.1111/j.1744-7917.2010.01320.x.

89. Cazember, A.E.; Verdores, J.C.; Reubsaat, F.A.; Hackstein, J.H.; van der Drift, C.; Den Camp, H.J. *Promicromonaspora pachnodae* sp. nov., a member of the (hemi) cellulolytic hindgut flora of larvae of the scarab beetle *Pachnoda marginata*. *Antonie van Leeuwenhoek* 2003, 83, 135–148, https://doi.org/10.1023/a:1023325817663.

90. Sheng, P.; Huang, S.; Wang, Q.; Wang, A.; Zhang, H. Isolation, screening, and optimization of the fermentation conditions of highly cellulolytic bacteria from the hindgut of *Holotrichia parallela* larvae (Coleoptera: Scarabaeidae). *Appl. Biochem. Biotechnol.* 2012, 167, 270–284, https://doi.org/10.1007/s12010-012-0970-3.

91. Sari, S.L.A.; Pangastuti, A.; Susilowati, A.; Purwoko, T.; Mahajoeno, I.; Kurniawati, D.; Anitasari, R. Cellulolytic and hemicellulolytic bacteria from the gut of *Oryctes rhinoceros* diversitas. *Biodiversitas* 2016, 17, 78–83.

92. Dini, I.R.; Wawan, W.; Hapsoh, H.; Sritawanyuni, S. Isolation and identification of cellulolytic and lignolytic bacteria from the gut of *Oryctes rhinoceros* Larvae decomposition of oil palm empty fruit bunches. *Indonesian J. Agr. Res.* 2018, 1, 193–203, https://doi.org/10.32734/injar.v1i2.314.

93. Shelomi, M.; Chen, M.J. Culturing-enriched metabarcoding analysis of the *Oryctes rhinoceros* gut microbiome. *Insects* 2020, 11, https://doi.org/10.3390/insects1110782.

94. Handique, G.; Phukan, A.; Bhattacharyya, B.; Baruah, A.A.; Rahman, S.W.; Baruah, R. Characterization of cellulose degrading bacteria from the larval gut of the white grub beetle *Lepidiotha mansueta* (Coleoptera: Scarabaeidae). *Arch. Insect Biochem. Physiol.* 2017, 94, https://doi.org/10.1002/arch.21370.

95. Mahbedeghe, M. Cellulolytic activities of the dung beetle, *Euoniticellus intermedius*, larva gut micro-flora. *The Open Biotechnol.* J. 2017, 11, 105–113, https://doi.org/10.2174/1874070701711010105.

96. Soko, K.M.; Bhattacharya, R.C.; Ramakrishnan, B.; Sharma, K.; Subramanian, S. Functional characterization of bacteria isolated from different gut compartments of white grub, *Anamala dimidiata*, larvae. *J. Environ. Biol.* 2020, 41, 1526–1535, http://doi.org/10.22438/jeb/41/6/MRN-1420.

97. Hu, X.; Yu, J.; Wang, C.; Chen, H. Cellulolytic bacteria associated with the gut of *Dendroctonus armandi* larvae (Coleoptera: Curculionidae: Scolytinae). *Forests* 2014, 5, 455–465, https://doi.org/10.3390/f5030455.

98. Hafezi, A.; Makhdoumi, A.; Asoodeh, A.; Mirshamis, O. Characterization of a bi-functional cellulase produced by a gut bacterial resident of Rosaceae branch borer Beetle, *Osphranderia coerulescens* (Coleoptera: Cerambycidae). *Int. J. Biol. Macromol.* 2017, 103, 158–164, https://doi.org/10.1016/j.ijbiomac.2017.05.042.

99. Bhuvaramwan, S.; Reshma, T.; Hilda, K.; Balaji, R.; Meenakumari, M.; Mathivanan, N.; Janarthanan, S. Purification and characterization of an endogenous cellulase from the digestive system of grub of banana pseudostem weevil *Odoiporus longicollis* (Olivier). *Research Square* 2020, https://doi.org/10.21203/rs.3.rs-38095/v1.
Dantur, K.I.; Enrique, R.; Welin, B.; Castagnaro, A.P. Isolation of cellulolytic bacteria from the intestine of *Diatraea saccharalis* larvae and evaluation of their capacity to degrade sugarcane biomass. *AMB Express* 2015, 5, https://doi.org/10.1038/s13568-015-0101-z.

Barbosa, K.L.; dos Santos Malta, V.R.; Machado, S.S.; Junior, G.A.L.; da Silva, A.P.V.; Almeida, R.M.R.G.; da Luz, J.M.R. Bacterial cellulase from the intestinal tract of the sugarcane borer. *Int. J. Biol. Macromol.* 2020, 161, 441–448, https://doi.org/10.1016/j.ijbiomac.2020.06.042.

Anand, A.A.; Vennison, S.J.; Sankar, S.G.; Gilwax Prabhu, D.J.; Vasan, P.T.; Raghuraman, T.; Jerome Geoffroy, C.; Vendan, S.E. Isolation and characterization of bacteria from the gut of *Bombbyx mori* that degrade cellulose, xylan, pectin and starch and their impact on digestion. *J. Insect Sci.* 2010, 10, https://doi.org/10.1673/031.010.10701.

Revathy, K.; Pandiarajan, J. Cellulolytic potential of gut bacterial biomass in silkworm *Bombbyx mori*. *L. Ecological Genetics and Genomics* 2020, 14, https://doi.org/10.1016/j.jegg.2019.100045.

Lee, F.J.; Rusch, D.B.; Stewart, F.J.; Mattila, H.R.; Newton, J.L. Saccharide breakdown and fermentation by the honey bee gut microbiome. *Environ. Microbiol.* 2015, 17, 796–815, https://doi.org/10.1111/1462-2920.12526.

Chakraborty, N.; Sarkar, G.M.; Lahirii, S.C. Cellulose degrading capabilities of cellulolytic bacteria isolated from the intestinal fluids of the silver cricket. *Environmentalist* 2000, 20, 9–11, https://doi.org/10.1023/A:1006691524607.

Banerjee, S.; Maiti, T.K.; Roy, R.N. Production, purification, and characterization of cellulase from *Acinetobacter junii* GAC 16.2, a novel cellulolytic gut isolate of *Gryllotalpa africana*, and its effects on cotton fiber and sawdust. *Ann. Microbiol.* 2020, 70, 1–16, https://doi.org/10.1186/s13213-020-01569-6.

Prasad, R.K.; Chatterjee, S.; Mazumder, P.B.; Sharma, S.; Datta, S.; Vaireale, M.G.; Dwivedi, S.K. Study on cellulase (β-1, 4-endoglucanase) activity of gut bacteria of *Sitophilus oryzae* in cellulotic waste biodegradation. *Bioreose. Technol. Rep.* 2019, 7, https://doi.org/10.1007/s12895-019-00274.

Azizah; Purwatiningsih; Wyono, H.T. Muzakhar, K. Morphological and biochemical characteristic of endosymbiotic cellulolytic bacteria from gut of *Hypothemenum hampei* Ferr. and its enzyme activity. In *AIP Conference Proceedings* 2020, 2296, https://doi.org/10.1063/5.0030576.

Nelson, K.; Muge, E.; Wamalwa, B. Cellulolytic *Bacillus* species isolated from the gut of the desert locust *Schistocerca gregaria*. *Scientific African* 2020, 11, https://doi.org/10.1016/j.sciaf.2020.e00665.

Yokoe, Y. Cellulase activity in the termite, *Leucotermes speratus*, with new evidence in support of a cellulase produced by the termite itself. *Scientific Papers of the College of General Education, University of Tokyo, Biology 1964, 14, 115–120.

Watanabe, H.; Noda, H.; Tokuda, G.; Lo, N. A cellulase gene of termite origin. *Nature* 1998, 394, 330–331, https://doi.org/10.1038/28527.

Lee, S.J.; Kim, S.R.; Yoon, H.J.; Kim, I.; Lee, K.S.; Je, Y.H.; Lee, S.M.; Soo, S.J.; Sohn, H.D.; Jin, B.R. cDNA cloning, expression, and enzymatic activity of a cellulase from the mulberry longicorn beetle, *Apriona germari*. *Comp. Biochem. Physiol. B Biochem. Mol. Biol.* 2004, 139, 107–116, https://doi.org/10.1016/j.cbpb.2004.06.015.

Wei, Y.D.; Lee, K.S.; Gui, Z.Z.; Yoon, H.J.; Kim, I.; Zhang, G.Z.; Guo, X.; Sohn, H.D.; Jin, B.R. Molecular cloning, expression, and enzymatic activity of a novel endogenous cellulase from the mulberry longicorn beetle. *Apriona germari*. *Comp. Biochem. Physiol. B Biochem. Mol. Biol.* 2006, 145, 220–229, https://doi.org/10.1016/j.cbpb.2006.07.007.

Kunieda, T.; Fujiyuki, T.; Kucharski, K.R.; Foret, S.S.; Ament, A.; Toth, A.L.; Ohashi, K.; Takeuchi, H.; Kamikouchi, A.; Kage, E.; Morioka, M. Carbohydrate metabolism genes and pathways in insects: insights from the honey bee genome. *Insect Mol. Biol.* 2006, 15, 563–576, https://doi.org/10.1111/j.1365-2583.2006.00677.x.

Kim, N.; Choo, Y.M.; Lee, K.S.; Hong, S.J.; Seol, K.Y.; Je, Y.H.; Sohn, H.D.; Jin, B.R. Molecular cloning and characterization of a glycosyl hydrolase family 9 cellulase distributed throughout the digestive tract of the cricket *Teleogryllus emma*. *Comp. Biochem. Physiol. B Biochem. Mol. Biol.* 2008, 150, 368–376, https://doi.org/10.1016/j.cbpb.2008.04.005.

Tokuda, G.; Watanabe, H.; Matsumoto, T.; Noda, H. Cellulose digestion in the wood-eating higher termite, *Nasutitermes takasagoensis* (Shiraki): distribution of cellulases and properties of endo-β-1, 4-glucanase. *Zool. Sci.* 1997, 14, 83–93, https://doi.org/10.2108/zsj.14.83.

Warnecke, F.; Luginbuhl, P.; Ivanova, N.; Ghassenian, M.; Richardson, T.H.; Stege, J.T.; Cayouette, M.; Mc Hardy, A.C.; Djordjevic, G.; Aboushadi, N.; Sorke, R. Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. *Nature 2007*, 450, 560–565, https://doi.org/10.1038/nature06269.

Liu, J.; Song, K.; Teng, H.; Zhang, B.; Li, W.; Xue, H.; Yang, X. Endogenous cellulolytic enzyme systems in the longhorn beetle *Mesosa myops* (Insecta: Coleoptera) studied by transcriptomic analysis. *Acta Biochim. Biophys. Sin.* 2015, 47, 741–748, https://doi.org/10.1093/abbs/gnv070.

Ferreira, A.H.; Marana, S.R.; Terra, W.R.; Ferreira, C. Purification, molecular cloning, and properties of a β-glucosidase isolated from midgut lumen of *Tenebrio molitor* (Coleoptera) larvae. *Insect Biochem. Mol. Biol.* 2001, 31, 1065–1076, https://doi.org/10.1016/S0965-1748(01)00054-6.
120. Slator, M. Cellulose digestion in termites and cockroaches: what role do symbionts play? *Comp. Biochem. Physiol. B Biochem. Mol. Biol. 1992*, 103, 775–784, https://doi.org/10.1016/0305-0491(92)90194-V.

121. Willis, J.D.; Klingman, W.E.; Oppert, C.; Oppert, B.; Jurat-Fuentes, J.L. Characterization of cellulolytic activity from digestive fluids of *Dissosteira carolina* (Orthoptera: Acrididae). *Comp. Biochem. Physiol. B Biochem. Mol. Biol. 2010*, 157, 267–272, https://doi.org/10.1016/j.cbpb.2010.06.012.

122. Su, L.J.; Liu, H.; Li, Y.; Zhang, H.F.; Chen, M.; Gao, X.H.; Wang, F.Q.; Song, A.D. Cellulolytic activity and structure of symbiotic bacteria in locust guts. *Genet. Mol. Res. 2014*, 13, 7926–7936, https://doi.org/10.4238/2014.september.29.6.

123. Beloqui, A.; Nechitaylo, T.Y.; López-Cortés, N.; Ghazi, A.; Guazzaroni, M.E.; Polaina, J.; Strittmatter, A.W.; Reva, O.; Waliczek, A.; Yakimov, M.M.; Golyshina, O.V. Diversity of glycosyl hydrolases from cellulase-depleting communities enriched from casts of two earthworm species. *Appl. Environ. Microbiol. 2010*, 76, 5934–5946, https://doi.org/10.1128/AEM.00902-10.

124. Shankar, T.; Mariappan, V.; Isaiaarasu, L. Screening cellulolytic bacteria from the mid-gut of the popular composting earthworm, *Eudrilus eugeniae* (Kinberg). *World J. Zool. 2011*, 6, 142–148.

125. Utekar, G.V.; Deshmukh, H.V. Characterization of *Bacillus* sp. from gut flora of earthworm *Eudrilus eugeniae* feed on sugar industry waste. *Res. J. Life Sci. Bioinform. Pharm. Chem. Sci. 2019*, 5, 887–895, https://doi.org/10.26479/2019.0502.66.

126. Shankar, T.; Sankaralingam, S.; Balachandran, C.; Chinnathambi, A.; Nasif, O.; Ali Alharbi, S.; Park, S.; Baskar, K. Purification and characterization of carboxymethylcellulase from *Bacillus pumilus* EWBCM1 isolated from earthworm gut (*Eudrilus eugeniae*). *J. King Saud Univ.-Sci. 2020*, 33, https://doi.org/10.1016/j.jsus.2020.101261.

127. Fuji, K.; Ikeda, K.; Yoshida, S. Isolation and characterization of aerobic microorganisms with cellulolytic activity in the gut of endogeic earthworms. *Int. Microbiol. 2012*, 15, 121–130, https://doi.org/10.2436/20.1501.01.165.

128. Jyotsna, K.P.; Vijayalakshmi, K.; Prasanna, N.D.; Shaheen, S.K. Isolation, characterization of cellulase producing *Lysinibacillus sphaericus* MTCC No. 9468 from gut of *Eisenia fetida*. *Bioscan 2011*, 6, 325–327.

129. Parihar, D.K. Isolation and screening of cellulolytic bacteria inhabiting gut of *Eisenia fetida* fed on municipal solid waste. *Int. Adv. Res. J. Sci. Eng. Technol. 2016*, 3, 84–88.

130. Dey, K.K.; Talukdar, N.C.; Nongkhlaw, F.M.; Thakuria, D. Isolation, characterization and practical significance of cellulose degrading bacteria from the gut wall of two ecologically distinct earthworms. *Curr. Sci. 2018*, 114.

131. Zhang, B.G.; Rouland, C.; Lattaad, C.; Lavelle, P. Activity and origin of digestive enzymes in gut of the tropical earthworm *Pontoxycolex corethrus*. *European J. Soil Biol. 1993*, 29, 7–11.

132. Lattaad, C.; Locati, S.; Mora, P.; Rouland, C. Origin and activities of glycolytic enzymes in the gut of the tropical geophagous earthworm *Millsonia anomala* from Lamto (Cô te d'Ivoire). *Pedobiologia 1997*, 41, 242–251.

133. Lattaad, C.; Zhang, B.G.; Locati, S.; Rouland, C.; Lavelle, P. Activities of the digestive enzymes in the gut and in tissue culture of a tropical geophagous earthworm, *Polypertherina elongata* (Megascolecidae). *Soil Biol. Biochem. 1997*, 29, 335–339, https://doi.org/10.1016/S0038-0717(96)00021-1.

134. Garvin, M.H.; Lattaad, C.; Trigo, D.; Lavelle, P. Activity of glycolytic enzymes in the gut of *Hormogaster elisae* (Oligochaeta, *Hormogastridae*). *Soil Biol. Biochem. 2000*, 32, 929–934, https://doi.org/10.1016/S0038-0717(99)00222-9.

135. Lattaad, C.; Mora, P.; Garvin, M.H.; Locati, S.; Rouland, C. Enzymatic digestive capabilities in geophagous earthworms-origin and activities of cellulolytic enzymes. *Pedobiologia 1999*, 43, 842–850.

136. Nozaki, M.; Miura, C.; Tozawa, Y.; Miura, T. The contribution of endogenous cellulase to the cellulose digestion in the gut of earthworm (*Phoretima hiligendorfii*; Megascolecidae). *Soil Biol. Biochem. 2009*, 41, 762–769, https://doi.org/10.1016/j.soilbio.2009.01.016.

137. Raut, S.K.; Ghose, K.C. Pestiferous land snail snail of India. *Technical Monograph ZSI, Calcutta 1984*, 11.

138. Biedermann, W.; Moritz, P. Beiträge zur vergleichenden physiologie der Verdauung. II. Über ein cellulolöselösendes enzyme im Lebersekreten der Schnecke (*Helix pomatia*). *Pflügers Archiv 1898*, 73, 219–287, https://doi.org/10.1007/BF01796256.

139. Seilliere, G. Utilisation des pentosanes par les organismes animaux. *C. R. Acad. Sci. Paris 1907*, 145, 1041–43.

140. Florkin, M.; Lozet, F. Origine bacterienne de la cellulase du contenu intestinal de L’Escargot. *Arch. Int. Physiol. Biochim. Biophys. 1949*, 57, 201–207.

141. Jeuniaux, C. Highlighting of a chitinolytic bacterial flora in the digestive tube of Esgargot (*"Helix Pomatia L."*). *Arch. Int. Physiol. 1950*, 58, 350–351, https://doi.org/10.3109/13813455009144965.

142. Jeuniaux, C. The intestinal chitinolytic bacterial flora of the snail (*Helix pomatia L.*): quantitative and qualitative analysis. *Bull. Soc. R. Sci. Liège.* 1955, 254–270.

143. Soedigdo, R.; Nio, I.S.; Adiwikarta, S.; Barnett, R.C. Cellulase from the snail *Achatina fulica* (Fer).*Physiol. Zool. 1970*, 43, 139–144, https://doi.org/10.1086/physzool.43.2.30155523.
144. Dar, M.A.; Chintalchere, J.M.; Pandit, R.S. Extraction and characterization of endogenous cellulases in *Achatina fulica* for lignocellulose digestion. *Fundam. Appl. Agric.* 2020, 5, 224–234, https://doi.org/10.5455/faa.91698.

145. Pinheiro, G.L.; Correa, R.; Soares, R.; Cardoso, A.; Chaia, C.; Clementino, M.M.; Garcia, E.; Souza De, W.; Frasès, S. Isolation of aerobic cultivable cellulolytic bacteria from different regions of the gastrointestinal tract of giant land snail *Achatina fulica*. *Front. Microbiol.* 2015, 6, https://doi.org/10.3389/fmicb.2015.00860.

146. Wijanjaarka, W.; Kusdiyantini, E.; Parman, S. Screening cellulolytic bacteria from the digestive tract of snail (*Achatina fulica*) and test the ability of cellulase activity. *Biosaintifikja: J. Biol. Educ.* 2016, 8, 385–391, https://doi.org/10.15294/biosaintifikja.v8i3.7263.

147. Aravind, K.K.; Sandeep, S.; Subramaniyan, S. Analysis of microbes and their enzymes in *Achatina fulica*. *Int. J. Sci. Res.* 2017, 6, 1897–1903.

148. Oyeleke, S.B.; Egwim, E.C.; Oyewole, O.A.; John, E.E. Production of cellulase and protease from microorganisms isolated from gut of *Archachatina marginata* (Giant African Snail). *SciTechnol* 2012, 2, 15–20, https://doi.org/10.5923/j.scit.20120201.03.

149. Ademolu, K.O.; Ojo, V.O.; Bamidele, J.A.B.; Adelabu, A.B.; Ebenso, I.; Idowu, A.B. Feeding pattern and gut enzymes activity of Giant African land snail (*Archachatina marginata*) during growth phases. *Arch. Zootec.* 2017, 66, 29–34, https://doi.org/10.21071/az.v66i253.2122.

150. Charrier, M.; Brune, A. The gut microenvironment of helicid snails (Gastropoda: Pulmonata): in-situ profiles of pH, oxygen and hydrogen determined by microsensors. *Can. J. Zool.* 2003, 81, 928–935, https://doi.org/10.1139/z03-003.

151. Charrier, M.Y.; Fonty, G.; Gaillard-Martini, B.; Ainouche, K.; Andant, G. Isolation and characterization of cultivable fermentative bacteria from the intestine of two edible snails, *Helix pomatia* and *Cornu aspersum* (Gastropoda: Pulmonata). *Biol. Res.* 2006, 39, 669–681, https://doi.org/10.4067/s0716-976020060000500010.

152. Charrier, M.; Combat-Blanc, Y.; Ollivier, B. Bacterial flora in the gut of *Helix aspersa* (Gastropoda Pulmonata): evidence for a permanent population with a dominant homolactic intestinal bacterium, *Enterococcus casseilavus*. *Can. J. Microbiol.* 1998, 44, 20–27.

153. Gomare, S.; Kim, H.A.; Ha, J.H.; Lee, M.W.; Park, J.M. Isolation of the polysaccharidase-producing bacteria from the gut of sea snail, *Batillus cornutus*. *Korean J. Chem. Eng.* 2011, 28, 1252–1259, https://doi.org/10.1007/s11814-010-0506-y.

154. Distel, D.L.; Morril, W.; Maclaren-Toussaint, N.; Franks, D.; Waterbury J. *Teredinibacter turnerae* gen. nov., sp. nov., a dinitrogen-fixing, cellulolytic, endosymbiotic gamma-proteobacterium isolated from the gills of wood-boring molluscs (*Bivalvia: Teredinidae*). *Int. J. Syst. Evol. Microbiol.* 2002, 52, 2261–2269.

155. O’Connor, R.M.; Fung, J.M.; Sharp, K.H.; Benner, J.S.B.; Mc Clung, C.; Cushing, S.; Lamkin, E.R.; Fomenkov, A.I.; Henriassat, B.; Londer, Y.Y.; Scholz, M.B. Gill bacteria enable a novel digestive strategy in a wood-feeding mollusk. *Proc. Nat. Acad. Sci.* 2011, 111, E5096–E5104, https://doi.org/10.1073/pnas.1113110111.

156. Altamia, M.A.; Shipway J.R.; Stein, D.; Betcher, M.A.; Fung, J.M.; Jospin, G.; Eisen, J.; Haygood, M.G.; Distel, D.L. *Teredinibacter* bacteriury sp. nov., a marine, cellulolytic endosymbiotic bacterium isolated from the gills of the wood-boring mollusc *Bankia setacea* (*Bivalvia: Teredinidae*) and emended description of the genus *Teredinibacter*. *Int. J. Syst. Evol. Microbiol.* 2020, 70, 2388–2394, https://doi.org/10.1099/ijsem.0.004049.

157. Maldonado, G.C.; Moura, M.; Skinner, L.F.; AraÚjo, F.V. Evaluation of wood degradation rates by *Teredinidae* (Mollusca: Bivalvia) in two ecologically distinct areas, and temperature and salinity influences on the cellulolytic activity of associated bacteria. *An. Acad. Bras. Ciênc.* 2020, 92, https://doi.org/10.1590/0013-76522020180970.

158. Joyson, R.; SWamy, A.; Bou, P.A.; Chapuis, A.; Ferry, N. Characterization of cellulolytic activity of the gut of the terrestrial land slug *Arion ater*: biochemical identification of targets for intensive study. *Comp. Biochem. Physiol. B Biochem. Mol. Biol.* 2014, 177, 29–35, https://doi.org/10.1016/j.cbpb.2014.08.003.

159. Tsuji, A.; Tominaga, K.; Nishiyama, N.; Yuasa, K. Comprehensive enzymatic analysis of the cellulolytic system in digestive fluid of the Sea Hare *Aplysia kurodai*. Efficient glucose release from sea lettuce by synergistic action of 45 kDa endoglucanase and 210 kDa b-glucosidase. *PLoS One* 2013, 8, https://doi.org/10.1371/journal.pone.0065418.

160. Yusuf, M.; Penid, N.; Danjumma, B.J.; Sahabi, B.M. Isolation of cellulolytic and methanogenic bacteria from the mid and hind gut of termites (Isoperta). *Int. J. Adv. Acad. Res. Sci. Technol. Eng.* 2018, 4, 1–13.

161. Gupta, P.; Samant, K.; Sahu, A. Isolation of cellulose-degrading bacteria and determination of their cellulolytic potential. *Int. J. Microbiol.* 2012, 2012, 1–5, https://doi.org/10.1155/2012/578925.

162. Shil, R.K.; Mojumder, S.M.; Sadida, F.F.; Uddin, M.; Sikdar, D. Isolation and identification of cellulolytic bacteria from the gut of three phytophagus insect species. *Brazilian Arch. Biol. Technol.* 2014, 57, 927–932, https://doi.org/10.1590/S1516-89132014042620.

163. Kakara, D.; Malothu, R.; Narayana, E.L. Isolation of cellulolytic bacteria from intestine of termites and their utility in saccharification and fermentation of lignocellulosic biomass. *Int. J. Eng. Res. Technol.* 2020, 9, 298–302.
164. Biswas, R.; Persad, A.; Bisaria, V.S. Production of cellulolytic enzymes. In: Bioprocessing of renewable resources to commodity bioproducts. Bisaria, V.S.; Kondo, A. (eds). John Wiley & Sons, New Jersey, 2014; pp. 105–132, https://doi.org/10.1002/9781118845394.ch5.

165. Galante, Y.M.; De Conti, A.; Monteverdi, R. Application of Trichoderma enzymes in textile industry. In: Trichoderma & Gliocladium—enzymes, biological control and commercial applications. Harman, G.F.; Kubicek, C.P. (eds). Taylor & Francis, London, 1998, pp. 311–326.

166. Baker, R.A.; Wicker, L. Current and potential applications of enzyme infusion in the food industry. Trends Food Sci. Technol. 1996, 7, 279–284, https://doi.org/10.1016/0924-2244(96)10030-3.

167. Hamer, J. Enzymes in the baking industry. In: Enzymes in food processing. Tucker, G.A.; Woods, L.F.J. (eds). Blackie Academic & Professional, Glasgow, 1991, pp. 168–193, https://doi.org/10.1007/978-1-4615-2147-1_6.

168. Maat, J.; Roza, M.; Verbakel, J.; Stam, H.; Santos da Silva, M.J.; Bosse, M.; Egmond, M.R.E.; Hagemans, M.L.D.; van Gorcom, R.F.M.; Hessing, J.G.M.; van den Hondel, C.A.M.J.J.; van Rotterdam, C. Xylanases and their applications in bakery. In: Xylans and xylanases, progress in biotechnology. Visser, J.; Beldman, G.; Kusters-van Someren, M.A.; Voragen, A.G.J. (eds). Elsevier, Amsterdam, 1992; pp. 349–360.

169. Gunata, Y.Z.; Bayonove, C.L.; Cordonnier, R.E.; Arnaud, A.; Galzy, P. Hydrolysis of grape monoterpenyl glycosides by Candida molischiana and Candida wickerhamii β-glucosidases. J. Sci. Food. Agric. 1990, 50, 499–506, https://doi.org/10.1002/jsfa.2740500408.

170. Prasad, D.Y.; Heitmann, J.A.; Joyce, T.W. Enzymatic de-inking of coloured offset newsprint. Nord. Pulp Paper Res. J. 1993, 8, 284–286, https://doi.org/10.3183/npprj-1993-08-02-p284-286.

171. Darwesh, O.M.; El-Maraghy, S.H.; Abdel-Rahman, H.M.; Zaghloul, R.A. Improvement of paper wastes conversion to bioethanol using novel cellulose degrading fungal isolate. Fuel 2020, 262, https://doi.org/10.1016/j.fuel.2019.116518.

172. Karthika, A.; Seenivasagan, R.; Kasimani, R.; Babalola, O.O.; Vasanthy, M. Cellulolytic bacteria isolation, screening and optimization of enzyme production from vermicompost of paper cup waste. Waste Management 2020, 116, 58–65, https://doi.org/10.1016/j.wasman.2020.06.036.

173. Ndlovu, T.M.; van Wyk, J.P.H. Isolation of cellulase enzyme from brown garden snail (Cornu aspersum) for the saccharification of waste paper materials. MethodsX 2019, 6, 1030–1035, https://doi.org/10.1016/j.mex.2019.04.019.