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REVIEW ARTICLE

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Microbial cellulase production and its potential application for textile industries

Gamachis Korsa[1,2*], Rocktotpal Konwarh[3], Chandran Masi[1,2], Abate Ayele[1,2] and Setegn Haile[1]

Abstract

Purpose The textile industry's previous chemical use resulted in thousands of practical particulate emissions, such as machine component damage and drainage system blockage, both of which have practical implications. Enzyme-based textile processing is cost-effective, environmentally friendly, non-hazardous, and water-saving. The purpose of this review is to give evidence on the potential activity of microbial cellulase in the textile industry, which is mostly confined to the realm of research.

Methods This review was progressive by considering peer-reviewed papers linked to microbial cellulase production, and its prospective application for textile industries was appraised and produced to develop this assessment. Articles were divided into two categories based on the results of trustworthy educational journals: methods used to produce the diversity of microorganisms through fermentation processes and such approaches used to produce the diversity of microbes through microbial fermentation. Submerged fermentation (SMF) and solid-state fermentation (SSF) techniques are currently being used to meet industrial demand for microbial cellulase production in the bio textile industry.

Results Microbial cellulase is vital for increasing day to day due to its no side effect on the environment and human health becoming increasingly important. In conventional textile processing, the gray cloth was subjected to a series of chemical treatments that involved breaking the dye molecule's amino group with Cl—, which started and accelerated dye(-resistant) bond cracking. A cellulase enzyme is primarily derived from a variety of microbial species found in various ecological settings as a biotextile/bio-based product technology for future needs in industrial applications.

Conclusion Cellulase has been produced for its advantages in cellulose-based textiles, as well as for quality enhancement and fabric maintenance over traditional approaches. Cellulase's role in the industry was microbial fermentation processes in textile processing which was chosen as an appropriate and environmentally sound solution for a long and healthy lifestyle.

Keywords Biopolishing, Cellulase, Industry, Microorganisms, Textile

Introduction

The textile industry has changed over time. In order to meet people's demands, a variety of fibers have been manufactured with polyester, cotton, and viscose being the most popular (Felgueiras et al. 2021). The 17 Sustainable Development Goals (SDGs) and 169 sub-targets included in the UN's 2030 Agenda serve as a global benchmark for the shift to sustainability. The agenda recognizes the interconnectedness of various challenges, including poverty, health, industry, innovation, and infrastructure,

*Correspondence:
Gamachis Korsa
gamachis.korsa@aastu.edu.et
[1] Department of Biotechnology, Addis Ababa Sciences and Technology University, Akaki Kality, P.O. Box 16417, Addis Ababa, Ethiopia
[2] Center of Excellence for Biotechnology and Bioprocess, Addis Ababa Science and Technology University, P.O. Box 16417, Addis Ababa, Ethiopia
[3] Uniglobe Scientific Pvt. Ltd, New Delhi, India

clean water and sanitation, and environmental degradation, among others, and that they can only be addressed jointly (Weiland et al. 2021; Provin et al. 2021). A microbial enzyme isolated from natural ecosystems has unique properties that could make them good candidates for improving biomass conversion efficiency into value-added goods, chemicals, and fuels. However, research into the composition of cellulosic biomass and the natural sources of microbial enzymes that drive biomass conversion efficiency is still in its early stages (Haile and Ayele 2022; Mukherjee et al. 2022). Cellulosic biomass bioconversion based on biotechnology has the potential to be a long-term solution for the creation of new products with added value. Enzyme-based bioprocessing can reduce the unfavorable effect of fiber damage due to the precise reaction specificity given by enzymes for particular or targeted textile finishing. Enzyme bioprocessing has the potential to improve the performance and quality of the textile materials produced, as well as save water, energy, and chemicals (Nayak et al. 2021; Boodhoo et al. 2022; Bilal et al. 2022). Cellulases have been routinely used throughout cellulose-based materials for their advantages over traditional processes, as well as for quality enhancement and texture maintenance. Microbial cellulase is effective in replacing pumice stones in biostoning and removing excess color to give denim a soft, worn appearance (Vélez-Mercado et al. 2021; Perumal et al. 2022). Novozymes, DSM, DuPont, Amano Enzymes Inc., etc. are prominent players in cellulase enzyme production worldwide (Singh et al. 2021). Cellulase-based products like DeniMax® (Novozymes) and ValumaxA 838 have permitted an easy and cost-effective creation of new shades and finishes in the textile industry (Agrawal 2017; da Silva et al. 2021).

Also, microbes such as bacteria, fungus, and actinobacteria produce cellulolytic enzymes, which have a wide range of applications in agriculture, textiles, pulp and paper, food and beverage, brewing and winemaking, detergent manufacturing, and bioconversion for value-added industrial products (Kumar et al. 2022; Lin 2022; Shukor et al. 2022).

The aim of this review begins with an overview of cellulase, classification and structure, cellulase-producing microbes and diversity of cellulase-producing microbes are also addressed, as well as fermentative processes for microbial cellulase production, strain improvement of microbes for enhanced cellulase production, and numerous textile industrial applications of microbial cellulase.

Microbial cellulase-classification and structure

Many reserves of powders, bagasse, shells, brans, and residual cakes have all been used to improve the production of microbial cellulases from residual lignocellulosic biomass (Liu 2020). These residues are ubiquitous and sufficient in all parts of the world, and incinerating them, which is the most common processing method, affects ecosystems' environmental quality. As a result, processing residual lignocellulosic biomass can be economically attractive for the bioproducts it can produce, in addition to being an appropriate environmental alternative (Luo et al. 2013; Roth et al. 2020). The most important strategy is the enzymatic hydrolysis of cellulosic biomass, which provides specificity, stereoselectivity, and greater conversion yields (Mumtaz et al. 2022; Wahart et al. 2022).

Microbial enzymes isolated from natural ecosystems have unique characteristics that could make them good candidates for improving biomass conversion efficiency into value-added products (Bussler et al. 2021). The term "cellulase" refers to all cellulolytic enzymes, systems, and structures, including cellulases produced by either cell-bound or extracellular microorganisms, as well as cellulase that differs in their mechanisms of action (Korsa et al. 2022; Mattam et al. 2022; Elsababty et al. 2022). The following types of cellulase have been described with their mechanisms of action and illustrated in Fig. 1; *endoglucanase* (EC 3.2.1.4) is a type of glucanohydrolase that cleaves glycoside linkages at random and binds to the noncrystalline component of cellulose, hydrolyzing amorphous sections more quickly due to weaker hydrogen bonds. It randomly breaks irregular cellulose chain sites, resulting in single polysaccharides or oligosaccharides of various lengths (Cremonesi and Casoli 2021; Berisio et al. 2022; de Souza et al. 2022). *Exoglucanase* (EC 3.2.1.91): 1, 4-β-D-glucan and cellobiohydrolases (I and II) are enzymes that bind and break elementary fibrils to create crystalline cellulose. It produces cello-oligosaccharides or disaccharides such as cellobiose or glucose by cleaving the ends of cellulose fibers (Islam and Roy 2018; Abuajah et al. 2022).

β-Glucosidase (EC 3.2.1.21): cleaves/hydrolyzes the disaccharide molecule cellobiose into simpler sugars and releases glucose monomers. From the nonreducing terminal glycosyl residues in cello-oligosaccharides, it cleaves cellobiose and other cello-oligomers into single sugars called glucose monomers (Saroj and Narasimhulu 2022; Raj et al. 2022).

Cellulase-producing microbes

No one microorganism in nature can produce a comprehensive and balanced collection of enzymes capable of efficiently degrading all types of lignocellulosic biomass, as demonstrated (Chukwuma et al. 2021; Gomes et al. 2022) (Fig. 2). This is to be expected, given that plant biomass is destroyed by a complete community of organisms in the natural environment (in fact, developing a single organism capable of decomposing

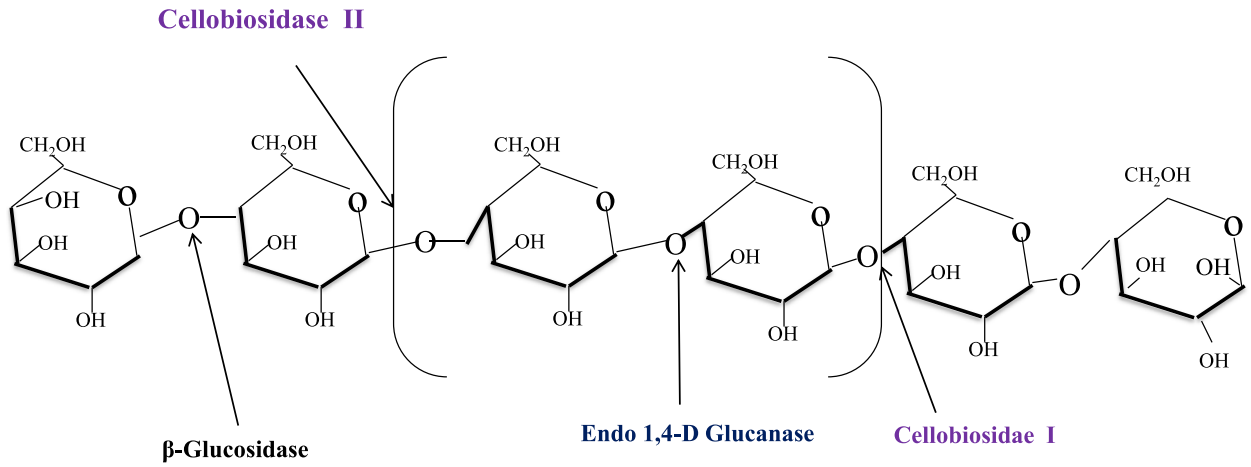

Fig. 1 The structures of cellulase (Linton 2020)

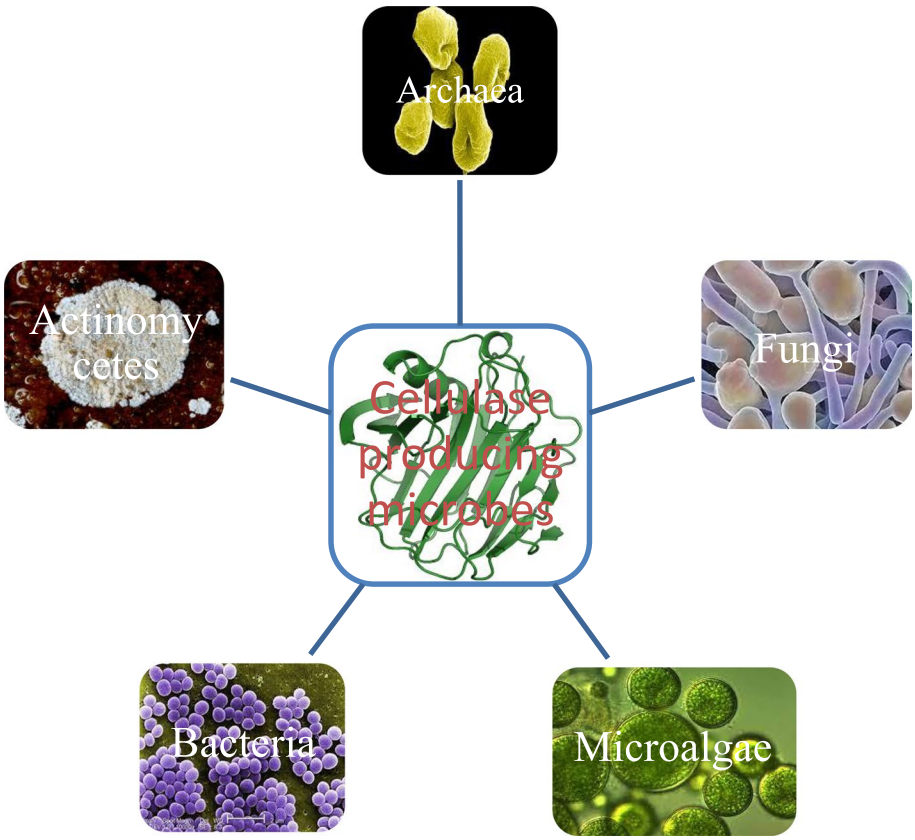

Fig. 2 The major cellulase-producing microorganisms modified from Leo et al. (2019)

lignocelluloses into sugars alone is a major goal of consolidated bioprocessing).

As a result, several solutions for enhancing the industrial lignocellulose degradation process have been explored (Guan et al. 2022; Saravanan et al. 2022; Zainudin et al. 2022).

Microalgae, bacteria, and fungi create more extracellular cellulase, which helps to dissolve crystalline cellulose. Due to its immense biochemical diversity, the ability to generate bulk cultures, and the simplicity of genetic modification, enzymes released by these microorganisms

are suitable for large-scale synthesis (Tapia-Tussell et al. 2020; Iram et al. 2022; Danso et al. 2022).

Diversity of cellulase-producing microbes

Microorganisms from a range of environmental environments have generated pathways for the creation of extracellular enzyme systems for the conversion of cellulosic substrates to simpler sugars and related products (Cheung and Vousden 2022). The decomposition of this cellulose material is discovered to be aided by cellulolytic microbes such as bacteria, actinomycetes, and fungi. Cellulolytic microorganism diversity and functions are generally influenced by soil structure and composition (Joshi et al. 2021; Greff et al. 2022; Tang et al. 2022). Since many enzyme-producing microorganisms are found in marine habitats, this environment is essential for exploring commercially useful enzymes (Vilela et al. 2021). For example, it has been found that forest soil has a higher number of cellulolytic microbes in comparison with agricultural, arid, garden soil, and compost (Tang et al. 2022). Cellulolytic microorganisms can be found in rotting grasses, leaves, and wood as well as in cotton bales, sewage sludge, silage, compost heaps, muds, decaying plant matter, and extreme environments like hot, acidified volcanic environments, and alkaline springs. They can also be found in soil, swamps, marshes, water bodies, and seawater sediments. They have also been associated with secondary microorganisms through symbiotic relationships (Wilson 2011; Leo et al. 2019; Kaur et al. 2020; Thapa et al. 2020). A number of seven bacterial isolates from the genera *Ochrobactrum*, *Acinetobacter*, *Pseudoxanthomonas*, *Paenibacillus*, *Stenotrophomonas*, and *Comamonas* were found in the composting leachate made from wheat straw (Mohammadipour et al. 2021). Three taxa of cellulolytic bacteria belonging to the families *Aeromonas*, *Bacillus*, and *Exiguobacterium* were isolated from sedimentary water samples of the lake (Chantarasiri 2021). In the Indo-Burma Biodiversity Hotspot, three cellulolytic fungi with significant FPase activity were isolated. *Talaromyces verruculosus* SGMNPf3 (KC937053), *Trichoderma gamsii* SGSPf7 (KC937055), and *Trichoderma atroviride* SGBMf4 were all characterized, identified, and reported to GenBank (KC937054) (Goyari et al. 2014). Also, microbial cellulases are produced by the green microalgae *Chlamydomonas reinhardtii*, *Gonium pectoral* and *Volvox carteri* (Guerriero et al. 2018).

Bacterial-producing cellulase

Cellulase-producing microorganisms distributed in the soil are broadly among many genera of a domain in the bacteria (Garcia et al. 2022). Enrichment of new microbial groups with high cellulase activity from uncultivated or forest soil is significant for the study of new species and functions that are relevant to fundamental concerns. *Micromonospora*, *Acidothermus*, *Paenibacillus*, *Streptomyces*, and *Pseudomonas* are examples of unique or new taxa of cellulolytic species that suggest that the ecosystem could be an attractive platform for the investigation of new enzymes for polysaccharide or cellulose degradation (Larson and Bagley 2022; Poulsen et al. 2022). Various bacteria could break down synthetic textile colors, such as azo dyes, triphenylmethane dyes, and anthraquinone dyes, have been researched. Bacterial degradation can be achieved using a single bacterial isolate or a consortium of microorganisms (Shukla et al. 2021).

As microbes secrete cellulose that is free of higher biopolymers, bacterial cellulose provides a low-cost feedstock (Kumar et al. 2019). Bacterial cellulose synthesis is a more cost-effective method of obtaining a quantity because microbial cellulose is pure and free of lignin, hemicelluloses, and pectin (Gedarawatte et al. 2021; Avcioglu 2022). Plant cellulose recovery is difficult and expensive due to the presence of nondegradable sources of polysaccharides of such components (Indumathi et al. 2022; Krishnaswamy et al. 2022). It is produced from coconut water by *Gluconacetobacter* (*Acetobacter*) *xylinus* for different applications (Singhania et al. 2022; Tureck et al. 2022). Bacterial cellulose is characterized by a three-dimensional structure made up of a superfine arrangement of cellulose nanofibers (3–8 nm). Their purity provides for successful application in biomedical products such as animal feeds, artificial cardiovascular tissues shown in (Table 1) below, and wound-covering scaffolds (Meng et al. 2019). The optimization of cellulase using bacterial species strain is used for the production of cellulase at the optimum condition of different parameters for industrial application (Gad et al. 2022; Montes et al. 2022).

Cellulase-producing fungi

Fungi are considered harmful microbes, although they are now an essential industrial raw material for a variety of applications (Bangar et al. 2022; Paul and Joshi 2022). It is possible that dynamic cellulose decomposers are to blame for the planet's decomposition. Furthermore, the framework for the synthesis of cellulases by fungal cellulosomes was more desirable, since it was resistant to environmental changes. When compared to *Aspergillus* and *Humicola* species, *Trichoderma* species are considered the most appropriate species for cellulase synthesis and use in the industry (Mattam et al. 2022; Christopher et al. 2022).

However, genetically modified strains of *Aspergillus* can produce cellulase in a relatively higher amount (Singh et al. 2021). Over the years, various cellulolytic

Table 1 Some cellulase-producing bacterial species strain

Bacteria							
S/no	**Species strain**	**Incubation time (days)**	**pH**	**Temp (°C)**	**Substrate**	**Max. enzyme activity (U/mL)**	**References**
1	*Pseudomonas fluorescens*	2	10	40	Glucose	1.5	Sethi et al. (2013)
2	*Enhydrobacter* sp. ACCA2	3	6.5	30	CMC	2.61	
3	*Micrococcus* sp	3	8	37	CMC	0.9490	Nisha (2015)
4	*Micrococcus* sp	4	5	25	CMC	102	Mmango-Kaseke et al. (2016)
5	*Bacillus licheniformis*	-	6.5	43.35	CMC	42.99	Shajahan et al. (2017)
6	*Pseudomonas* sp	4	7	40	CMC	0.0067	Shaikh et al. (2013)
	Bacillus sp	4	7.5	50	CMC	0.0093	
7	*Paenibacillus terrae* ME27-1	2.5	8	28	Wheat bran	2.08	Liang et al. (2014)
8	*Streptomyces*	2.5	6	40	CMC	0.26	Fatokun et al. (2016)
9	*Ochrobactrum haematophilum*	-	6.3	44.2	CMC	3.55	Parkhey et al. (2017)
10	*Bacillus* sp. C1AC55.07	2.25		32	-	0.366	Diasa et al. (2014)
11	*Paenibacillus* sp.	1	7	40	CMC	2655	Islam and Roy (2018)
12	*Bacillus* VITRKHB	1	7.83	25.84	Xylose	192	Singh et al. 2014
13	*Bacillus licheniformis* HI-08	-	7	45	Sugarcane bagasse	393.99	Afzal et al. (2019)
14	*Bacillus* sp. SM3-M8	2	7	45	CMC	3.198	Rasul et al. (2015)
15	Bacillus sp.	-	6	50	CMC	5.21	Shah et al. (2015)
16	*Bacillus subtilis* (KFY-40)	2	6	55	CMC	16.62 ± 1.85	Naresh et al. (2019)

CMC carboxymethyl cellulose, *°C* Celsius, *Hr* hours, *S/No*. species number, *Temp*. temperature, *Max* maximum

fungal spectrums have been collected and identified, and these numbers have continued to produce significant. An impressive assemblage of over 14,000 fungi that were active together with cellulose and added insoluble fibers were previously reported. *Trichoderma viride* and *Trichoderma reesei*, for example, support cellulase formation in suitable conditions, such as solid and submerged fermentation (Idris et al. 2017; Zhao et al. 2021). Fungal species are favored for cellulase synthesis because they release large volumes of extremely versatile extracellular cellulase (Monclaro et al. 2022; Lübeck and Lübeck 2022). By secreting a variety of hydrolytic and oxidative catalysts, fungal cellulases can hydrolyze lignocellulosic biomass. The best-characterized cellulolytic organisms are white-rot fungi, such as *Phanerochaete chrysosporium*, and soft-rot fungi, also including *Fusarium solani*, *Penicillium funiculosum*, *Talaromyces emersonii*, *Trichoderma koningii*, and *Trichoderma reesei*, as shown in Table 2 below. *Aspergillus fumigatus*, *Aspergillus nidulans*, *Aspergillus aculeatus*, *Aspergillus niger*, *Aspergillus oryzae*, and *Aspergillus niger* are the most widely used commercial microorganisms with high cellulolytic potential (Faheina Junior et al. 2022 et al. 2022; Isola et al. 2022; Santos et al. 2022; Vasco-Correa et al. 2022). A total of 88 filamentous fungal strains were identified, and cellulase-producing fungi screening revealed that 16 strains from the genera *Penicillium*, *Trichoderma*, *Aspergillus*, and *Talaromyces* had variable cellulolytic activity (Tomico-Cuenca et al. 2021; Lübeck and Lübeck 2022). *Trichoderma harzianum* isolate LZ117 is the most potent generator of these strains. A comparison of the transcriptomes of *Trichoderma harzianum* LZ117 and *Trichoderma harzianum* K223452, a control strain purified on cellulose, revealed a focused control of gene transcription essential to protein synthesis (Li et al. 2020; Pang et al. 2021; Mondal et al. 2022). Cellulase production optimization utilizing fungal species strains for the industry is critically shown in Table 2 below. Optimizing the parameters for cellulase production at the optimum condition of different parameters for industrial applications is critical (Gad et al. 2022; Helal et al. 2022).

Cellulase-producing actinomycetes

Actinomycetes are gram-positive mycelial microscopic organisms that are ubiquitous in soil and are particularly important for their role in the utilization of organic materials and the delivery of bioactive chemicals, with most isolates being indicated to do so (Al-Shaibani et al. 2021; Rani et al. 2021). A few studies suggested that separating actinomycetes from marine sediments could be useful for isolating novel actinomycetes with the potential to produce a useful new product. Actinomycetes, on the other hand, are known for producing a variety of extracellular enzymes that degrade polymers, including chitinase, lipase, and cellulase (Phuoc et al. 2020; Javed et al. 2021; Sudarshan et al. 2022). Actinomycetes have long

Table 2 Some cellulase-producing fungi species strain

Fungi							
S/no	**Species strain**	**Inc. time (days)**	**pH**	**Temp (°C)**	**Carbon source**	**Enzyme activity (U/mL)**	**References**
1	*Scopulariopsis brevicaulis*	5	5	40	Sugarcane bagasse	18.18	Akinyele et al. (2020)
2	*Trichoderma* sp.	5	5	40	Sugarcane bagasse	4.11	Akinyele et al. (2020)
3	*Trichoderma longibrachiatum*	7	4	55	Cellulose	10.61	Leghlimi et al. (2013)
4	*Penicillium bilaiae*	2	5	40	Cellulose	5.9	Soeka and Ilyas (2020)
5	*Aspergillus niger*	–	4.5	28	Sawdust	0.1813	Acharya et al. (2008)
6	*Aspergillus niger*	-	4.5	30	Oil palm frond	2.38	Tai et al. (2019)
7	*Aspergillus fumigatus*	4	5	50	CMC	526.3	Liu et al. (2011)
8	*Trichoderma viride*	4	4	-	CMC	1.066	El Baz et al. (2018)
9	*Trichoderma* sp.		6.5	45	CMC	1.98	Gautam et al. (2011)
10	*Aspergillus tubingensis*	4	4.8	40	Corn stover	86.4	Imran et al. (2017)
11	*Penicillium* sp.	–	5	30	Corncob	15.787	Ire et al. (2018)
12	*Aspergillus niger*	3	5	40	Glucose	0.9	Sethi and Gupta (2014)
13	*Trichoderma reesei*	6	5.5	37.5	Pineapple	9.23	Saravanan et al. (2012)
14	*Penicillium chrysogenum*	6	5	30	CMC	0.552	Kaur and Joshi (2015)

CMC carboxymethyl cellulose, *°C* Celsius, *Hr* hours, *S/No*. species number, *Temp*. temperature, *Max* maximum

been thought of as intermediate species between bacteria and fungi. They create a mycelial network of branching filaments, similar to fungi, but they are thinner, have muramic acid-containing cell walls, prokaryotic nuclei, and are susceptible to bactericidal antibiotics, just like bacteria (Gong et al. 2020). They are therefore real bacteria, despite their obvious fungal appearance. Mycobacteria and Corynebacteria are related to actinomycetes (Melgarejo et al. 2021; Streletskii et al 2022). They include the aerobic *Nacardia*, *Actinomadura*, *Dermatophilus*, and *Streptomyces* species, as well as the anaerobic *Actinomyces*, *Arachnia*, *Bifidobacterium*, and *Rothia* species. *Actinomyces*, the most common pathogenic genus, is anaerobic or microaerophilic and non-acid fast, whereas *Nacardia* species are aerobic and maybe acid fast (Viswanathan and Rebecca 2019; Patel et al. 2020; Subathra Devi et al. 2022).

Swarna and Gnanadoss. (2020) reported that *Streptomyces* sp. LCJ10A, *Streptomyces* sp. LCJ11A, *Streptomyces* sp. LCJ13A, *Streptomyces* sp. LCJ14A, and *Streptomyces* sp. LCJ16A identified from *Pichavaram mangroves* are indeed very efficient in producing economically important enzymes such as lipase, cellulase, and asparaginase. Such enzymes can be valuable resources for novel biotechnological processes and can contribute to the discovery of new biological understanding (Vijayakumar 2021; Abdel-Azeem et al. 2021; Sengupta et al. 2020) which was shown in (Table 3) below.

Actinomycetes that produce cellulase have been isolated and characterized as belonging to the following genera: *Asanoa*, *Dactylosporangium*, *Kitasatospora*, *Nonomuraea*, *Streptomyces*, and *Streptosporangium* (Putri and Setiawan 2019), *Streptomyces* and *Nocardia* (Meliani et al. 2022), and *Streptomyces* sp. MS-S2 (Danso et al. 2022). The optimization of cellulase using *Actinomycetes* species strain for the industry is of immense importance to optimize the parameters for cellulase production (Sivasankar et al. 2022; Sudarshan et al. 2022; Rodrigues et al. 2022) in Table 3.

Cellulase-producing archaea

In-depth studies have been carried out on the structure and development of the methanogenic archaeal species that participate in the biomass-degrading microbial communities found in biogas plants (Maus et al. 2018). The majority of the Archaea cellulase observed comes from intensive surroundings. Certain cellulase genes were identified in *Desulfurococcus fermentans* and *Thermogladius cellulolyticus*, whereas *hyperthermophilic* Archaea include *Pyrococcus furiosus*, *Pyrococcus horikoshii*, and *Sulfolobus solfataricus* (Graham et al. 2011; Leo et al. 2019; Larson and Bagley 2022; Kabaivanova et al. 2022). Maus et al. (2017) studied that the hydrogenotrophic route, which represents the final phase of the anaerobic digestion (AD) chain, was anticipated to create CH4 by seven of the examined methanogenic Archaea. Two species, *Methanoculleus bourgensis* and *Defuviito gatunisiensis*, were found to have a dominant role in biogas microbial communities among the microorganisms investigated (Camargo et al. 2021; Malik and Furtado

Table 3 Some cellulase-producing actinomycetes species strain

Actinomycetes							
S/no	**Species strain**	**Inc. time (days)**	**pH**	**Temp (°C)**	**Carbon source**	**Enzyme activity (U/mL)**	**References**
1	*Streptomyces* DSK59	4	6.5	45	CMC	0.027	Budihal et al. (2016)
2	*Streptomyces auranticus*	8	7	30	CMC	233.56	Abou-Dobara et al. (2015)
3	*Streptomyces viridobrunneus* SCPE-09	5	4.9	50	Wheat bran	2.00	Da Vinha et al. (2010)
4	*Streptomyces* sp.	12	-	35	CMC and husk	59.56	Ishchi and Ragi (2019)
5	*Streptomyces thermocoprophilus* TC13W	5	6.5	40	CMC	925	Sinjaroonsak and Chaiyaso (2020)
6	*Streptomyces drozdowiczii*	3	5	50	CMC	0.595	Grigorevsk et al. (2005)
7	*Thermomonospora*	3	5	50	CMC	23	George et al. (2001)
8	*Streptomyces* sp. Bse 7–9	4	7	30	Bagasse	4.496	Ratnakomala et al. (2019)
9	*Microbispora cellulosiformans* sp.	-	7	28	D-Fructose, D-glucose, lactose	-	Gong et al. (2020)
10	*Streptomyces anulatus* NEAE-94	5	7	37	D(+) glucose(−) fructose	27.31	El-Naggar and El-Shweihy (2020)
11	*Streptomyces mexicanus* NRRLB 24,916	5	7.5	35	Glucose	23.10	Das et al. (2017)
12	*Streptomyces griseorubens* AB184139	6	7	45	CMC	4.5	Prasad et al. (2013)
13	*Streptomyces* sp. F2621	-	9	30	Ball-milled wheat straw	22.41	Tuncer et al. (2004)

CMC carboxymethyl cellulose, *°C* Celsius, *Hr* hours, *S/No.* species number, *Temp* temperature, *Max* maximum

2022; Jo et al. 2022). Das et al. (2019) studied the characterization of extremely halophilic archaeal isolates from Indian salt pans, and screening for hydrolytic enzyme production Halophilic archaea is multi-stress-tolerant organisms, and their catalysts are of specific importance because they are generally stable and functional under extreme temperatures and low water activity. Because of their improved functionality in extreme circumstances encountered in numerous industries, the search for novel extremozymes is continuing. *Haloferax*, *Halorubrum*, *Halococcus*, *Haloarcula*, *Halogeometricum*, and *Haloterrigena* were among the six genera studied (Junior et al. 2022; Leoni et al. 2022).

Cellulase-producing microalgae

Microalgae are microscopic organisms that contain chlorophyll and are found in freshwater and marine habitats (Shokrkar and Keighobadi 2022; Melendez et al. 2022). Cellulase is produced by the microalgae *Chlorella homosphaera*, *Nannochloropsis* sp., *Rhizoclonium* sp., *Chlorococcum infusionum*, *Haematococcus pluvialis*, *Chlorella* sp., and *Scenedesmus* sp (Zuorro et al. 2016; Sharma and Yazdani 2016). Because of its high abundance of vital nutrients and minerals, microalgal biomass has gained a lot of interest in the industrial world. Low biomass production, an uneven carbon-to-nitrogen (C/N) ratio, refractory cellular components, and the high cost of microalgal harvesting are all key roadblocks to algal biomass valorization (Shah and Mishra 2020; Tawfik et al. 2022).

Fermentative processes for microbial cellulase production

Today, industrial demand for microbial production of cellulase is being met by production methods using submerged fermentation (SMF) processes and solid-state fermentation (SSF). Cellulolytic microorganisms are known as true cellulolytic microorganisms, which can degrade natural cellulose (Faheina Junior et al. 2022 et al. 2022; Santos et al. 2022). Microbial enzymes that dominate commercial applications due to their high levels of expression and secretion can create free cellulases. Solid-state fermentation (SSF) and submerged fermentation (SMF) are the two basic techniques for producing cellulases, and they differ in terms of environmental conditions and modes of conduction (El Sheikha and Ray 2022; Nascimento et al. 2022; Chmelová et al. 2022). Verifiable analysis of the volume of water present in the reaction is one of the most important characteristics in separating these types of cycles. Water activity to support cell growth and metabolism, on the other hand, does not approach the water's maximum binding capacity with a solid matrix (Teles et al. 2019; Nisar et al. 2022; Kalogeropoulou et al. 2022).

Submerged fermentation (SMF)

Industrially important enzymes have traditionally been obtained from submerged fermentation (SMF) because of the case of handling and greater control of environmental factors such as temperature and pH (Oh and Jin 2020; Mitri et al. 2022; Intasit et al. 2022). Because of the consumption and high cost of enzymes, submerged fermentation currently produces commercial enzymes, and several of the possible uses have been industrialized. When compared to SSF, SMF offers better control of environmental characteristics, lower labor costs, fewer space requirements, and lower scale-up requirements (Libardi et al. 2019). Ramamoorthy et al. (2019) reported that when utilizing an SMF to make cellulase, the following issues are frequently encountered: the production of cellulase causes an increase in the viscosity of the culture broth. Enhanced agitation to counteract it may result in uncontrollable foaming, secreted cellulase within the culture broth may cause partial saccharification (of the lignocellulosic biomass) and concentration of sugars (glucose and xylose), a lower dissolved oxygen percent (DO%) in the broth due to the growing fungus's accelerated uptake of oxygen, and a decreased oxygen hold up due to an increase in the viscosity (Hosseini et al. 2022; Kabatesi and Wang 2022).

In the submerged fermentation, extracellular endoglucanase activity was also detected, and the four strains had similar enzyme excretion patterns. The extracellular activity was lowest in the *Klebsiella* sp. (B2) strain, albeit this difference was not significant when compared to the other strains. In Petri dishes, the results were found to be consistent with CMC growth patterns and enzymatic hydrolysis profiles (Barbosa et al. 2020; Kurt and Cekmecelioglu 2021).

Solid-state fermentation (SSF)

Solid-state fermentation relies on the utilization of less expensive substrates for cellulase synthesis, making it more cost-effective (Dessie et al. 2022; Chilakamarry et al. 2022). The technology is promising because of the high product concentration, low dewatering costs, and low infrastructure and expertise requirements. Solid-state fermentation offers higher cellulase yields than submerged fermentation, and production costs are decreased significantly with the right technology, improved bioreactor design, and a competitive cellulase production process. The ingredients of the medium also influence the synthesis of enzymes by different bacteria (Kieliszek et al. 2021; Nabot et al. 2022). For the production of microbial metabolites, solid-state fermentation used complex substrates such as sugarcane bagasse, wheat bran, wheat straw, rice bran, rice straw, corncobs, banana waste, wheat flour, cornflour, mustard oil cake, sesame oil cake, cotton oil cake, cassava flour, steamed rice, sayo hulls, sago humps, and apple pomance (El Sheikha and Ray; 2022; Santos et al. 2022). For example, the filamentous fungus *Trichoderma reesei* RUT C30 was used for cellulase production using wheat bran as substrate under SSF (Singhania et al. 2007). SSF methods are mostly employed for enzyme production as this process is very simple and cost-effective (Bala and Singh 2019; Siqueira et al. 2020). The temperature maintenance, pH maintenance, moisture maintenance, lack of homogeneous mass transfer, uneven fungal growth in the SSF media, and lack of a methodology to estimate the exact fungal biomass concentration are all problems with scaling up SSF in an industrial application (Ramamoorthy et al. 2019; Pandey and Negi 2020; Prabhu et al. 2022).

Strain improvement of microbes for enhanced cellulase production

Strain improvement is inevitable if cellulase production has to be reached an industrially feasible level. Engineering cellulases to improve their properties to meet robust industrial applications is often required (Dey et al. 2021; Ugbenyen and Ikhimalo 2021; Adnan et al. 2022). Filamentous fungi natively secrete various cellulases when growing on lignocellulose wastes. Improving cellulase expression by random mutagenesis is the classical approach. Random mutagenesis, site-specific mutagenesis, or their combinations have been used to obtain tailor-made enzymes for industrial applications (Bhati and Sharma 2021; Jeennor et al. 2022). Improved cellulase production from *Aureobasidium pullulans* Y-2311–1, thanks to genome shuffling and bacteria. On day 1, one strain produced through genome shuffling (*Aureobasidium pullulans* GS23) had the highest overall cellulase activity, which was sixfold higher than the wild-type strain. In comparison with the wild-type strain, the *Aureobasidium pullulans* GS23 strain reported a 6.95-fold and 1.52-fold increase in exoglucanase and b-glucosidase activity, respectively (Baldwin et al. 2020). Understanding the whole-genome sequence and functions makes determining the target regions for genetic changes much easier. Targeted strain engineering, whether for better cellulase production in fungi or metabolic engineering, necessitates effective ways of introducing controlled genetic changes into an organism (Jiao et al. 2021; Olukunle et al. 2021).

For a long time, the low effectiveness of gene targeting has made obtaining a reasonable number of transformants by homologous integration or deletion of the expression cassette a considerable difficulty. Because of their ability to grow on the less expensive substrate, they had become prospective sources of metabolites for industrial use. Years of research and industrial use have

gathered knowledge about fungal genetics (Papzan et al. 2021; Poonsrisawat et al. 2022). Engineering CBDs (cellulose-binding domains) of cellulases, molecular cloning, and gene expression were used to boost cellulase activity (Sharma et al. 2022; Calzada et al. 2021). A novel approach for enhancing catalytic activity is to use a new technique called substrate-induced gene-expression screening (SIGEX) in conjunction with fluorescence-activated cell sorting (FACS). Through bacterial mutagenesis, cellulase activity in cellulase-producing thermophiles was also increased. For example, *Bacillus* sp. strain C1 was mutagenically treated with NTG (N-methyl-N′-nitro-N-nitrosoguanidine), and altered clones were obtained (Singhania et al. 2021). The cost of the cellulase enzyme and its stability are the two most important considerations in its application. Cotton preparations, wool, and dyeing treatment all require cellulases. Novel cellulases with higher process compatibility, high specific activity, better specificity, and stability are being identified from new lineages of cellulolytic organisms due to their broad uses and ever-increasing demand (Adebami and Adebayo-Tayo 2020; Srivastava et al. 2022). Because of its effectiveness, strain enhancement for cellulase production using mutagenesis agents has gotten a lot of interest. UV, X-rays, gamma radiation, ethyl methanesulfonate (EMS), N-methyl-N-nitro-N-nitrosoguanidine (NTG), and mustards have all been used as mutagenic agents (Sangkharak et al. 2012; Faheina Junior et al. 2022 et al. 2022). Lu et al. (2020) studied, based on phylogenetic position and phenotypic characteristics, the high-yield bacteria cellulase-producing strain *Komagataeibacter* sp. nov. CGMCC 17,276 was assigned as a novel species in the *Komagataeibacter* genus with good properties of rapid cell growth and high bacterial cellulase production. Under static and agitated conditions, properties analysis of bacterial cellulose generated by *Komagataeibacter* sp. nov. CGMCC 17,276 revealed strongly cross-linked cellulose nanomaterial (Betlej et al. 2021).

Ryngajłło et al. (2020) reported that a recombinant strain of *Komagataeibacter xylinus* 10,245 was produced for the composite synthesis of bacterial cellulose and chitin. In *Komagataeibacter xylinus*, an operon including three *Candida albicans* UDP-GlcNAc synthesis genes (AGM1, NAG5, and UAP1) was expressed under the control of a promoter. The modified strain was able to produce activated cytoplasmic UDPGlcNAc monomers that cellulose synthase could use to join glucose and GlcNAc to form a chimeric polymer. To boost transformation efficiency, pyr4 deletion in the fungus *Trichoderma reesei* SN1 was used to create a pyr4 Disruption Strain from a uracil auxotroph strain, SP4 (Saravanakumar et al. 2020; Zheng et al. 2020). The glucose output of SPB2 is 65.0% higher than that of SP4 when corncob residues are saccharified with crude enzyme (Fierro et al. 2022; Rosolen et al. 2022).

These results reveal the feasibility of strain improvement through the development of an efficient genetic transformation platform to construct a balanced cellulase system for biomass conversion (Qian et al. 2016). After UV irradiation and NTG treatment, *Cellulomonas* sp. strain M23, a significant strain that produces a high amount of cellulase, was selected from 328 mutant strains to boost cellulase production from *Cellulomonas* sp TSU-03 (Kothari et al. 2019; Yanagisawa et al. 2022). In comparison with the wild type, the maximum value of cellulase activity 2008 U/mg protein was attained, as well as a significant potential for cellulase production by fermentation using a growth medium containing carboxymethyl cellulose (CMC) as the major substrate (Sangkharak et al. 2012). Sadhu et al. (2013) studied that after mutagenesis with N-methyl-N′-nitro-N-nitrosoguanidine (NTG) as a mutagenic agent, a putative mutant (C1M26) of *Bacillus* sp. (MTCC10046) was screened from the wild C1 strain. In comparison with the wild-type C1 strain, the mutant C1M26 generated more cellulase. These results in increased cellulase synthesis due to regulatory gene mutations or cellulase mRNA stability. Sequential mutagenesis with three mutagens of ultraviolet irradiation (UV), N-methyl-N′-nitro-N-nitrosoguanidine (NTG), and ethyl methanesulfonate improved the activity of *Streptomyces durhamensis* (EMS) (Golinska et al. 2020; Lakshmi et al. 2020; Azouz 2021). The cellulase activity of the mutant *Streptomyces durhamensis* GC23 was improved to 1.86-fold compared to the wild strain (vs15) after mutagenesis, and the cellulase activity of the mutant *Streptomyces durhamensis* GC23 was further optimized to twofold that of the wild type (Lakshmi et al. 2020).

Application of microbial cellulase for textile industries

Cellulases are a type of hydrolase that can degrade lignocelluloses. They are widely applied in numerous sectors because they are made from renewable resources and waste. They have a wide range of uses in textiles, detergents, and other biotechnology fields, with a recent concentration on the textile industry (Ejaz et al. 2021). Denim washing with cellulase is a common eco-friendly procedure for achieving a pleasing look and non-abrasiveness in cotton textures and denim. However, previous enzymatic denim washing methods used acid cellulase (*Trichoderma reesei*) and neutral cellulase (*Humicola isolens*), both of which had the problem of causing indigo color back staining on the cloth. Although it has been suggested that pH is the most important factor in preventing back stains, there have been no reports on the use of cellulase for denim washing under soluble

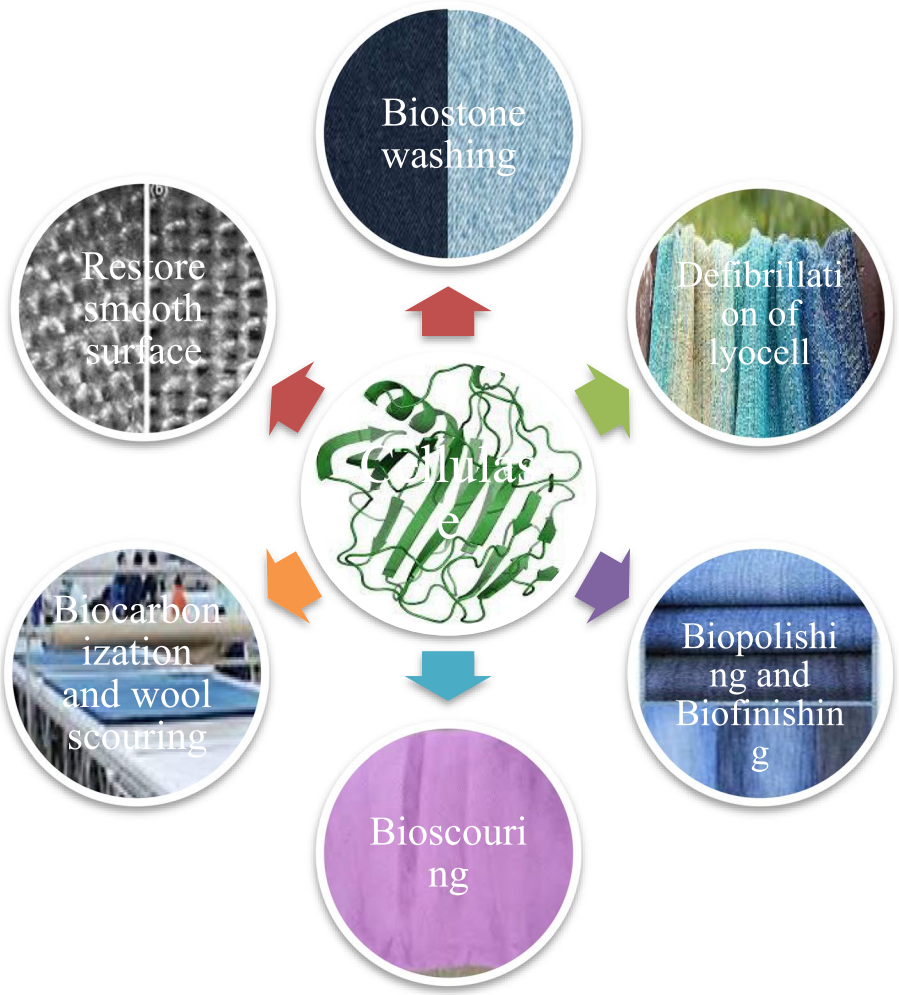

Fig. 3 Microbial cellulase application for textile industries (Biernat 2019; Jayasekara and Ratnayake 2019)

circumstances. Under basic conditions, a soluble base stable endoglucanase from alkalothermophilic *Thermomonospora* sp. (T-EG) was used for denim finishing (Imran et al. 2019; Sampathkumar et al. 2019). The textile industry meets one of humanity's most fundamental necessities while also contributing significantly to many country's economic growth. The demand for textile materials is increasing as the population grows and per capita consumption of textiles rises (Ahmed and Bibi 2018; Provin et al. 2021; Skiba et al. 2022). The traditional method of textile wet processing, on the other hand, involves a series of steps before it leads to a finished fabric, which requires the use of high salt concentrations, harsh chemicals, and a large amount of water and energy consumption, all of which are critiqued due to their environmental cost. The employment of enzymes in textile wet processing is guided by an understanding of the environment (Son et al. 2022; Ambaye et al. 2022). Enzymes introduce biotechnology into the textile industries, which appears to strike a reasonable compromise between industrial demands and environmentally responsible product development (Aggarwal et al. 2020; Singhania et al. 2022). It is important to note that recent technological breakthroughs in the field of bio-based processing have resulted in significant changes in the textile industry, which is increasingly becoming more ecologically conscious (Fasiku et al. 2020; Nursyirwani et al. 2020; Kabir and Koh 2021). Resizing, scouring, dyeing, coloring, and finishing are five key applications of textile wet processing, as illustrated in Fig. 3. However, the most common enzyme-based industrial processes, such as biodesizing, bioscouring, and biobleaching, have experienced industrial biotechnological breakthroughs and now outperform the efficacy and effectiveness of chemical-based processing for wet textile preparatory processes (Rahman et al. 2020; Rajulapati et al. 2020).

Biostone washing

One of the most important aspects of producing a faded look is denim washing. Previously, stone washing was done by providing it with a soft feel and the desired appearance. The pumice stone removes color particles from the yarn surface in the denim fabric after washing. The faded effect is obtained by ring dyeing denim fabric and heavy abrasion during the stone washing process (Mazotto et al. 2021; Periyasamy and Tehrani-Bagha 2022). To achieve the fading effects, oxidative bleaching chemicals with or without the inclusion of stones have also been used. Denim washing is one of the key areas in getting a faded look. Earlier stone washing is used to be done to achieve a soft feel and the desired appearance. During washing, the pumice stone, and scraps of the dye particles from the yarn surface in the denim fabric. Due to the ring dyeing of denim fabric and heavy abrasion during the stone washing process, the faded effect is achieved. Oxidative bleaching agents with or without the addition of stones have also been used to get the fading effects (Costa et al. 2021; Mustafa et al. 2022). Denim, which is made of twill weave fabric colored in indigo colors and has a well-worn appearance, has gained a lot of favor over the years. The traditional use of pumice stones (with or without an oxidizing agent such as potassium permanganate) for stone washing denim has some drawbacks (Korsa et al. 2022), including machine damage, drainage system blockage, issues with residue removal on the pumice stones, the need for a large number of stones for even small batches, and the risk of excessive abrasion damaging the fabric. Over the years, denim-heavy-grade cotton twill, dyed with indigo colors and a well-worn look, has churned commendable popularity. The conventional use of pumice stones (with or without oxidizing agent like potassium permanganate) for "stone washing" of denim suffers from numerous practical snags including impairment of machine parts, blockage of the drainage system, issues of removal of residues on the pumice stones, requisite for a large number of stones for even small batches, and the possibility of excessive abrasion that may damage the fabric (Bağıran et al. 2021; Hasan et al. 2021; Islam 2021).

Among others, cellulases have received considerable interest in the textile industry for mercerization, scouring, bio-polishing, laundering, and "stone" finishing (Korsa et al. 2022). Periyasamy and Venkatesan (2019) reviewed that the indigo dye on the denim surface is loosened by the cellulase, which is referred to as "biostoning." Several pumice stones can be replaced by a tiny quantity of enzymes, making handling easier. The biostoning procedure decreases denim fabric degradation, processing machinery wear, and pumice dust production (Rahman et al. 2020; Eid and Ibrahim 2021; Pandit et al. 2022). During the process, a pumice stone can lose up to 50% of its weight and produce a large amount of pumice grit, which can result in pumice sludge. The use of enzymes instead of pumice stones is environmentally friendly (Eid and Ibrahim 2021; Hoque et al. 2021; Mevada et al. 2022). Pazarlioğlu et al. (2005) reported that back staining and tissue stiffness have previously limited the use of acid cellulases, such as those produced by *Trichoderma*, in biostoning, and anti-redeposition chemicals or bleaching agents have been employed to counteract this during washing phases. Neutral cellulases, on the other hand, have a less aggressive effect. Another widely used application of enzymes in the finishing of textile products (cotton and other cellulose-based fibers) is biopolishing. The indigo dye is on the fabric's surface, and cellulases remove the surface fibers to reveal the white string (Aggarwal et al. 2019; Islam 2021; Arbab et al. 2022). Rashid and Rahman (2020) studied that due to its great differences and attractive color look, acid wash on denim jeans is becoming increasingly fashionable. Clothes with an indigo or sulfur base can be washed in acid. Tumbling denim garments with pumice stones presoaked in a solution containing sodium hypochlorite (5 to 10%) or potassium permanganate is the most common method of acid washing (3 to 6%).

Biopolishing and finishing

Cellulases act on small-fiber ends that protrude from the fabric surface in biopolishing, where mechanical action removes these fibers and polishes the fabrics, resulting in a smooth glossy appearance with improved color brightness, hydrophilicity, and moisture absorbance, an environmentally friendly process, and uniformly improved finishing (de Souza Lima et al. 2022; Gupta and Kelkar-Mane 2022). *Trichoderma reesei's* endoglucanase II is thought to be the most effective enzyme for finishing cotton fabrics and biostoning denim garments. However, during finishing and biostoning, commercially available endoglucanase II is frequently blended with other cellulase components, particularly endoglucanase I, resulting in hydrolysis and weight loss of garments (Kinet et al. 2015; Pandit et al. 2022). To eliminate the presence of additional cellulose components, we extracted the endoglucanase II gene from *Trichoderma reesei* and expressed it in *Pichia pastoris* under the control of a methanol-inducible AOX1 promoter. When the endoglucanase II gene of *Trichoderma reesei* is heterologously produced in *Pichia pastoris*, it produces an enzyme that does not cause cellulosic fiber weight loss when used in denim washes (Amengual et al. 2022; Saif et al. 2022) and biopolishing, a great improvement over the use of commercially

available *Trichoderma reesei* cellulase (Rather et al. 2022; Khan et al. 2022; Sivasankar et al. 2022).

Bioscouring

The scouring method of today is chemically based and incredibly alkaline. Chemical procedures are unspecific; thus, they attack not just the contaminants but also the cellulose, causing harm to the strength qualities. Furthermore, due to high COD, BOD, and TDS levels in the effluents, present procedures are harmful to the environment. In the last 10–12 years, a wide range of studies on cotton bio-preparation have been performed (Chavan et al. 2020; Sen et al. 2021; Laga 2022). Bioscouring, an environmentally friendly way of eliminating impurities from fabrics using enzymes, is one of the alternative processes that has been studied in recent years to improve scouring efficiency while lowering ecological impact. The conventional scouring method, which uses a harsh environment, is gradually being replaced by an enzyme-based method that is more environmentally friendly (Jagajanantha et al. 2022; Sharma et al. 2022). Bioscouring is a wettability-boosting method in which enzymes remove non-cellulosic sticky molecules from a piece of fabric without destroying its cellulose content, such as pectin, natural waxes, esters, grease, dirt, and oil. Bioscouring is a process in which enzymes remove non-cellulosic viscous compounds from a piece of fabric without degrading its cellulose content, such as pectin, natural waxes, esters, grease, dirt, oil, and so on, to boost the fabric's wettability (Jagajanantha et al. 2022; Pandit et al. 2022). Degumming and scouring have traditionally been done in alkaline and high-temperature environments (pH 10 and 95 °C). This requires rigorous treatment of alkali-containing effluent after the process, which consumes a lot of energy and damages fibers. This results in poor fabric quality and stability, as well as a labor-intensive and costly process. Toxic effluents are produced during chemical treatment, which is hazardous to the environment and also damages the fabric material (Al-Dhabi et al. 2020; Rajulapati et al. 2020). High heterologous expression of an alkaline pectate lyase (APL) as a key enzyme is used in mild bioscouring pretreatment processes with reduced environmental pollution and energy consumption, whereas traditional chemical treatment methods are carried out under high pH and temperature conditions with high-energy and effluent treatment costs, particularly in the textile industry (Radhakrishnan 2022; Tatta et al. 2022). However, due to the slim profits of the textile industry, the production cost of APL restricts its application in the bio-textile industry (De Oliveira et al. 2021; Nguyen et al. 2021a, b; Ramesh et al. 2021).

Due to their high price, APLs produced by *Bacillus subtilis*, *Pichia pastoris*, or *Aspergillus niger* now on the market are mainly food grade for use in food and fodder and were not suited for the bio-treatment of textiles. As a result, it is critical to raise APL's fermentation output and lower production costs to optimize its applicability for the bio-treatment of textiles (Singh et al. 2020; Zhen et al. 2020).

Biocarbonization and wool scouring

The dyeing of wool with suitable dyes usually necessitates an acidic bath, the pH of which is determined by the dyestuff levelling qualities. It is well established that using low pH values results in improved dye exhaustion (greater dye uptake). However, in terms of the excellent performance and quality of wool goods, the reliance on levelling qualities on pH is equally crucial (Gouveia et al. 2008; El-Sayed et al. 2021). Wool carbonization, a procedure that uses sulfuric acid to remove plant residues from wool, has unfavorable environmental and wool quality consequences. Enzymatic treatment of wool with cellulases and pectinases may increase the decomposition of vegetable matter, allowing it to be easily removed and reducing the amount of sulfuric acid required for the carbonizing process (Chowdhury and Pandit 2022). Wool scouring is an essential part of the manufacturing process that removes contaminants from raw wool such as wool greases, detergents, dirt, and other impurities (Awchat 2022; Chowdhury and Pandit 2022).

Because of the tightening of environmental standards, the cost of effluent treatment and sludge disposal generated during the traditional scouring process utilizing an aqueous solution or solvents is becoming a growing concern for the textile industry (El-Newashy et al. 2021; Kaur and Verma 2021). In wool scouring, enzymes such as xylanase, pectinase, savinase, and resinase can be used to improve process efficiency and reduce water consumption and scouring effluents (Maiti et al. 2018; Sharma et al. 2022).

Defibrillation of lyocell

Surface fibrils released during fibrillation treatment are removed during the enzyme treatment of the fibrillated lyocell fabric. Because of the specific hydrolysis that occurs during enzymatic treatment, the mechanical characteristics are degraded more quickly. The enzyme treatment can affect all of the fibers in the fabric, whereas the mechanical defibrillation treatment affects only the surface fibers (Ibbett et al. 2013; Berto et al. 2021; Mazotto et al. 2021).

Lyocell fibers were exposed to different doses of a cross-linking substance to investigate the fibrillation propensity.

An ideal concentration was discovered to minimize fibrillation. Held to account was the influence of physical

parameters on the fibrillation index. Birefringence, inherent viscosity, and relative crystallinity are among them (Rahman et al. 2021; Abbasi Moud 2022).

A large degree of irregular superficial fibrillation can be found in lyocell fabric. There are no quantifiable modifications in linear density or fiber diameter since the underlying fibers that make up the majority of the fabric are unaffected by the mechanical treatment (Zhang et al. 2018; Artigas-Arnaudas et al. 2022).

Fabrics made from cellulosic fibers such as cotton, viscose, ramie, linen, and lyocell (lyocell is a pure cellulosic fiber made from wood pulp that shows fibrillation on the surface after being solvent spun with amino oxide) were used. These fibers tended to generate "fuzz" (short fibers protruding from the surface) and "pilling" (fluffy/loosened fuzz adhered to the surface), both of which were regarded as unfavorable characteristics of cellulosic fabrics (Hildebrandt et al. 2021; Tian et al. 2022).

Conclusion

The biological aspects of cellulosic biomass processing will be the focus of future cellulase and cellulolytic microbe research. The use of cellulase at appropriate levels for the purpose has various advantages, including being ecologically friendly, causing less damage to clothes without sacrificing fabric strength, reducing equipment wear, increasing garment load in the machine, and improving garment quality. The various cellulases are expected to attack the cellulosic fibers' surface (representing bundles of fibrils), then attach to the exposed fibrils on the yarn surface, and hydrolyze the latter, leaving the fiber core intact. The release of the surface-adhered dye is enhanced by mechanical action as a result of controllable/tunable hydrolysis of the fiber surface. Enzyme-based textile processing is cost-effective, environmentally benign, non-hazardous, and uses little water. In cellulose-based textiles, cellulases have been extensively recognized for their advantages over traditional processes, as well as for quality enhancement and fabric maintenance. Microorganisms' cellulases are effective in replacing pumice stones for bio-stoning and removing excess color from denim to give it softness and a worn appearance. Finding innovative cellulolytic enzymes with higher functioning necessitates the use of cutting-edge technologies.

Abbreviations

AD	Anaerobic digestion
CBD	Cellulose-binding domains
NTG	N-Methyl-N′-nitro-N-nitrosoguanidine
SIGEX	Substrate-induced gene-expression screening
SMF	Submerged fermentation
SSF	Solid-state fermentation

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Consent for publication

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Competing interests

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