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Potential of lignocellulolytic biocatalysts of native and proposed genetically engineered microbial cell factories on jute fiber modification and jute waste recycling: A review

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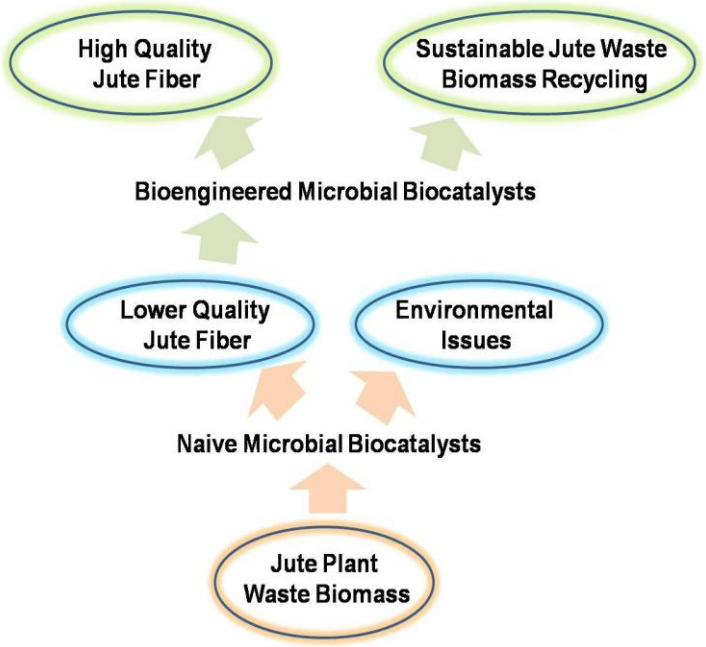
GRAPHICAL ABSTRACT



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ABSTRACT

The lignocellulolytic microbial systems from different parts of the world responsible for lignocellulosic biomass (LCB) like jute (*Corchorus* spp.) waste degradation, fiber modification, and bioenergy production are not limited to a specific prokaryotic or eukaryotic group. The industrial applications of these highly efficient bacterial, fungal and algal communities are related to the production of lignocellulolytic enzymes such as cellulase, hemicellulase, lignin-peroxidase, versatile peroxidase, laccase, thermostable oxidants, pectinase, etc. They are a blessing for the jute, dye, paper, pulp, and biofuel industries as they help to generate a sustainable ecosystem. The jute plant is lignocellulosic biomass so it can be utilized in various ways, from everyday goods to power generation. Jute industries generally use different physicochemical strategies to generate quality fiber and post-retting activities, but these approaches cannot produce desired products; hence microbial routes are best for quality fiber generation, waste remediation, and biofuel generation. To this end, this review summarizes the most important milestones of the development of the leading enzyme-producing cell factories and their engineering by genetic, metabolic, and synthetic biology approaches with the emergence of high throughput methods, such as site-directed mutagenesis and others that can analyze the relevant mutations to accelerate our understanding of lignocellulolytic enzymology.

1 Introduction

Jute resides in the genus of *Corchorus* under the family named *Tiliaceae* and is one of the most important and cheapest natural fibers as well as lignocellulosic biomass, having high sustainability and economic value (cash crop), just after cotton concerning its production and use in the South Asian countries like India, Bangladesh, etc. (Hossen et al. 2020; Jha et al. 2022). Retting defines the post-harvest operation that is the extraction of mature jute fiber from non-fibrous tissues and the woody part of the stem through various ways that helps to yield high-graded jute fiber. The Retting process can be carried out through different strategies like the conventional method of whole plant retting, chemical retting, microbial retting, mechano-microbial retting, in-situ retting with the microbial consortium, etc. (Majumdar et al. 2013). No single method can provide optimum results regarding retting time, fiber quality, cost, and environmental pollution. During microbial retting, microbial enzymes help to consume non-fibrous cementing materials like lignin, pectin, and hemicellulose (Manimekalai and Kavitha 2017). The Retting step is crucial as if improper retting takes place, it may lead to the generation of inferior quality fiber which ultimately results in a loss for the farmers. One problematic scenario observed every year in these countries, is the unavailability of a sufficient amount of free-flowing good, quality mild water during jute harvesting season for irregular climatic behavior that causes uncertainty of rainwater (Singh et al. 2019a). If water scarcity occurs, groundwater is used; as a result, the groundwater level goes down, and more water is required for soil saturation. The problem with chemical retting is that the fibers obtained after chemical treatment are rough, stiff, and coarser (Van sumere 1992). Van sumere (1992) reported that the bacterial retting process is much better than the chemical method as it provides better quality fiber and lower environmental pollution. In contrast, chemical retting is a high-energy process that generates costly waste. For that reason, different biological routes are used to get different microbial systems. It is known that the economic value of jute fiber depends on its fiber phenotypic and morphological characteristics like strength, weight, length, color, and luster of fibers (Islam et al. 2013). The jute retting period always varies with the thickness of the stem and the retting proceeds from top to bottom, but the base portion is highly complex, having to recalcitrate structure and thus very tough to ret. As a result, microorganisms attack most of the cambium portion and secondary phloem and cannot attack as well as ret the hardwood. The decomposition of the parenchymatous tissues proceeds due to microbial enzyme secretion (Haque et al. 2001). In recent years, microbial consortium approaches have been highly used to shorten the retting time and to upgrade the retting and fiber quality (Ghorai and Chakraborty 2020). Water absorption and liberation of soluble constituents like sugar, glucosides, and nitrogenous compounds from jute plants favor initial microbial growth. Further, these microbes utilize free sugars, pectin, hemicelluloses, and proteins of the plants as essential nutrients for their development, and multiplication occurs under favorable conditions (Ahmed and Akhter 2001). Microorganisms used for the single treatment or consortium approach are bacterial or fungal. Though extensive research has been done on different bacterial and fungal strains, there are still so many organisms that are untouched and can be used for jute retting enhancement as these organisms can produce the enzymes required for the breakdown of lignocellulosic biomass. Jute itself is a composition of lignocelluloses made by lignin, pectin, cellulose, and

hemicelluloses, and thus it can be retted by the ligninolytic enzyme-producing organisms (Hossain et al. 2021). Pectin is the cementing material that helps to stick the phloem fiber with the bark of the stem. It is the main target of most scientists as the breakdown of pectin without hampering the cellulosic domain (59-61%) improves the quality of the fiber, and on the other hand, hemicelluloses (21-24%) are the non-fibrous part of jute and its removal enhance the softness and the golden shiny nature of the fiber (Sfiligoj Smole et al. 2013). Hemicellulose is the structural backbone of the plant cell wall composed of a branched polymer of different sugars (i.e., hexose and pentose form). It is the second highest abundant polysaccharide in the plant cell wall. Based on the sugar residues present in the structural polymer as the backbone, hemicelluloses are classified likely into xylan, galacto-(gluco) mannans, and xyloglucans (Scheller and Ulvskov 2010). Jute fiber contains 12-14% of lignin which plays a major role in the photo-yellowing problem of fiber. This is an oxidative photochemical reaction caused by lignin photosensitization (Achwal and Sinkar 1994; Liew et al. 2017). Lignin loses its methoxyl groups due to light and degrades that form ortho-quinones which discolor the fiber (Cogulet et al. 2016). Fiber decolorization is another reason for strength loss. The removal of lignin resists discoloration of the fiber due to sunlight. Thus, pectinolytic, xylanolytic, and ligninolytic microbial agents are in much demand in the scientific community. In jute industries, many wastes are generated (Figure 1); jute root cuttings have not usually been utilized for jute product production and thus are dumped in the trash. This can lead to soil pollution. Effluents that are produced during the jute retting are used for irrigation purposes and have a very negative impact on seed germination of different types of plants and also in pisciculture (Sinha and Paul 2014). However, the effluents can be used in agricultural fields after their proper treatment by the microbial system that can break the organic loads in the wastewater effluents. Thus, the importance of microbial pathways has a tremendous impact on the jute fiber modification and treatment of the jute waste effluents, as we know that water scarcity is a grave problem in most South Asian countries. Thus, the utility of the treated effluent water is immense. In the current review article, an extensive literature survey has been done to find the bacterial and fungal systems already used in retting systems and are highly established. Another report is used to discover the microbiological systems that can break lignocellulosic biomass. One observable thing during these surveys is that most of the organisms used in the retting process are native and not genetically modified. When it comes to biofuel genesis, most organisms used for the breakdown of lignocellulosic biomass are genetically modified and metabolically engineered (Ghosh and Hallenbeck 2012; Chukwuma et al. 2021). Another thing is that genetic alteration in the genome of an organism modifies its substrate- binding affinity, which is determined by its Michaelis Menten constant, which is the Km value. In maximum cases, the Km value is reduced, which signifies the increased amount of substrate specificity of the enzymes (Ghosh and Das 2020). When the bacterial, fungal, and algal systems are modified,

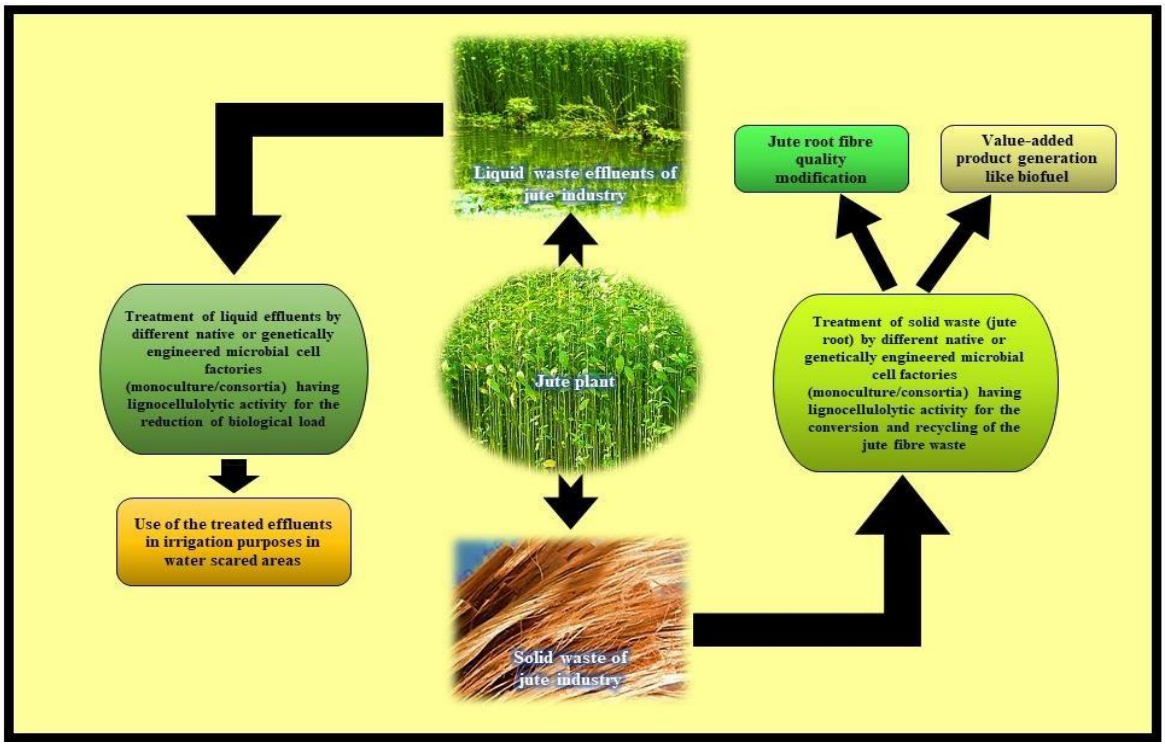

Figure1 Jute industry waste treatment, recycling and conversion

positive results have been generated. This review article emphasized the identification of native, genetically engineered, and consortia-based microbial systems that could gradually increase the product-producing rate and can enhance the jute fiber modification process, jute waste remediation, recycling, and biofuel generation.

2 Lignocellulosic biomass pretreatment process

Lignocellulose is a plant material and is highly recalcitrant. Its breakdown is very tough due to the presence of the protective layer of phenolic polymer lignin surrounding the lignocellulosic biomass. However, for any modification, conversion, or recycling, we need to break that rigid portion to get the polysaccharide part cellulose, hemicellulose, etc., that can be converted to value-added products (Islam et al. 2022a). Besides that, fiber modification also depends on the plant material's lignin content. The higher the lignin content, the lower the fiber quality, and vice-versa. Hence lignin breakdown is essential for any industry to generate economic products. Different physical, chemical, physicochemical, and biological strategies have been applied in different industries to get the treated lignocellulosic biomass that can be treated further by multiple microbial systems as well as consortium approaches to get the best value-added products starting from biofuel to decorative products (Shahinur et al. 2022; Ivanovska et al. 2022). In the acid pretreatment process (Chemical method), LCB has been treated with diluted or concentrated acids of 0.2 to 2.5 w/w% with vigorous mixing at 130°C to 210°C. This treatment has an expensive recovery process and costly equipment. Fermentation inhibitors like hydroxyl methyl furfural are produced during the process. Lignin is not removed properly (Naseeruddin et al. 2013; Harmsen et al. 2010). In the alkaline pretreatment process (chemical method), LCB has been soaked with alkaline solutions like sodium and ammonium hydroxide at an optimal temperature for a specific period. In this process, the total operational cost and the catalysts are also very expensive (Zhao et al. 2008). Organosolv is a chemical method in which LCB is treated with organic solvents like acetone, ethanol, methanol, or their mixture with water to remove lignin and hemicelluloses (Limayem and Ricke 2012). Oxidative Delignification is a chemical process that is performed by mixing LCB with ozone, oxygen, and hydrogen peroxide to convert lignin polymer into carboxylic acids (Sun and Chen 2007). Ionic Liquid treatment is a physicochemical method in which LCB is mixed with the ionic solvent at an optimal temperature between 90°C to 130°C and optimal pressure. Then the water added ends up forming precipitation of biomass and enhancing the accessibility of cellulose (Zhu et al. 2013; Cox and Ekerdt 2013). Wet oxidation is a physicochemical treatment process in which drying and milling of the LCB waste occur at 195 °C for 10 min to 20 min. After that, water is added along with Na_2CO_3. Then the mixture is aerated, which results in fractionated LCB. The sugar-yielding capacity of this process is deficient (Harmsen et al. 2010). Microwave heating with catalyst technology is a physicochemical treatment associated with heating LCB in the microwave between the temperatures of 100°C– 200°C. After heating, maleic acid is added in different concentrations, generating pentose sugar (Kim et al. 2012). The combinational culture approach is a biological pretreatment method in which combining combinational microbial inoculums has been used for the lignocellulosic biomass. However, it is a less productive pretreatment method (Katiyar et al. 2015). Physical pretreatment methods that can process LCB into more accessible materials include milling, microwave irradiation, ultrasound technology, mechanical extrusion, and pyrolysis. In the milling process, rotary cutters separate the material by varying the cutter direction on different axes, changing cutter speed and pressure. Milling processes are different, like ball milling, hammer milling, vibro-milling, colloid milling, two-roll milling, etc. Among all milling processes, ball milling can only be used for the treatment of dry as well as wet LCB wastes. However, it is incapable of removing lignin properly, as well as an energy-consuming process that makes it a less suitable physical pretreatment option. Microwave irradiation is the most common method of plant biomass pretreatment. This is an advantageous method as it is straightforward to conduct, has increased heating capacity, less processing time, fewer inhibitors, and low energy requirement. In extrusion pretreatment, LCB materials are mixed, heated, and sheared, which results in modification of the physical and chemical properties of the biomass. Low cost along with the best- controlled monitoring process makes extrusion pretreatment better than any other physical pretreatment method. Zero sugar degradation with good adaptable capacity makes it a perfect physical system more feasible for bioethanol production by pretreating lignocellulosic waste. Pyrolysis is a thermal breakdown method of lignocellulosic waste at a temperature ranging between 500 and 800°C, without any oxidizing agent generally used to produce bio-oil from LCB waste (Aftab et al. 2019). The ultrasound approach is a green technology that is novel as well as environmentally friendly. The ultrasound sonication technique reduces pretreatment time and the requirement for chemicals or enzymes. Lignocellulosic biomass fractionation takes ultrasonic waves with subsequent hydrolysis for biofuel generation (Subhedar and Gogate 2016; Patil et al. 2022).

3 Jute fiber modifications by different lignocellulolytic enzymes

Jute fiber is a lignocellulosic biomass. Hence its breakdown, conversion, and modification are possible using lignocellulolytic enzymes. The most treated enzymes for jute fiber modification are laccase, cellulase, and pectinase (Autore et al. 2009). In this review article, we will analyze the promising enzyme function and the physical and chemical modification of these enzymes (Figure 2).

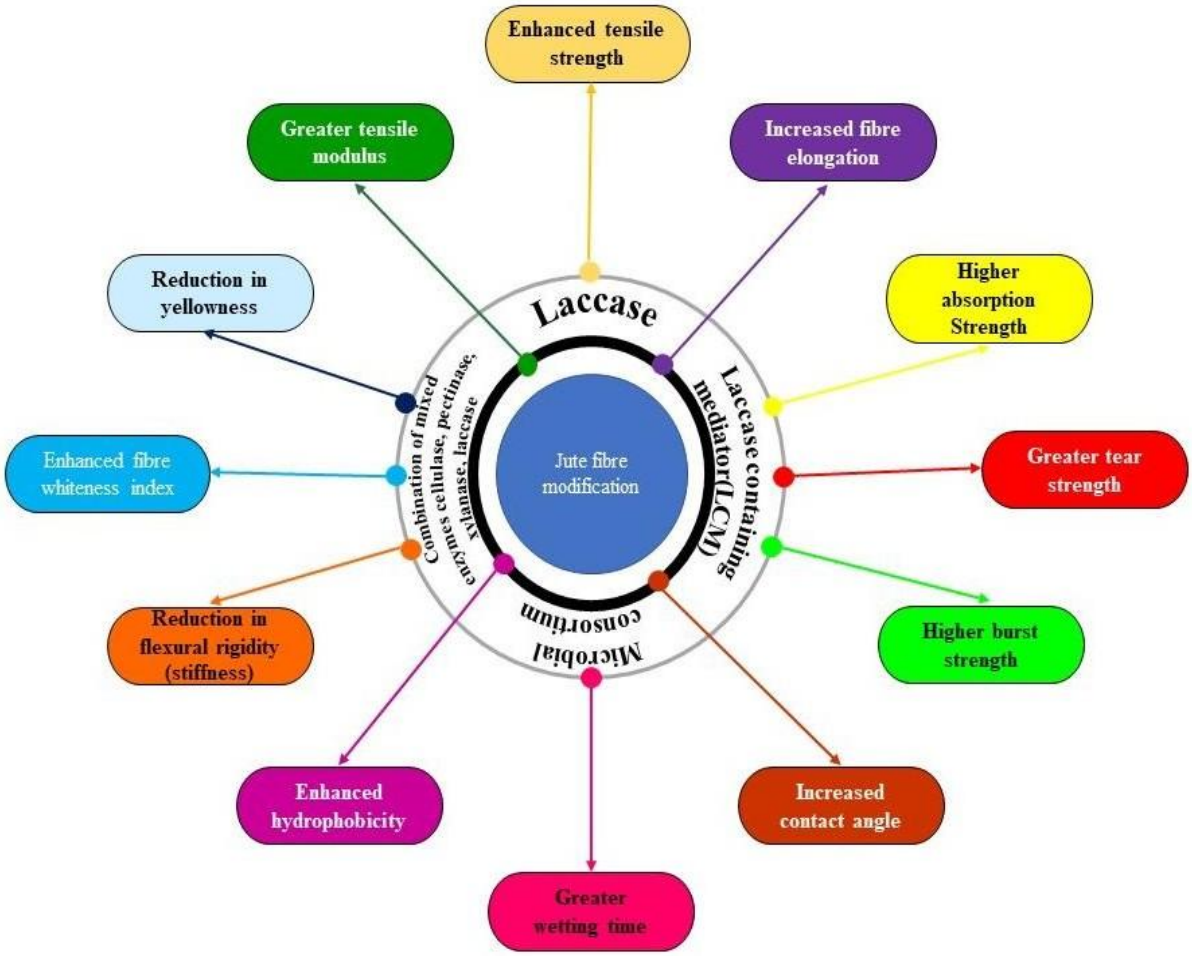

Figure 2 Jute fiber modification by laccase and combination of mixed enzymes (cellulase, pectinase, xylanase, and laccase)

3.1 Jute Fiber Modification by Laccase

Jute has gained massive attention because it is readily biodegradable and has significant mechanical properties, low cost, vast raw sources, etc. (Zhou et al. 2017; Wang et al. 2019). Due to the disadvantages of physical and chemical processing methods, using enzymes or enzyme technology to modify fiber draws the researcher's attention (Table 1). Laccase is a kind of oxidoreductase enzyme that causes the catalysis of jute lignin by oxidation and produces free radicals. It contributes to the formation of hydrophobic monomers. These glycoproteins oxidize phenols and aromatic or aliphatic amines, giving rise to reactive radicals where molecular oxygen is reduced to water in a simultaneous redox reaction (Riva 2006). The substrate containing cellulose, hemicellulose, and lignin is oxidized, which further continues for degradation and grafting (Table 3, 4). Grafting is the co-polymerization of the jute fiber with other chemicals like vinyl monomers, methacrylonitrile, and acrylonitrile that provide extra strength with enhanced thermal stability and modified surface smoothness to the jute fiber (Mondal et al. 2016). On the other hand, Jute fiber composite is an excellent alternative to synthetic fiber composite due to its easy availability, low weight and cost, non-toxicity, high flexural strength, and biodegradability (Song et al. 2021). Laccase oxidizes the phenolic hydroxyl groups in lignin, present in the jute fiber, leading toward the biogenesis of radicals of phenoxyl residues which have been coupled to end up with ether structures (Dong et al. 2018). Laccase-mediated reactions increase hydrophobicity on this fabric's surface and tensile properties (Kudanga et al. 2010; Zhou et al. 2013; Thakur et al. 2015; Nayab-Ul-Hossain et al. 2020). In the case of laccase/ mediator systems, laccase leads to the activation of synthetic mediators, including 2,2 - azino-bis- (3-ethylthiazoline-6-sulfonate) (ABTS) and 1-hydroxy benzotriazole and natural mediators like acetosyringone and syringaldehyde that result in the oxidization of the non-phenolic parts in the lignin structure (Reynaud et al. 2013; Witayakran and Ragauskas 2009). Jute fiber modification by using laccase after defibrillation is depicted in Table 2.

Table 1 Jute fiber modification by laccase and LCM (Laccase containing mediators)

Enzyme/ Enzyme plus mediator	Properties of jute fiber	Control	Modified result	Reference
Laccase	Tensile strength (N.m/g)	6.3±0.2	8.8±0.1	Dong et al. 2016
	Elongation percentage	0.40±0.04	0.60±0.04	
	Absorption Strength (mJ/g)	15.7±0.9	30.8±1.5	
	Tear strength (mN.m^2/g)	1.4±0.3	1.8±0.2	
	Burst strength (kPa.m^2/g)	1.038±0.003	1.098±0.003	
	Contact Angle	-	95.48°	
	Wetting time	-	3058s	
Laccase and ABTS	Tensile strength (N.m/g)	6.3±0.2	Decrease by 17%	
Laccase and 2,6-dimethoxyphenol (DMP)	Tensile strength (N.m/g)	6.3±0.2	Decrease by 9.1%	
Laccase and Alkali lignin (AL)	Tensile strength (N.m/g)	6.3±0.2	Increased by 13.6%	
Laccase and AL	Elongation percentage	0.40±0.04	0.60±0.04%	
	Absorption Strength (mJ/g)	15.7±0.9	35.9±2.2	
	Tensile strength (N.m/g)	1.4±0.3	2.0±0.2	
	Burst strength (kPa.m^2/g)	1.038±0.003	1.194±0.005	
	Contact Angle	-	68.69°	
	Wetting time	-	1438s	
Laccase and Guaiacol (G)	Tensile strength (N.m/g)	6.3±0.2	Increased by 14.8%	
Laccase and G	Elongation percentage	0.40±0.04	0.60±0.02	
	Absorption Strength (mJ/g)	15.7±0.9	36.6±2.3	
	Tear strength (mN.m^2/g)	1.4±0.3	2.0±0.1	
	Burst strength (kPa.m^2/g)	1.038±0.003	1.202±0.003	
	Contact Angle	-	106.26°	
	Wetting time	-	4199s	

Table 2 Jute fiber modification by using laccase after defibrillation

Laccase plus, defibrillation				
Enzyme	Properties of jute fiber	Control	Modified result	Reference
Laccase plus, defibrillation	Contact Angle	-	Increased to 95.48°	Dong et al. 2016
	Wetting time	-	3058s	
	Tensile strength (N.m/g)	-	Increased by 39.7%	
	Tear strength (mN.m^2/g)		Increased by 28.6%	
	Burst strength (kPa.m^2/g)	-	Increased by 5.8%	

Table 3 Jute fiber modification by Grafting process

Jute/polypropylene Composites with laccase	Tensile strength (MPa)	Tensile modulus (MPa)	Reference
Control jute/pp	34.58±1.74	2669.57±99.66	Ni et al. 2015
PG-grafted jute/PP	36.81±2.02	2757.71±100.69	
OG-grafted jute/PP	37.06±1.44	2925.37±105.48	
DG-grafted jute/PP	40.30±0.36	3139.43±44.45	
Retention of tensile strength and modulus of different jute fiber composites after water immersion of 216 hours			
Control jute/pp	86.58±1.56	55.75±0.63	Ni et al. 2015
PG-grafted jute/PP	89.89±1.35	56.85±1.05	
OG-grafted jute/PP	90.21±0.97	58.43±1.62	
DG-grafted jute/PP	92.93±0.74	60.23±2.15	

Table 4 Enhancement in mechanical properties of jute fibers by grafting process

Composite type	Properties of jute fiber	Modified result	Reference
Grafted Dodecyl gallate (DG) onto jute fabric by laccase for the enhancement of surface hydrophobicity of jute fiber	Water contact angle (°)	Increased to 133.01	Ni et al. 2015
	Water absorption	Increased by 22.21 %	
	Thickness swelling	Increased by 17.05%	
	Tensile strength (MPa)	Increased by 16.54%	
	Tensile modulus (MPa)	Increased by 17.60%	
	Elongation at break (%)	2.78%	
	Loss of modulus (E")	Higher than control	
Grafted Octal gallate (OG) onto jute fabric by laccase for the enhancement of surface hydrophobicity of jute fiber	Water contact angle (°)	Increased to 121.70°	
	Tensile strength (MPa)	Increased by 70.17%	
	Tensile modulus (MPa)	Increased by 9.58%	
	Elongation at break (%)	2.57%	
Grafted Propyl gallate (PG) onto jute fabric by laccase for the enhancement of surface hydrophobicity of jute fiber	Water contact angle (°)	Increased to 117.54°	
	Tensile strength (MPa)	Increased by 6.45%	
	Tenacity loss	Increased by 3.30%	
	Elongation at break (%)	2.51%	

3.2 Jute Fiber Modification by Cellulase

Jute has been considered as one of the most primeval cash crops in South Asian countries. Several disadvantages of jute fiber include harshness, stiffness, and complex structural properties because of the presence of lignin (Vigneswaran and Jayapriya 2010). Jute contains 58-63% of cellulose, 21-24% of hemicellulose, 12-14% of lignin, 0.2-0.5% of pectin, and other compounds including wax (0.4-0.8%), protein (0.8- 2.5%), mineral matter (0.6-1.2%). Nevertheless, it has been reported that cellulase has significant potential in softening the jute fiber and working with other enzymes (Table 5, 6, 7) (Samanta et al. 2005, 2006). However, pretreatment methods, i.e., mixed enzyme treatment and amino silicone treatments, have been executed by Basu et al. (2008). The enzymatic intervention has been executed involving a mixture of cellulase, pectinase, and xylanase in different ratios. Though -CHO group of oxidated cellulose or hemicellulose of jute induces a reaction with the -NH_2 group of amino silicone substance and leads to the formation of an inter-fiber bond and further durable film coverage on the surface of jute. Treatment with the mixed enzyme at 55°C for 2 hrs converts the fiber into more improved quality in fineness, brightness, and softness and lowers bundle tenacity (Chakrabarti and Sinha 2001).

Table 5 Action of cellulase in jute fiber modification

Jute fiber	Cellulase concentration	Modified result	Application	Reference
Tenacity loss	2%	9.05%	Loss of fiber strength	Vigneswaran and Jayapriya 2010
	3%	14.76%		
	4%	19.83%		
Improved fiber elongation	2%	0.96%	Improved elongation	
	3%	3.87%		
	4%	5.26%		
Reduction in flexural rigidity (stiffness)	2%	20.49%	Enhanced suppleness and softness in fibers	
	3%	25.47%		
	4%	34.67%		
Enhanced whiteness index	2%	12.35%	Improved whiteness index	
	3%	16.02%		
	4%	3.47%		
Reduction in yellowness	2%	54.90%	Enhanced brightness	
	3%	58.02%		
	4%	54.97%		

Table 6 Jute fiber modification by mixed enzymes

Mixed enzymes treatment of jute fiber				
Enzymes	Properties of jute fiber	Control	Modified result	Reference
Xylanase/Laccase	Contact Angle	0.00°	96.17±0.12°	Dong et al. 2016
	Wetting time (s)	664.0±45.5	3454.4±58.9	
	Tensile strength (N.m/g)	6.3±0.2	Increased by 10.2%	
	Tear strength ($mN.m^2/g$)	1.4±0.3	1.9±0.2	
	Burst strength ($kPa.m^2/g$)	1.038±0.003	1.106±0.005	
Cellulase/Laccase	Contact Angle	0.00°	97.53±0.29°	
	Wetting time (s)	664.0±45.5	3655.6±39.5	
	Tensile strength (N.m/g)	6.3±0.2	Increased by 26.1%	
	Tear strength ($mN.m^2/g$)	1.4±0.3	2.2±0.2	
	Burst strength ($kPa.m^2/g$)	1.038±0.003	1.182±0.003	

3.3 Jute Fiber Modification by Pectinase

Pectinases are the enzymes that catalyze the degradation of complex molecules called pectin. Depolymerization or de-esterification reactions are to be performed by this enzyme (Singh et al. 2019b). Three types of pectinases are generally found; i.e., (1) pectin methylesterases, (2) Polygalacturonases, and (3) pectin transaminases (Ramos and Malcata 2011). When commercial pectinases or xylanases are added, it shows the ability to loosen the protruding fiber bundle of jute in an enzyme treatment under 50°C (Sreenath et al. 1996). Interest in Bio degumming is growing day by day because of its low-cost, environment-friendly, and high efficiency (Banik et al. 2007; Biswas et al. 2013). Non-Cellulosic components like pectin, lignin, and hemicelluloses in jute are broken down by the activity of enzymes produced by microorganisms (Kozlowski et al. 2006). *Pectobacterium* sp. DCE-01 has the potential to secrete pectinase along with other enzymes (Duan et al. 2016). A *Micrococcus* sp. strain exhibits the ability to accomplish the jute degumming in 6 days (Haque et al. 2003). Several bacteria such as *Bacillus pumilus*, *B. subtilis*, *B. cereus*, and *B. licheniformis* are used in fiber retting, whereas *B. pumilus* has been reported to produce exo- pectinase (Tepe and Dursun

Table 7 Jute fiber modification by mixed enzymes (mixture of cellulase, xylanase, and pectinase)

Jute fiber parameter	Mixed enzyme concentration	Modified result	Application	Reference
Tenacity loss	2%	11.96%	Loss of fiber strength	Vigneswaran and Jayapriya 2010
	3%	13.47%		
	4%	23.81%		
Improved fiber Elongation	2%	3.44%	Improved elongation	
	3%	5.00%		
	4%	5.48%		
Reduction in flexural rigidity (stiffness)	2%	13.61%	Enhanced suppleness and softness in fibers	
	3%	29.87%		
	4%	36.97%		
Enhanced whiteness index	2%	14.66%	Improved whiteness index	
	3%	15.49%		
	4%	26.37%		
Reduction in yellowness	2%	52.84%	Enhanced brightness	
	3%	55.58%		
	4%	58.02%		

2014; Liang et al. 2015). Bacterial consortia consisting of *P. aeruginosa*, *Bacillus* sp, *B. subtilis*, and *Enterococcus* sp. show enzymatic potential by producing pectinase, mannase, and xylanase (Tamburini et al. 2003; Hossain et al. 2021).

4 Native bacterial communities involved in jute fiber modification

Lignocellulosic biomass like jute fiber is cemented to adjacent cells inside the stem with pectin extracted through retting, also known as the degumming process. Different pectinolytic anaerobic bacteria are responsible for water retting treatment that helps to decompose pectic substances from jute stems and produce high-quality fiber. In this process, pectin is depolymerized by a different group of pectinolytic enzymes: Polygalacturonases, pectin lyase, pectate lyase, and pectin esterase. Additionally, xylanase selectively removes the non-fibrous hemicelluloses without affecting cellulosic fiber resulting in soft fiber generation. Hence Pectinolytic microorganisms having xylanase activity and negative cellulase activity is of great importance. Another substance called lignin is a phenolic polymer that protects the outermost layer of jute and is one of the most critical restriction generators for improving fiber quality. Without breaking the lignin polymer, we cannot get the economic jute fiber (Barai et al. 2020). Thus pectinase, xylanase, and ligninase are the three most critical enzymatic factors contributing to the science behind jute fiber improvement. Water-based microbiological retting is the most economical and promising avenue that mainly involves bacterial communities along with different types of fungal, protozoan, algal, and diatom-based biological systems. Bacterial regimes can be classified as aerobic and anaerobic. The most crucial aerobic retting bacteria belonging to the genus *Bacillus* are *B. subtilis, B. polymyxa, B. mesenteric, B. pumilus, B. cereus, B. megaterium, and B. macerans*. Some other gram-negative genera including *Erwinia* and *Pseudomonas* are involved in microbial retting. During the post-retting period, some anaerobic bacteria like *Clostridium acetobutylicum, C. stercorarium*, and *C. tertium* are playing a vital role in the retting process. The best bacterial strains for degumming comprise *Bacillus cereus, B. megaterium, B. subtilis, B. koreensis, B. xiamenensis, Proteus mirabilis, Enterobacter tabaci, Kosakonia oryzae, Serratia nematodiphila* and *Aeromonas jandaei*. Further, *B. megaterium* has the highest pectinolytic and xylanolytic activity (Hasan et al. 2020). *Micrococcus* spp. has been identified as an accelerator of jute retting. Referring to the recent advancements made in isolating completed/partial genes controlling desirable traits, it is suggested to use modern molecular techniques to improve not only the quality of jute fibers but also to bioengineer microbial flora to further reduce the retting time without sacrificing fiber qualities (Haque et al. 2003). On the other hand, several aerobic bacteria like *Bacillus subtilis, B. polymyxa, B. mesenteric, B. maserans, C. tertium, C. aurantibutyricum, C. felsinium*, etc. have been isolated from the retting water. These aerobic microbial systems grow first, utilize dissolved oxygen, and promote the growth of aerobes. It has been stated that a more significant part of decomposition is carried out by aerobic species (Hasan et al. 2020). In the last decade, genetic engineering approaches have been used extensively to enhance the productivity of desired enzymes. Some of the modifications have been depicted in Table 8.

Table 8 Most promising genetically engineered bacterial systems that can be used in jute fiber modification and jute waste recycling

Bacterial Strain	Mutated Strain	Mutation Strategy	Engineered Enzyme	Substrate	Reduction % of Km Or fold of enzyme activity	Application	Reference
Rhodococcus jostii	*R. jostii* N246A	Oligonucleotide directed mutagenesis	versatile peroxidase	H_2O_2	44.44	Fiber modification, Dye decolorization, Biofuel Production	Roberts et al. 2011
Paenibac illus polymyxa Z6	*P. polymyxa* Z6 H218D	Site-directed mutagenesis	Pectinase	Linear 1,5-alpha-L-arabinan	--		Wang et al. 2014
Bacillus pumilus	*B. pumilis* L386Q/G4 17I	Site- directed mutagenesis	Laccase	guaiacol	77.14		Ihssen et al. 2017
Bacillus subtilis	*B. subtilis* M502F	Site-directed mutagenesis	Laccase	ABTS	90.80		Durão et al. 2006
Pyrococcus horikoshii	*P. horikoshii* C106A/C159A	Site-directed mutagenesis	Hyperthermophilic beta-1, 4 endoglucanase (EGPh)	Carboxymethyl cellulose	1.7 fold higher		Kang et al. 2007
	P. horikoshii C106A/C1 59A/C372A/C4 12A	Site-directed mutagenesis	Hyperthermophilic beta-1, 4 endoglucanase (EGPh)	p- nitrophenyl cellobiose	2.1 fold higher		
	P. horikoshii C372/AC4 12A	Site-directed mutagenesis	Hyper thermophilic beta-1, 4 endoglucanase (EGPh)	p- nitrophenyl cellobiose	1.6 fold higher		
	P. horikoshii E201, H297, H299 and E342	Site-directed mutagenesis (alanine scanning method)	Endogluc anase	p- nitrophen yl cellobiose	Enhanced enzyme activity		Kim et al. 2007
Clostridi um cellsulov orans	*C. cellsulovo rans* K94R, S365P, K9 4R-S365P	Site-directed mutagenesis	Mesophilic endogluca nase (EngZ)	carboxym ethyl cellulose	Enhanced enzyme activity		Kim et al. 2009
Bacillus subtilis JA18	*B. subtilis* JA18 Egl330	Truncation of the cellulose binding domain (CBD)	Endo- beta-1, 4- glucanase	CMC	78% higher catalytic efficiency		Wang et al. 2009

5 Native fungal communities involved in jute fiber modification

Wide ranges of fungi from different origins are capable of retting different wet and dry ribbons of jute under controlled laboratory conditions. Post-retting treatments of jute fiber using fungal cultures can be used to minimize the negative effects of jute root by removing the hard bottom part. Many fungal species are beneficial in improving the fiber quality of jute. During and after retting, the microbial load per ml of retting water increment occurs. Different methods like ribbon, dry and chemical retting can be an alternative system to conventional retting that can overcome the scarcity of retting water. Multiple attempts have already been made to isolate and screen different fungal systems like *Aspergillus niger*, *Macrophomina faciolina*, *Mucor*, *Chaetomium* sp., *Phoma* sp., *and Penicillium* sp., etc. All these systems have been good retting agents. The microbial population varies from place to place in the jute-growing areas in Asian countries. Diverse research has found that post-retting water contains a higher fungal load. In the in-vitro test, the addition of post-retting fungal strains increases the amount of retting in a significant way and also reduces the time required for the retting technique. The retting period becomes almost half after using post-retting water. Isolated fungi of *Aspergillus clavatus*, *Rhizopus* sp., *Zygorinchous* sp., *Sporotrichum* sp., *Trichoderma* sp., *Penicillium* sp., *Curvularia* sp. has examined for the retting efficacy of green jute ribbons. In laboratory and field conditions, *Sporotrichum* sp. retted the jute material in 7 days, whereas *Trichoderma* sp. and *Curvularia* sp. retted the green ribbon in 11 days. In the case of retting by *Sporotrichum* sp., no adverse effect on the fiber bundle strength and fiber yield has been observed, and according to the Pressley index, fiber strength is found to be 10.82 lbs/mg, and fiber yield is about 2.8kg out of 40kg green ribbons (Haque et al. 2003). Other multi-diverse fungal communities can produce multiple enzymes like ligninase, laccase, cellulase, and hemicellulase that can convert lignocellulosic biomass like jute fiber into value-added products like bioethanol, etc. That means these ligninolytic microbial systems can be able to ret jute as well. Some of these fungal communities with their pivotal impacts have been discussed here. *Trichoderma reesei* is a mesophilic filamentous fungus capable of secreting many cellulolytic enzymes like endoglucanase, exoglucanase, and β-glucosidase that have huge industrial applications in substrate conversion, that is, cellulose which is a major ingredient of jute plant biomass (Bayram Akcapinar et al. 2015). In contrast, strain *T. harzianum* contains only endoglucanase, exoglucanase and lacks β-glucosidase for generation of six carbon sugar. *Pestalotiopsis* is an ascomycete fungus with pathogenic activity against plants and can grow in aerobic and anaerobic situations on polyurethane synthetic polymer as the sole carbon source, hence helps in bioremediation (Sánchez 2009; Elgamsy et al. 2022). Enzymes produced by this microbial system are endoglucanase and exoglucanase to generate value-added products from cellulose-containing jute plant waste biomass (Islam et al. 2022b). Anaerobic fungus like *Neocallimastix frontalis*, which lives in the rumen, have been captive to producing endoglucanase and exoglucanase and has a high demand in the cellulose conversion industry. *Rhizopus oryzae* is a well-known micro-fungus having heterothallic filamentous construction that is found as a saprotrophic in soil and rotting vegetation and has an efficiency of cellulose breakdown by producing industrially important 1,3-β-D-Glucosidase. *Fomitopsis palustris* is a polypore fungus that causes brown rot disease by the enzymatic breakdown of the woody part cellulose. Further, *F. palustris* possess three different cellulase enzymes i.e. EG-II, exoglucanase, and β-glucosidase, which assist in loosening cell-wall structural polysaccharide network by disassembling hemicellulose portion joined with cellulose. Similarly, *Phanerochaete chrysosporium* is the most studied white rot fungus that possesses a Secretome and secretes an array of peroxidases, oxidases, and cellulases. Endoglucanase, exoglucanase, and β-glucosidase are the enzymes of this fungus that can help to convert cellulose into glucose to produce energy-producing components (Sánchez 2009). *Penicillium brefeldianum* can produce 1,6-β-D-Glucosidase, whereas *Myceliophthora* sp., *Humicola* sp., *Fusarium oxysporum*, and *Eichhornia crassipes* produce different types of cellulases (Sánchez 2009; Dashtban et al. 2009). *Aspergillus niger* is a fungus that causes "black mold" disease on certain fruits and vegetables and is responsible for the production of multiple enzymes like α-L Arabino-furanosidase, a feruloyl esterase, Exo-β-1,4-mannosidase, endogalactanase, endo- α-1,5-arabinanase for detachment and breakdown of hemicellulose. Another species that can break hemicellulose is *A. nidulans* which is a potentially resourceful organism having the capability of the production of naïve and different heterologous enzymes for industrial applications like Exo-1,4-β- Xylosidase, endogalactanase for the breakdown of hemicellulose. *Neocallimastix* sp. is a type of fibrolytic fungi that causes colonization and breakdown of the structural polysaccharides of plants by producing the enzyme p-Coumaroyl Esterase. *T. longibrachiatum* is responsible for large-scale commercial production of hemicellulases like Endo- 1,4-β-xylanase, xylan α-1,2-glucuronosidaseetc (Sánchez 2009). *Sclerotium rolfsii* is a necrotrophic fungal plant pathogenic community that acquires hemicellulolytic enzymes like Endo-β-1,4- mannanase. Other fungal origins responsible for hemicellulose detaching enzymes are *A. fumigatus* (Xylan α-1,2-glucuronosidase), *Humicola insolvens* (β-Glucosidase), *T. reesei* (Acetyl esterase, acetyl xylan esterase, glucuronyl methyl esterase), *Phanerochaete chrysosporium* (Glucuronyl methyl Esterase), *Acremonium alcalophilum* (Glucuronyl methyl Esterase) (Sánchez 2009). Lignin, the phenolic polymer in lignocellulosic biomass, is the toughest part of the plant's structural organization. Hence different chemical, physical and physicochemical processes have been done to separate lignin from lignobiomass to produce six

Table 9 Most promising genetically engineered fungal systems that can be used in jute fiber modification and jute waste recycling

Fungal Strain	Mutated Strain	Mutation Strategy	Mutated Enzyme	Substrate	Reduction % of Km Or enzyme activity	Application	Reference
Trichoderma reesei	*T. ressei* Q126F, K272F, Q274V	Site directed mutagenesis	Endoglucanase I	cellulosic material	Enhanced enzyme activity	Fiber modification, Dye Decolourisation, Biofuel Product ion	Roberts et al. 2011
Thermotoga maritime	*T. maritime mutant*	Inverse polymerase chain reaction (IPCR)	Endoglucanase Cell 12B	Carboxy methyl cellulose	Enhanced enzyme activity		Zhang et al. 2015
Aspergillus awamori	*A. awamori* D71I, D77N, and D77I	Site-directed mutagenesis	Feruloyl esterase- A	alpha- naphthyl butyrate	12.12/ 45.45/54.54		Koseki et al. 2005
Aspergillus niger CIB 423.1	*A. niger* CIB 423.1 D93G	Site-directed mutagenesis	Feruloyl esterase	furalate	10.625		Zhang and Wu 2011
Phanerete chrysosporium	*P. chrysosporium* P106R/Q10H/L211V/ A243R/F255L	Alteration of amino acid sequences	Lignin peroxidase	H_2O_2	Enhanced enzyme activity		Ryu et al. 2008a, b.
	P. chrysosporium A140G/S190P/P193A /S196F/E20Q	Alteration of amino acid sequences	Lignin peroxidase	2,4-dichlorophenol	Enhanced enzyme activity		
Pleurotus eryngii	*P. eryngii* A260F and R257A	Site-directed mutagenesis	versatile peroxidase	lignin	20-to-50-fold higher enzyme activity		Ruiz-Duenas et al. 2008
Pleurotus ostreatus	*P. ostreatus* W170A, R263N, Q266F, and V166/168L	homologous gene expression system	Laccase	H_2O_2	Enhanced enzyme activity		Tsukihara et al. 2008
	P. ostreatus Mutant POXA1bDEL TA16/P OXA1bDELT A4	Site-directed mutagenesis	Laccase	Syringalda zine	Enhanced enzyme activity		Autore et al. 2009
Melanocarpus albomyces	*M. albomyces Mutant L559A*	Site-directed mutagenesis	Laccase	Syringalda zine	Enhanced enzyme activity		

carbon sugars that can be used for different value-added products generation. In jute industries, the multi-faced physicochemical system has been used to generate quality fiber, but the problem is that not a single system can generate grade one fiber. Hence microbial communities like fungal systems became very popular for their large-scale enzyme production like lignin peroxidase and laccases. Fungal toxicity is a barrier in this system. However, *Phanerochaete chrysosporium* is a saprophytic fungus that breaks the woody part of dead plants by using the enzymes lignin peroxidase, glyoxylate oxidase, manganese peroxidase, horseradish peroxidase, cellobiose dehydrogenase (Fujian et al. 2001; Sánchez 2009). On the other hand, *Neurospora crassa* can produce a special type of lignin-breaking enzyme, laccase, a powerful enzymatic system among all other ligninolytic enzymes. *Aspergillus sclerotiorum* is a genetically identified fungal system indexed in the Environmental Relative Moldiness Index (ERMI) that releases lignin peroxidase and manganese peroxidase for the breakdown of lignin in woody plants. *Cladosporium* species are ubiquitous and represent isolated airborne fungi that can release lignin peroxidase and manganese peroxidase for uncovering the lignocellulosic biomass. *Mucor racemosus* is a fast-growing mold that has a global distribution and capable of producing enzymes like lignin peroxidase and manganese peroxidase, responsible for the generation of sugary materials by breaking down the lignin segment from lignocellulosic biomass (Tsukihara et al. 2006; Sánchez 2009; Bonugli-Santoset et al. 2010; Rathner et al. 2017; Frommhagen et al. 2017). No single fungal community can produce all lignocellulolytic enzymes needed to break down waste lignocellulosic biomass. This is because the structural integrity of the biomass is very complex and has very high physicochemical

constraints. To meet the industrial need, various efforts have been carried out to develop effective genetic engineering approaches that can increase biomass accessibility (Table 9).

6 Native and genetically engineered promising algal systems that can be used for jute fiber modification

The jute plant is a complex mixture of cellulose, hemicellulose, pectin, and lignin, and a network of carbon sugar monomers links these components. The most critical factors to be considered in managing jute wastes (solid and liquid) are the reduction of organic loads present in jute industry effluents used in agricultural fields near jute industries and water scars areas (Das and Ghosh 2021). Using solid jute waste as cheaper feedstocks could help to produce biofuels (Ochoa- Chacón et al. 2022). Two types of biomasses are present in nature: traditional and modern. The former refers to the plant residue utilized for heating and cooking. In contrast, the latter refers to the waste biomass used for transportation fuels and electricity generation. Waste biomass refers to the lower-value by-product of various industrial sectors such as agriculture, forestry, etc. Energy crops can be used as raw materials for second-generation biofuel production. Jute, textile, paper, and pulp industrial waste conversion to value-added products is carried out through three sequential steps (i) lignocellulosic waste pretreatment, (ii) Physico-chemical as well as biological lysis of polymeric sugar, (iii) separation and purification (Ghosh and Talukdar 2020; Ghosh and Das 2021; Chares Subash and Muthiah 2021). The increasing popularity of alternative fuel sources and lignocellulosic waste conversion has prompted scientists to explore the potential of bioconversion of lignocellulose. The main challenge is the delignification of lignocellulose for its recalcitrance composition and toxicity. Multiple biological regimes have disintegrated lignocellulosic biomass like bacteria, fungi, etc. However, analyzing algal systems for producing ligninolytic enzymes is a newly emerging field of research for biofuel and high-quality jute fiber generation. To this end, the different algal system has been introduced that can produce required biocatalysts for the breakdown of lignocellulosic biomass like lignin peroxidase, laccase, thermostable oxidants, etc. Laccases are multi-copper oxidases commonly found in fungi, bacteria, and higher plants. They also show their presence in the algal system of *Tetracystis aeria*, which was first observed by Otto et al. (2010). This organism can produce the extracellular laccase-like enzyme. The strain has been characterized by its ability to biodegrade various xenobiotics, such as phenanthrene and azo dyes. Its ability to effectively convert lignocellulosic solid waste into lignin has been identified. It has been assumed that algae can convert phenolic compounds into complex polymers by a ring cleavage mechanism and these can be oxidized indirectly through redox mediators. Lignin biosynthesis and degradation is a natural function of laccase in bioremediation. Genus *Tetracystis* is a green alga that inhabits the soil and can be studied for its laccase-like enzymes. This model could support the study of different phenolic compounds released from lignocellulosic waste. Purification of *T. aeria* laccase has been done by Otto and Schlosser (2014), which contains two polypeptides of molecular weight of 110kDa and 71 kDa. High substrate specificity has been observed in purified laccase. Chlorophyceae algae like *T. aeria* can show ABTS oxidizing properties. *Scenedesmus* clade can oxidize phenolic constituents by its thermostable low-molecular-weight enzyme. True laccase has been secreted by *Chlamydomonas moewusii* that optimally act at neutral to alkaline pH. Oxidation of 17α-ethinylestradiol, bisphenol A, nonylphenol, and triclosan are carried out by laccase of *Tetracystis aeria* in the presence of ABTS, which is a redox mediator. Green algal regimes can help in the bioremediation of the ecosystem by breaking down the phenolic pollutants found in contaminated industrial surface waters (Otto et al. 2010; Otto and Schlosser 2014; Otto et al. 2015). *Spirulina platensis* CFTRI, a cyanobacterial strain, can produce an extracellular thermostable laccase of 66 kDa that efficiently shows ligninolytic action in the presence of ABTS at alkaline pH. Enhanced laccase activity has been observed in the presence of Cu^{+2}, Zn^{+2}, and Mn^{+2}. It shows dye decolorization activity that can help bioremediation (Afreen et al. 2017). Seven microalgal species that have been isolated and screened by Abd Ellatif et al. (2021) can show dye decolorization of orange G, crystal violet, malachite green, brazilwood, Naphthol Green B dyes, etc. These are *Nostoc humifusum*, *N. muscorum*, *Oscillatoria* sp., *A. oryzae*, *S. platensis*, *Chlorella vulgaris* and *W. saccata*. Ligninolytic activity has been determined in all strains by ligninase assay. *C. vulgaris* shows maximum lignin peroxidase activity, whereas *A. oryzae* and *W. saccata* show maximum laccase activity. Optimum decolorization by *C. vulgaris*, *A. oryzae*, and *W. saccata* indicates their potentiality for breaking down lignocellulosic waste like jute root waste biomass and its conversion efficacy into value-added products (Abd Ellatif et al. 2021). Jute waste degradation and biofuel generation not only depend on ligninolytic enzymes but also on cellulase and hemicellulase enzymes that are being produced by genetically modified marine algal systems like *Chlamydomonas* sp. and *Dunaliella* sp. that help in algal biofuel genesis and can be used as waste converting tools into value-added products (Subhadra 2010; Georgianna and Mayfield 2012; Arora et al. 2019). Algal Xylanase is capable of breaking the hemicellulosic part of lignocellulosic biomass. Photosynthesis is the most promising property of marine algae and hence can fix carbon dioxide in the presence of solar energy. Metabolic engineering and synthetic biology strategies help us to convert chloroplasts in *C. reinhardtii* and *Dunaliella tertiolecta* by forming recombinant proteins inside the algal system. Growth in long pH ranges and different brine densities make these systems a true candidate for biofuel production and waste remediation. Chloroplast transformation of *D. tertiolecta* has been done by homologous

recombination. Erythromycin has been used in the antibiotic resistance selection process. Five recombinant enzymes, i.e., phosphate- hydrolase, α-galactosidase, β-mannanase, xylanase, and phytase, have been produced in the plastids of *D. tertiolecta* and *C. reinhardtii*. The particle bombardment method has been used to transform the plastid using 5′UTR, psbD promoter, psbA terminator, and 3′-UTR in the algal genetic systems (Georgianna et al. 2013). In recent years, genetic and metabolic alteration of the algal system opened the opportunity for generating recombinant proteins like xylanase, which is being used for the depolymerization of hemicelluloses, cellulase for the disintegration of plant structural polysaccharides, etc. (Subhadra and Grinson-George 2011). Hence, the enzymes required for the fragmentation of lignocellulosic biomass are now available from both naive and genetically and metabolically engineered algal strains. So, a mono algal culture or a hypothetical algal consortium with all the required enzymes for bioremediation of a lignocellulosic waste, jute retting, or bioethanol production would be the environmentally sustainable key player that will provide growth in both the jute and fuel industry from the economic aspect. These activities are interrelated with lignocellulosic biomass breakdown as well as fiber modification. Besides the native algal system, some genetically engineered marine algae can produce different cellulolytic enzymes like hemicellulase, cellulase, mannase, xylanase, glucosidase, etc. A hypothetical concept depicts that an algal consortium may act better than individual treatment for good-quality fiber and biofuel genesis. The consortium approach is a mixed naïve and genetically altered algal system capable of faster retting and stable process mechanism instead of monoculture.

7 Proposed microbial Consortium that can be used in jute fiber modification

Jute fiber modification can be enriched by the hub of multiple lignocellulolytic symbiotic microbial strains due to the presence of lignocellulose degrading genes in the consortia. The enrichment culture technique can help to make the consortia with specific and mixed enzymatic properties by maintaining functional diversity, distribution, environmental relationships, and abundance of the participating co-members. The fascinating microbial consortia responsible for the breakdown of lignocellulose is XDC-2 composed by Guo et al. (2010) from the compost, which was studied further by Hui et al. (2013). It has been reported that the consortium cultures can efficiently degrade the lignocellulose rapidly and 17.6% of unpretreated corn stalks can be degraded by this consortium, along with cellulose, hemicellulose, and lignin degradation in 10.4%, 16.5%, and 9.6% ratios, respectively (Hui et al. 2013). Zhang et al. (2015) produced a microbial consortium TMC7, which can degrade 79.7% of rice straw at 65˚C within 15 days. Similarly, Lu et al. (2019) produced a thermophilic consortium TC-Y, which can degrade 49.5% of corn stalks in just 20 days. A synthetic fungal-bacterial mixed consortium has been designed by Hu et al. (2017) that can efficiently improve the activity of the lignocellulolytic enzyme. Their consortium analysis has made it clear that the bacterial members are more critical than the fungi for lignocellulolytic enzyme activity (Hu et al. 2017). Liang et al. (2018) also produced a consortium OEM2, which can degrade 41.5% rice straw in 9 days and 85% hemicelluloses in 12 days (Liang et al. 2018). Cortes-Tolalpa et al. (2018) have constructed a salt-tolerant lignocellulosic-biomass breaking microbial consortium system by enriching a halo-marsh soil microbiome with carbon and energy source, i.e., wheat straw and the consortia results in higher lignin as well as cellulose breakdown. Results indicate that compared to fungi, the bacterial system shows the primary role in the degradation of the recalcitrant substrate under salt conditions (Cortes-Tolalpa et al. 2018). It has been observed that pretreated substrates can be easily hydrolyzed, which is not cost-friendly as the pretreatment process is responsible for additional expense and pollution. Hence, the industries highly need a consortium with the capability of breaking down the unpretreated jute fiber.

8 Conclusion and Future Outlook

Jute fiber and jute waste (lignocellulosic waste biomass) are cheaper substrates and can be used to produce different types of value-added products and biofuel. Hence, historical evidence of jute-based research outcomes by the industry and by different academic research organizations is glorious and triumphant. Along with the positive side, jute fiber has some lacuna like lower flax than other natural fibers, sensitivity to water absorption, poor bonding capacity with different matrices, non-uniform fiber, limited fiber volume, etc. The various steps of the lignocellulosic jute waste treatment or jute fiber modification process are economically unfeasible and adversely affect the environment. In addition, the use of industrial waste effluent harms human health and the environment. All these gaps can be filled by the proper biological treatment methods for generating various kinds of necessary products for humankind. The monoculture retting method is now old. The microbial consortia-based retting process is in high demand as it can provide the best economic product. Nevertheless, shortly, mixed microbial consortia and genetically modified microbial consortia will be the workhorse for generating valuable lignocellulolytic enzymes required for jute retting. The rapid emergence and improvement of lignocellulolytic enzymes through protein engineering have ameliorated the laccase, lignin-peroxidase, pectinase, and cellulase/hemicellulase production rates. This process is regulated through various factors such as substrate-binding affinities, transcriptional regulatory factors, and enzyme-specific activities. A paradigm shift has been observed during genetically modified microbes are developed and used in the consortia-based approach. However, this paradigm shift requires

compromises in terms of time consumption. Metabolic engineering is a suitable key for generating cell factories but identifying the ideal targeted gene cluster and alteration in metabolic pathways is challenging; hence, sophisticated genetic tool-box and target-oriented methodologies are needed to improve the efficacy of lignocellulosic waste recycling and jute fiber modification. A rational design of a synthetic metabolic pathway could be utilized to improve the lignocellulosic waste biomass for bioenergy and high-grade fiber generation. An accelerated enzymatic degradation approach can be used to improve the utilization of lignocellulosic waste. Systems biology, metabolic engineering, and synthetic biology could play critical roles in mass LCB degradation and minimize the toxicity of lignocellulosic waste. On the other hand, the genetic consortium can be the key player in producing all the required lignocellulolytic enzymes in a single microbial host that can change the line of limitation.

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Author's contribution

All the authors contributed equally.

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Abd Ellatif, S., El-Sheekh, M. M., & Senousy, H. H. (2021). Role of microalgal ligninolytic enzymes in industrial dye decolorization. *International Journal of Phytoremediation, 23*(1), 41– 52. https://doi.org/10.1080/15226514.2020.1789842

Achwal, W. B., & Sinkar, U. W. (1994). Modified processing of jute fabrics to minimize photo yellowing: Part II-Use of UV absorbers. *Indian Journal of Fiber and Textile Research, 19,* 30–33.

Afreen, S., Shamsi, T. N., Baig, M. A., Ahmad, N., et al. (2017). A novel multicopper oxidase (laccase) from cyanobacteria: Purification, characterization with potential in the decolorization of anthraquinonic dye. *PloS One, 12*(4), e0175144. https://doi.org/10.1371/journal.pone.0175144

Aftab, M. N., Iqbal, I., Riaz, F., Karadag, A., & Tabatabaei, M. (2019). Different pretreatment methods of lignocellulosic biomass for use in biofuel production. In Abd El-Fatah Abomohra (Ed), *Biomass for bioenergy-recent trends and future challenges* (pp. 1-24). Intech open. https://10.5772/intechopen.84995

Ahmed, Z., & Akhter, F. (2001). Jute Retting: An Overview. *Journal of Biological Sciences (Faisalabad, Pakistan), 1*(7), 685–688. https://doi.org/10.3923/jbs.2001.685.688

Arora, P., Shukla, V. K., & Tiwari, A. (2019). Algal Cellulases. In N. Srivastava, M. Srivastava, P.K. Mishra, P.W. Ramteke, R.L. Singh (Eds), *New and Future Developments in Microbial Biotechnology and Bioengineering* (pp. 283-295). Elsevier. https://doi.org/10.1016/B978-0-444- 64223-3.00016-3

Autore, F., Del Vecchio, C., Fraternali, F., Giardina, P., Sannia, G., & Faraco, V. (2009). Molecular determinants of peculiar properties of a *Pleurotus ostreatus* laccase: Analysis by site- directed mutagenesis. *Enzyme and Microbial Technology*, *45*(6–7), 507–513. https://doi.org/10.1016/j.enzmictec.2009.08.004

Banik, S., Basak, M. K., & Sil, S. C. (2007). Effect of inoculation of pectinolytic mixed bacterial culture on improvement of ribbon retting of jute and Kenaf. *Journal of Natural Fibers, 4*(2), 33– 50. https://doi.org/10.1300/j395v04n02_03

Barai, S., Chattopadhyay, L., & Majumdar, B. (2020). Studies on delignification in jute (*Corchorus* spp L.) fiber with promising lignin degrading bacterial isolates. *Journal of Environmental Biology. 41,* 703-710. http://doi.org/10.22438/jeb/41/4/MRN-1252

Basu, G., Samanta, A. K., & Ghosh, P. (2008). Enzyme and silicone treatments on jute fiber. Part II: Effect on process performance during yarn making and yarn properties. *Journal of the Textile Institute*, *99*(4), 307–316. https://doi.org/10.1080/00405000701414816

Bayram Akcapinar, G., Venturini, A., Martelli, P. L., Casadio, R., & Sezerman, U. O. (2015). Modulating the thermostability of Endoglucanase I from *Trichoderma reesei* using computational approaches. *Protein Engineering, Design and Selection, 28*(5), 127–135. https://doi.org/10.1093/protein/gzv012

Biswas, D., Nandi, A. K., Chakrabarti, S. K., & Ray, P. (2013). Development of sustainable technology to produce jute-ramie blended textile and its applications. Conference Papers in *Materials Science, 2013,* 1–4. https://doi.org/10.1155/2013/578690

Bonugli-Santos, R. C., Durrant, L. R., da Silva, M., & Sette, L. D. (2010). Production of laccase, manganese peroxidase and lignin peroxidase by Brazilian marine-derived fungi. *Enzyme and*

Microbial Technology, 46(1), 32–37. https://doi.org/10.1016/j.enzmictec.2009.07.014

Chakrabarti, S. K., & Sinha, S. N. (2001). Enzyme additives technology for productivity improvement and cost reduction in jute processing. *Journal of the Institution of Engineers (India), 82*, 1–4. https://bit.ly/3J4ywDG

Chares Subash, M., & Muthiah, P. (2021). Eco-friendly degumming of natural fibers for textile applications: A comprehensive review. *Cleaner Engineering and Technology, 5*, 1-11, https://doi.org/10.1016/j.clet.2021.100304

Chukwuma, O. B., Rafatullah, M., Tajarudin, H. A., & Ismail, N. (2021). A review on bacterial contribution to lignocellulose breakdown into useful bio-products. *International Journal of Environmental Research and Public Health, 18*(11), 6001. https://doi.org/10.3390/ijerph18116001

Cogulet, A., Blanchet, P., & Landry, V. (2016). Wood degradation under UV irradiation: A lignin characterization. *Journal of Photochemistry and Photobiology. B: Biology, 158*, 184–191. https://doi.org/10.1016/j.jphotobiol.2016.02.030

Cortes-Tolalpa, L., Norder, J., van Elsas, J. D., & Falcao Salles, J. (2018). Halotolerant microbial consortia able to degrade highly recalcitrant plant biomass substrate. *Applied Microbiology and Biotechnology, 102*(6), 2913–2927. https://doi.org/10.1007/s00253-017-8714-6

Cox, B. J., & Ekerdt, J. G. (2013). Pretreatment of yellow pine in an acidic ionic liquid: extraction of hemicellulose and lignin to facilitate enzymatic digestion. *Bioresource Technology, 134*, 59–65. https://doi.org/10.1016/j.biortech.2013.01.081

Das, S., & Ghosh, D. (2021). Isolation of ligninolytic microbial regime from mangrove ecosystem for the bioremediation of lignocellulosic waste generated from jute plant. *Advanced International Journals of Research Abstracts*, 55.

Dashtban, M., Schraft, H., & Qin, W. (2009). Fungal bioconversion of lignocellulosic residues; opportunities and perspectives. *International Journal of Biological Sciences, 5*(6), 578–595. https://doi.org/10.7150/ijbs.5.578

Dong, A., Fan, X., Wang, Q., Yu, Y., & Cavaco-Paulo, A. (2016). Enzymatic treatments to improve mechanical properties and surface hydrophobicity of jute fiber membranes. *Bioresources, 11*(2), 3289-3302. https://doi.org/10.15376/biores.11.2.3289-3302

Dong, A., Li, F., Fan, X., Wang, Q., et al. (2018). Enzymatic modification of jute fabrics for enhancing the reinforcement in jute/PP composites. *Journal of Thermoplastic Composite Materials, 31*(4), 483–499. https://doi.org/10.1177/0892705717706538

Duan, S., Feng, X., Cheng, L., Peng, Y., Zheng, K., & Liu, Z. (2016). Bio-degumming technology of jute bast by Pectobacterium sp. DCE-01. *Applied Microbiology and Biotechnology Express, 6*(1), 86. https://doi.org/10.1186/s13568-016-0255-3

Durão, P., Bento, I., Fernandes, A. T., Melo, E. P., Lindley, P. F., & Martins, L. O. (2006). Perturbations of the T1 copper site in the CotA laccase from *Bacillus subtilis*: structural, biochemical, enzymatic and stability studies. *Journal of Biological Inorganic Chemistry: JBIC: A Publication of the Society of Biological Inorganic Chemistry, 11*(4), 514–526. https://doi.org/10.1007/s00775-006-0102-0

Elgamsy, R., Allah Abo Elmagd, A., Elrahman Mokhtar, A., Khalid, I., et al. (2022). Developing fire retardant composites of biodegradable polyethylene reinforced with agricultural wastes. *Ain Shams Engineering Journal, 13*(6), 1-10. https://doi.org/10.1016/j.asej.2022.101768

Frommhagen, M., Mutte, S. K., Westphal, A. H., Koetsier, M. J., et al. (2017). Boosting LPMO-driven lignocellulose degradation by polyphenol oxidase-activated lignin building blocks. *Biotechnology for Biofuels, 10*(1), 121. https://doi.org/10.1186/s13068-017-0810-4

Fujian, X., Hongzhang, C., & Zuohu, L. (2001). Solid-state production of lignin peroxidase (LiP) and manganese peroxidase (MnP) by *Phanerochaete chrysosporium* using steam-exploded straw as substrate. *Bioresource Technology, 80*(2), 149–151. https://doi.org/10.1016/s0960-8524(01)00082-7

Georgianna, D. R., & Mayfield, S. P. (2012). Exploiting diversity and synthetic biology for the production of algal biofuels. *Nature, 488*(7411), 329–335. https://doi.org/10.1038/nature11479

Georgianna, D. R., Hannon, M. J., Marcuschi, M., Wu, S., et al. (2013). Production of recombinant enzymes in the marine alga *Dunaliella tertiolecta*. *Algal Research, 2*(1), 2–9. https://doi.org/10.1016/j.algal.2012.10.004

Ghorai, A. K., & Chakraborty, A. K. (2020). Sustainable in-situ jute retting technology in low volume water using native microbial culture to improve fiber quality and retting waste management. *International Journal of Current Microbiology and Applied Sciences, 9*(11), 1080– 1099. https://doi.org/10.20546/ijcmas.2020.911.126

Ghosh, D., & Das, S. (2020). Genetic and metabolic engineering approaches for improving accessibilities of lignocellulosic biomass toward biofuels generations. In A. Kuila and V. Sharma (Eds),

Genetic and Metabolic Engineering for Improved Biofuel Production from Lignocellulosic Biomass (pp. 13–35). Elsevier. https://doi.org/10.1016/B978-0-12-817953-6.00002-6

Ghosh, D., & Das, S. (2021). Engineering of microbial cellulases for value-added product generations. In D.K. Tuli & A. Kuila (Eds), *Current Status and Future Scope of Microbial Cellulases* (pp. 171–187). Elsevier. https://doi.org/10.1016/B978-0-12-821882-2.00008-9

Ghosh, D., & Hallenbeck, P. C. (2012). Advanced Bioethanol Production. In P.C. Hallenbeck (Ed), *Microbial Technologies in Advanced Biofuels Production* (pp. 165–181). Springer US. https://10.1007/978-1-4614-1208-3

Ghosh, D., & Talukdar, P. (2020). Relevance of Microbial Enzymes in Textile Industries Emphasizing Metabolic Engineering Panorama. In H. Thatoi, P.K.D., Mohapatra, S., Mohapatra, & Mondal, K.C. (Eds.), *Microbial Fermentation and Enzyme Technology* (1st ed.) (pp. 195-205). CRC Press. https://doi.org/10.1201/9780429061257

Guo, P., Zhu, W., Wang, H., Lü, Y., Wang, X., Zheng, D., & Cui, Z. (2010). Functional characteristics and diversity of a novel lignocelluloses degrading composite microbial system with high xylanase activity. *Journal of Microbiology and Biotechnology, 20*(2), 254–264. https://doi.org/10.4014/jmb.0906.06035

Haque, M. S., Zakaria, A., Adhir, K. B., & Firoza, A. (2003). Identification of Micrococcus sp. responsible for the acceleration of jute retting. *Pakistan Journal of Biological Sciences, 6*, 686-687. https://10.3923/pjbs.2003.686.687

Haque, Md Shamsul, Asaduzzaman, M., Akhter, F., & Ahmed, Z. (2001). Retting of Green Jute Ribbons (Corchorus capsularis var. CVL-1) with Fungal Culture. *Journal of Biological Sciences (Faisalabad, Pakistan), 1*(11), 1012–1014. https://doi.org/10.3923/jbs.2001.1012.1014

Harmsen, P. F., Huijgen, W., Bermudez, L., & Bakker, R. (2010). *Literature review of physical and chemical pretreatment processes for lignocellulosic biomass (No.1184).* Wageningen University and Research: Wageningen, The Netherlands. https://library.wur.nl/WebQuery/wurpubs/fulltext/150289.

Hasan, R., Aktar, N., Kabir, S. M. T., Honi, U., et al. (2020). Pectinolytic bacterial consortia reduce jute retting period and improve fiber quality. *Scientific Reports, 10*(1), 5174. https://doi.org/10.1038/s41598-020-61898-z

Hossain, M. M., Siddiquee, S., & Kumar, V. (2021). Critical factors for optimum biodegradation of bast fiber's gums in bacterial retting. *Fibers (Basel, Switzerland), 9*(8), 52. https://doi.org/10.3390/fib9080052

Hossen, M. Z., Akhter, S., Tahmina, S. A., & Dayan, M. A. R. (2020). Jute Fiber: A Suitable Alternative to Wood Fiber for Paper and Pulp Production. *American Journal of Pure and Applied Biosciences, 2*(6), 177-182. https://doi.org/10.34104/ajpab.020.01770182

Hu, J., Xue, Y., Guo, H., Gao, M.T., et al. (2017). Design and composition of synthetic fungal-bacterial microbial consortia that improve lignocellulolytic enzyme activity. *Bioresource Technology, 227*, 247–255. https://doi.org/10.1016/j.biortech.2016.12.058

Hui, W., Jiajia, L., Yucai, L., Peng, G., et al. (2013). Bioconversion of un-pretreated lignocellulosic materials by a microbial consortium XDC-2. *Bioresource Technology, 136*, 481–487. https://doi.org/10.1016/j.biortech.2013.03.015

Ihssen, J., Jankowska, D., Ramsauer, T., Reiss, R., et al. (2017). Engineered Bacillus pumilus laccase-like multi-copper oxidase for enhanced oxidation of the lignin model compound guaiacol. *Protein Engineering, Design and Selection: PEDS, 30*(6), 449–453. https://doi.org/10.1093/protein/gzx026

Islam, M. M., & Rahman, M. M. (2013). Advances in jute and allied fibers post-harvest processing technologies in Bangladesh: Adoption constraints, prospect and future thrust. *WebPub Journal of Scientific Research, 1*(2), 20–30.

Islam, M. N., Hossain, S. M., Khatton, A., Rahman, M. M., et al. (2022a). Microcrystalline Cellulose from Jute Fiber: A Bright Prospect for Pharmaceutical Industry. *Scholars International Journal of Chemistry and Material Sciences, 5*(6), 100-104. https://10.36348/sijcms.2022.v05i06.003

Islam, M. N., Khatton, A., Sarker, J., Sikder, H. A., & Chowdhury, A. S. (2022b). Modification of Jute Fiber by Etherification Method for Diverse Textile Uses. *Saudi Journal of Engineering and Technology, 7*(2), 107-111. https://10.36348/sjet.2022.v07i02.007

Ivanovska, A., Maletić, S., Djokić, V., Tadić, N., & Kostić, M. (2022). Effect of chemical modifications and coating with Cu-based nanoparticles on the electro-physical properties of jute fabrics in a condition of high humidity. *Industrial Crops and Products, 180*, 114792. https://doi.org/10.1016/j.indcrop.2022.114792

Jha, S. K., Roy, M. L., Shamna, A., Kumar, S., Samajdar, T., & Naik, R. K. (2022). Performance evaluation of CRIJAF nail weeder in jute growing areas of North 24 Parganas district of west Bengal. *Indian Research Journal of Extension Education, 22*(2), 156–159. https://doi.org/10.54986/irjee/2022/apr_jun/156-159

Kang, H.J., Uegaki, K., Fukada, H., & Ishikawa, K. (2007). Improvement of the enzymatic activity of the hyperthermophilic cellulase from *Pyrococcus horikoshii*. *Extremophiles: Life under Extreme Conditions*, *11*(2), 251–256. https://doi.org/10.1007/s00792-006-0033-2

Katiyar, P., Srivastava, S. K., & Tyagi, V. K. (2015). A current scenario and novel approaches to degrade the lignocellulosic biomass for the production of biodiesel. *Journal of Fundamentals of Renewable Energy and applications*, *5*(161), 2.

Kim, E. S., Liu, S., Abu-Omar, M. M., & Mosier, N. S. (2012). Selective conversion of biomass hemicellulose to furfural using maleic acid with microwave heating. *Energy and Fuels: An American Chemical Society Journal*, *26*(2), 1298–1304. https://doi.org/10.1021/ef2014106

Kim, H.W., Takagi, Y., Hagihara, Y., & Ishikawa, K. (2007). Analysis of the putative substrate binding region of hyperthermophilic endoglucanase from *Pyrococcus horikoshii*. *Bioscience, Biotechnology, and Biochemistry*, *71*(10), 2585–2587. https://doi.org/10.1271/bbb.70322

Kim, S., Silva, C., Zille, A., Lopez, C., Evtuguin, D. V., & Cavaco-Paulo, A. (2009). Characterisation of enzymatically oxidised lignosulfonates and their application on lignocellulosic fabrics. *Polymer International*, *58*(8), 863–868. https://doi.org/10.1002/pi.2600

Koseki, T., Takahashi, K., Fushinobu, S., Iefuji, H., et al. . (2005). Mutational analysis of a feruloyl esterase from *Aspergillus awamori* involved in substrate discrimination and pH dependence. *Biochimica et Biophysica Acta*, *1722*(2), 200–208. https://doi.org/10.1016/j.bbagen.2004.12.016

Kozlowski, R., Batog, J., Konczewicz, W., Mackiewicz-Talarczyk, M., et al. (2006). Enzymes in bast fibrous plant processing. *Biotechnology Letters*, *28*(10), 761–765. https://doi.org/10.1007/s10529-006-9044-4

Kudanga, T., Prasetyo, E. N., Sipilä, J., Nyanhongo, G. S., & Guebitz, G. M. (2010). Chemo- enzymatic functionalisation of lignocellulose materials using oxiranes. *Process Biochemistry (Barking, London, England)*, *45*(9), 1557–1562. https://doi.org/10.1016/j.procbio.2010.06.008

Liang, C., Gui, X., Zhou, C., Xue, Y., Ma, Y., & Tang, S.-Y. (2015). Improving the thermoactivity and thermostability of pectate lyase from *Bacillus pumilus* for ramie degumming. *Applied Microbiology and Biotechnology*, *99*(6), 2673–2682. https://doi.org/10.1007/s00253-014-6091-y

Liang, J., Fang, X., Lin, Y., & Wang, D. (2018). A new screened microbial consortium OEM2 for lignocellulosic biomass deconstruction and chlorophenols detoxification. *Journal of Hazardous Materials*, *347*, 341–348. https://doi.org/10.1016/j.jhazmat.2018.01.023

Liew, F. K., Hamdan, S., Rahman, M. R., & Rusop, M. (2017). Thermomechanical properties of jute/bamboo cellulose composite and its hybrid composites: The effects of treatment and fiber loading. *Advances in Materials Science and Engineering*, *2017*, 1–10. https://doi.org/10.1155/2017/8630749

Limayem, A., & Ricke, S. C. (2012). Lignocellulosic biomass for bioethanol production: Current perspectives, potential issues and future prospects. *Progress in Energy and Combustion Science*, *38*(4), 449–467. https://doi.org/10.1016/j.pecs.2012.03.002

Lu, J., Yang, Z., Xu, W., Shi, X., & Guo, R. (2019). Enrichment of thermophilic and mesophilic microbial consortia for efficient degradation of corn stalk. *Journal of Environmental Sciences (China)*, *78*, 118–126. https://doi.org/10.1016/j.jes.2018.07.010

Majumdar, B., Das, Suparna, Saha, A.R., Chowdhury, H., Kundu, D. K. & Mahapatra, B. S. (2013). *Improved Retting Of Jute and Mesta with Microbial Formulation (Bulletin No. 04 /2013).* Central Research Institute for Jute and Allied Fibers (ICAR), Barrackpore, Kolkata, pp. – 32.

Manimekalai, G., & Kavitha, S. (2017). A review on application of retting techniques for naturalfiber extraction. *International Journal of Creative Research Thoughts*, *5*(4), 372-377. https://rb.gy/iv3qpa

Mondal, M., Ibrahim, H., Khan, M., Rahman, M., Islam, M., & Rabbi, M. A. (2016). Characterization of grafted jute fiber using acrylate monomers pretreated with alkali. *Fashion and Textiles*, *3*(1), 1-14. https://doi.org/10.1186/s40691-016-0060-2

Naseeruddin, S., Srilekha Yadav, K., Sateesh, L., Manikyam, A., Desai, S., & Venkateswar Rao, L. (2013). Selection of the best chemical pretreatment for lignocellulosic substrate *Prosopis juliflora*. *Bioresource Technology*, *136*, 542–549. https://doi.org/10.1016/j.biortech.2013.03.053

Nayab-Ul-Hossain, A. K. M., Sela, S. K., Hassan, M. N., & Sarkar, A. (2020). Surface modification of ligno-cellulosic fiber (jute) to increase electrical conductivity. *Materials Letters: X*, *5*(100036), 100036. https://doi.org/10.1016/j.mlblux.2019.100036

Ni, X., Dong, A., Fan, X., Wang, Q., Yu, Y., & Cavaco-Paulo, A. (2015). Jute/polypropylene composites: Effect of enzymatic modification on thermo-mechanical and dynamic mechanical properties. *Fibers and Polymers*, *16*(10), 2276–2283. https://doi.org/10.1007/s12221-015-5475-7

Ochoa-Chacón, A., Martinez, A., Poggi-Varaldo, H. M., Villa-Tanaca, L., Ramos-Valdivia, A. C., & Ponce-Noyola, T. (2022). Xylose metabolism in bioethanol production: *Saccharomyces cerevisiae* vs non-Saccharomyces yeasts. *Bioenergy Research, 15*(2), 905–923. https://doi.org/10.1007/s12155-021-10340-x

Otto, B., & Schlosser, D. (2014). First laccase in green algae: purification and characterization of an extracellular phenol oxidase from *Tetracystis aeria*. *Planta, 240*(6), 1225–1236. https://doi.org/10.1007/s00425-014-2144-9

Otto, B., Beuchel, C., Liers, C., Reisser, W., Harms, H., & Schlosser, D. (2015). Laccase-like enzyme activities from chlorophycean green algae with potential for bioconversion of phenolic pollutants. *Federation of European Microbiological Societies Microbiology Letters, 362*(11), 1-8. https://doi.org/10.1093/femsle/fnv072

Otto, B., Schlosser, D., & Reisser, W. (2010). First description of a laccase-like enzyme in soil algae. *Archives of Microbiology, 192*(9), 759–768. https://doi.org/10.1007/s00203-010-0603-7

Patil, H., Mudaliar, S., & Athalye, A. (2022). Ultrasound-assisted enzymatic scouring of jute optimised by response surface methodology and its natural dyeing. *Coloration Technology, 138*(5), 1-12. https://doi.org/10.1111/cote.12638

Ramos, O. S., & Malcata, F. X. (2011). Food-Grade Enzymes. In Murray Moo-Young (Ed.), *Comprehensive Biotechnology* (pp. 555–569). Elsevier. http://dx.doi.org/10.1016/B978-0-08 088504-9.00213-0

Rathner, R., Petz, S., Tasnádi, G., Koller, M., & Ribitsch, V. (2017). Monitoring the kinetics of biocatalytic removal of the endocrine disrupting compound 17α-ethinylestradiol from differently polluted wastewater bodies. *Journal of Environmental Chemical Engineering, 5*(2), 1920–1926. https://doi.org/10.1016/j.jece.2017.03.034

Reynaud, C., Tapin-Lingua, S., Elegir, G., Petit-Conil, M., & Baumberger, S. (2013). Hydrophobic properties conferred to Kraft pulp by a laccase-catalysed treatment with lauryl gallate. *Journal of Biotechnology, 167*(3), 302–308. https://doi.org/10.1016/j.jbiotec.2013.07.014

Riva, S. (2006). Laccases: blue enzymes for green chemistry. *Trends in Biotechnology, 24*(5), 219–226. https://doi.org/10.1016/j.tibtech.2006.03.006

Roberts, J. N., Singh, R., Grigg, J. C., Murphy, M. E. P., Bugg, T. D. H., & Eltis, L. D. (2011). Characterization of dye-decolorizing peroxidases from *Rhodococcus jostii* RHA1. *Biochemistry, 50*(23), 5108–5119. https://doi.org/10.1021/ bi200427h

Ruiz-Dueñas, F. J., Morales, M., Mate, M. J., Romero, A., et al. (2008). Site-directed mutagenesis of the catalytic tryptophan environment in *Pleurotus eryngii* versatile peroxidase. *Biochemistry, 47*(6), 1685–1695. https://doi.org/10.1021/bi7020298

Ryu, K., Hwang, S. Y., K. H., Kang, J. H., & Lee, E. K. (2008a). Functionality improvement of fungal lignin peroxidase by DNA shuffling for 2,4-dichlorophenol degradability and H2O2 stability. *Journal of Biotechnology, 133*(1), 110–115. https://doi.org/10.1016/j.jbiotec.2007.09.008

Ryu, K., Kang, J. H., Wang, L., & Lee, E. K. (2008b). Expression in yeast of secreted lignin peroxidase with improved 2,4-dichlorophenol degradability by DNA shuffling. *Journal of Biotechnology, 135*(3), 241–246. https://doi.org/10.1016/j.jbiotec.2008.04.007

Samanta, A. K., Mitra, S., & Mahalanabis, K. K. (2006). Effect of selective chemical and bio- chemical softening treatment of jute fabric. *Journal of the Institution of Engineers (India), Part TX: Textile Engineering Division, 86*, 21–33. https://rb.gy/khi74k

Samanta, A. K., Singhee, D., Basu, G., & Mahalanabis, K. K. (2005). Effect of selective pretreatments and subsequent mixed enzyme treatment on properties of jute-cotton union fabric. *Indian Journal of Fiber and Textile Research, 30*, 451-467.

Sánchez, C. (2009). Lignocellulosic residues: biodegradation and bioconversion by fungi. *Biotechnology Advances, 27*(2), 185–194. https://doi.org/10.1016/j.biotechadv.2008.11.001

Scheller, H. V., & Ulvskov, P. (2010). Hemicelluloses. *Annual Review of Plant Biology, 61*(1), 263–289. https://doi.org/10.1146/annurev-arplant-042809-112315

Sfiligoj, M., Hribernik, S., Stana, K., & Kree, T. (2013). Plant Fibers for Textile and Technical Applications. In S. Grundas and A. Stepniewski (Eds.), *Advances in Agrophysical Research* (pp. 369-398). IntechOpen. https://doi.org/10.5772/52372

Shahinur, S., Sayeed, M. M. A., Hasan, M., Sayem, A. S. M., Haider, J., & Ura, S. (2022). Current development and future perspective on natural jute fibers and their biocomposites. *Polymers, 14*(7), 1445. https://doi.org/10.3390/polym14071445

Singh, A. K., Jha, S. K., Majumdar, B., Roy, M. L., Sarkar, S., & Ghorai, A. K. (2019a). Impacts of climate smart jute farming on resource use efficiency, productivity and economic benefits in rural Eastern India. *Outlook on Agriculture, 48*(1), 75–82. https://doi.org/10.1177/0030727019829488

Singh, R. S., Singh, T., & Pandey, A. (2019b). Microbial Enzymes—An Overview. In R.S. Singh, R.R. Singhania, A.

Pandey and C. Larroche, *Advances in Enzyme Technology* (pp. 1–40). Elsevier. https://10.1016/B978-0-444-64114-4.00001-7

Sinha, S. N., & Paul, D. (2014). Impact of jute mill waste water on seed germination and vigour index of *Cicer arietinum* l. And *Pisum sativum* l. *Journal of Biological and Scientific Opinion*, *2*(1), 66–69. https://doi.org/10.7897/2321-6328.02115

Song, H., Liu, J., He, K., & Ahmad, W. (2021). A comprehensive overview of jute fiber reinforced cementitious composites. *Case Studies in Construction Materials*, *15*, e00724. https://doi.org/10.1016/j.cscm.2021.e00724

Sreenath, H. K., Shah, A. B., Yang, V. W., Gharia, M. M., & Jeffries, T. W. (1996). Enzymatic polishing of jute/cotton blended fabrics. *Journal of Fermentation and Bioengineering*, *81*(1), 18–20. https://doi.org/10.1016/0922-338x(96)83113-8

Subhadra, B. G. (2010). Sustainability of algal biofuel production using integrated renewable energy park (IREP) and algal biorefinery approach. *Energy Policy*, *38*(10), 5892–5901. https://doi.org/10.1016/j.enpol.2010.05.043

Subhadra, B., & Grinson-George. (2011). Algal biorefinery-based industry: an approach to address fuel and food insecurity for a carbon-smart world: Algal biorefinery-based industrial ecology. *Journal of the Science of Food and Agriculture*, *91*(1), 2–13. https://doi.org/10.1002/jsfa.4207

Subhedar, P. B., & Gogate, P. R. (2016). Use of ultrasound for pretreatment of biomass and subsequent hydrolysis and fermentation. In S.I. Mussatto (Ed.), *Biomass Fractionation Technologies for a Lignocellulosic Feedstock Based Biorefinery* (pp. 127–149). Elsevier. https://10.1016/B978-0-12-802323-5.00006-2

Sun, F., & Chen, H. (2007). Evaluation of enzymatic hydrolysis of wheat straw pretreated by atmospheric glycerol autocatalysis. *Journal of Chemical Technology and Biotechnology*, *82*(11), 1039–1044. https://doi.org/10.1002/jctb.1764

Tamburini, E., León, A. G., Perito, B., & Mastromei, G. (2003). Characterization of bacterial pectinolytic strains involved in the water retting process. *Environmental Microbiology*, *5*(9), 730–736. https://doi.org/10.1046/j.1462-2920.2003.00462.x

Tepe, O., & Dursun, A. Y. (2014). Exo-pectinase production by Bacillus pumilus using different agricultural wastes and optimizing of medium components using response surface methodology. *Environmental Science and Pollution Research International*, *21*(16), 9911–9920. https://doi.org/10.1007/s11356-014-2833-8

Thakur, K., Kalia, S., Kaith, B. S., Pathania, D., & Kumar, A. (2015). Surface functionalization of coconut fibers by enzymatic biografting of syringaldehyde for the development of biocomposites. *Royal Society of Chemistry Advances*, *5*(94), 76844–76851. https://doi.org/10.1039/c5ra14891j

Tsukihara, T., Honda, Y., Sakai, R., Watanabe, T., & Watanabe, T. (2006). Exclusive overproduction of recombinant versatile peroxidase MnP2 by genetically modified white rot fungus, *Pleurotus ostreatus*. *Journal of Biotechnology*, *126*(4), 431–439. https://doi.org/10.1016/j.jbiotec.2006.05.013

Tsukihara, T., Honda, Y., Sakai, R., Watanabe, T., & Watanabe, T. (2008). Mechanism for oxidation of high-molecular-weight substrates by a fungal versatile peroxidase, MnP2. *Applied and Environmental Microbiology*, *74*(9), 2873–2881. https://doi.org/10.1128/aem.02080-07

Van Sumere, C. (1992). Retting of flax with special reference to enzyme-retting. In HS Shekhar Sharma and CF Van Sumere (Eds.), *The biology and processing of flax* (pp. 153–193). M Publications. http://hdl.handle.net/1854/LU-222219

Vigneswaran, C., & Jayapriya, J. (2010). Effect on physical characteristics of jute fibers with cellulase and specific mixed enzyme systems. *Journal of the Textile Institute*, *101*(6), 506–513. https://doi.org/10.1080/00405000802542333

Wang, H., Memon, H., AM Hassan, E., Miah, M. S., & Ali, M. A. (2019). Effect of jute fiber modification on mechanical properties of jute fiber composite. *Materials*, *12*(8), 1226. http://dx.doi.org/10.3390/ma12081226

Wang, S., Yang, Y., Yang, R., Zhang, J., et al. (2014). Cloning and characterization of a cold-adapted endo-1,5-α-L-arabinanase from *Paenibacillus polymyxa* and rational design for acidic applicability. *Journal of Agricultural and Food Chemistry*, *62*(33), 8460–8469. https://doi.org/10.1021/jf501328n

Wang, Y., Yuan, H., Wang, J., & Yu, Z. (2009). Truncation of the cellulose binding domain improved thermal stability of endo-β-1, 4-glucanase from *Bacillus subtilis* JA18. *Bioresource Technology*, *100*(1), 345–349. https://10.1016/j.biortech.2008.06.001

Witayakran, S., & Ragauskas, A. J. (2009). Modification of high-lignin softwood kraft pulp with laccase and amino acids. *Enzyme and Microbial Technology*, *44*(3), 176–181. https://doi.org/10.1016/j.enzmictec.2008.10.011

Zhang, J., Shi, H., Xu, L., Zhu, X., & Li, X. (2015). Site-directed Mutagenesis of a hyperthermophilic endoglucanase Cel12B from *Thermotoga maritima* based on rational design. *PloS One*, *10*(7), e0133824. https://doi.org/10.1371/journal.pone.0133824

Zhang, S.B., & Wu, Z.L. (2011). Identification of amino acid residues responsible for increased thermostability of feruloyl esterase A from *Aspergillus niger* using the PoPMuSiC algorithm. *Bioresource Technology*, *102*(2), 2093–2096. https://doi.org/10.1016/j.biortech.2010.08.019

Zhao, Y., Wang, Y., Zhu, J. Y., Ragauskas, A., & Deng, Y. (2008). Enhanced enzymatic hydrolysis of spruce by alkaline pretreatment at low temperature. *Biotechnology and Bioengineering*, *99*(6), 1320–1328. https://doi.org/10.1002/bit.21712

Zhou, C., Wang, Q., Yu, Y., Fan, X., Cao, Y., & Li, T. (2017). Functional Modification of Jute Fiber by Enzymatic Grafting of Gallate Esters. *Chemical Engineering Transactions*, *62*, 193-198. https://10.3303/CET1762033

Zhou, H., Yang, D., Qiu, X., Wu, X., & Li, Y. (2013). A novel and efficient polymerization of lignosulfonates by horseradish peroxidase/H(2)O(2) incubation. *Applied Microbiology and Biotechnology*, *97*(24), 10309–10320. https://doi.org/10.1007/s00253-013-5267-1

Zhu, S., Yu, P., Wang, Q., Cheng, B., Chen, J., & Wu, Y. (2013). Breaking the barriers of lignocellulosic ethanol production using ionic liquid technology. *Bioresources*, *8*(2), 1510-1512. https://doi.org/10.15376/biores.8.2.1510-1512