Review Article

Microbial Lytic Polysaccharide Monooxygenases: Production, Purification and Bio-Industrial Applications: A Comprehensive Review

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Abstract | Lytic polysaccharide monooxygenases EC 1.14.99 are copper-dependent oxidative enzymes that play an essential role in the degradation of highly recalcitrant polysaccharides such as cellulose and chitin. They are widely distributed in fungi, bacteria and some marine organisms where they are secreted extracellularly. During degradation, LPMOs activate oxygen species at the copper center and introduce oxidation at specific positions of polysaccharide chains leading to chain disruption and significantly increasing the efficiency of overall biomass conversion. These enzymes play a major role in petrochemical industry especially in biofuel production. Moreover, it facilitates the conversion of lignocellulosic biomass into fermentable sugars so the use of these enzymes in food processing aid in the production of value-added materials such as nanocellulose and oligosaccharides.

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Introduction

Lytic Polysaccharide Monooxygenases (LPMOs) are formally included in the copper-dependent oxidative enzyme class known as the enzyme commission group EC 1.14.99. These biocatalysts are classified into a number of Auxiliary Activity (AA) families, specifically ranging from AA9 to AA17. Each AA family has evolved to be more adept at substrates like cellulose, chitin, or starch than others. The "histidine brace" motif, a structural feature in which a single copper ion is coordinated by two conserved histidine residues to drive catalysis, is the hallmark of these families at the molecular level. While members of some families, such as AA9 and AA16, primarily target cellulose, members of other families, such as AA10 and AA11, are necessary for shredding resilient chitin structures.

Auxiliary Activity families of LPMOs comprise a diverse group of copper-dependent oxidative enzymes that enhance the degradation of recalcitrant

polysaccharides by oxidatively cleaving glycosidic bonds. Based on sequence similarity and substrate specificity, LPMOs are classified in the CAZy database into eight AA families: AA9, AA10, AA11, AA13, AA14, AA15, AA16 and AA17. The AA9 family is predominantly found in fungi and acts mainly on cellulose, catalyzing oxidation at the C1 or C4 carbon positions to improve cellulose accessibility for cellulases. AA10 enzymes occur primarily in bacteria but are also present in archaea, viruses and some fungi. They exhibit broader substrate specificity acting on chitin, cellulose and xylan (Vu *et al.*, 2014). The fungal AA11 family consists mainly of chitin-active LPMOs involved in chitin degradation and cell-wall remodeling. AA13 enzymes are unique among LPMOs because they target starch facilitating oxidative starch depolymerization and enhancing the action of amylolytic enzymes (Loleggio *et al.*, 2015). The AA14 family acts on xylan associated with plant cell walls thereby increasing the accessibility of cellulose within lignocellulosic biomass. AA15 LPMOs are widespread among insects, other animals, algae, oomycetes and some viruses where they participate in chitin and cellulose degradation and various biological processes such as molting and biomass digestion (Forseberg *et al.*, 2011). AA16 represents a more recently identified fungal family that is mainly associated with cellulose oxidation and acts synergistically with cellulases during biomass conversion. The newest family AA17 has been identified predominantly in oomycetes and is distinguished by its activity on pectin significantly expanding the known substrate range of LPMOs beyond cellulose, chitin and starch (Couturier *et al.*, 2018; Sabbadin *et al.*, 2018). Collectively, these families demonstrate their crucial role in the enzymatic deconstruction of complex polysaccharides for both natural carbon cycling and industrial biorefinery applications (Li *et al.*, 2019; Wang *et al.*, 2022; Zhang *et al.*, 2023).

Structure of LPMO enzymes

LPMOs are a highly diverse family of enzymes in terms of sequence, but they share a highly conserved 3D structure primarily composed of a β-sandwich fold placing the catalytic copper in a surface position (Frandsen *et al.*, 2021).

In LPMOs, the histidine brace motif is the distinguishing feature where the N-terminal histidine and an internal histidine coordinate a single copper ion. Oxygen activation for oxidative polysaccharide cleavage requires the copper center, and recent studies have elucidated several active site configurations that allow for this unique enzymatic function. The catalytic surface of LPMOs are generally flat and contain aromatics or polar residues that facilitate interaction with solid crystalline substrates such as cellulose and chitin. The surface loops surrounding the catalytic site play a crucial role in fine-tuning substrate selectivity and regioselectivity of oxidation (LoLeggio *et al.*, 2015).

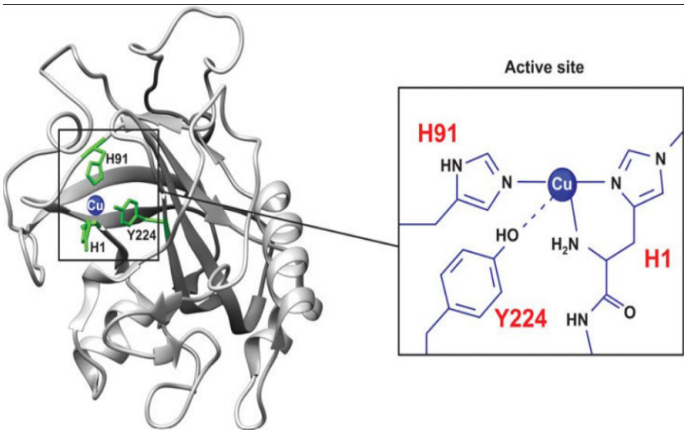

Figure 1: Structural representation of the LPMO active site highlighting the conserved histidine brace motif, where a copper ion (Cu) is coordinated by histidine residues (H1 and H91) and tyrosine residue (Y224). This copper-centered catalytic site is responsible for the oxidative cleavage of polysaccharides such as cellulose and chitin (Vandhana *et al.*, 2022).

Sources of LPMOs

The natural footprint of Lytic Polysaccharide Monooxygenases (LPMOs) is incredibly broad, reaching across various branches of the tree of life. These enzymes are currently divided into a number of Auxiliary Activity (AA) families, from AA9 to AA17. Each family is specialized, with some focusing on breaking down cellulose while others are specifically adapted to act on chitin or starch.

Fungal sources

Fungi are essentially nature's most efficient powerhouses for producing LPMOs, particularly within the AA9, AA11, and AA13 families. In the industrial biotechnology sector, *Trichoderma reesei* and *Aspergillus niger* remain the undisputed gold standard because they are incredibly good at pumping out massive amounts of protein. These thermophilic organisms are a total game changer for the industry; because their enzymes stay stable even under extreme heat, they can easily survive the intense temperatures

needed to pull apart tough biomass (Armenta *et al.*, 2023).

Bacterial sources

Bacterial LPMOs mainly from the AA10 family, are essentially the heavy lifters of the enzyme world because of their sheer physical toughness. These enzymes are experts at shredding chitin that incredibly stubborn, rugged material you find in shrimp shells and insect skeletons. We have even seen fresh breakthroughs in 2024 that uncovered entirely new versions from *Streptomyces* and marine dwelling *Vibrio* species. What really gives these bacterial enzymes an edge is their grit; they thrive in salty or alkaline environments that would stop others cold, making them the perfect candidates for marine biorefining or cleaning up harsh industrial wastewater (Tidke *et al.*, 2023).

Recombinant and metagenomic sources

Because nature doesn't always provide these enzymes in the massive quantities factories need, scientists often rely on recombinant production. Essentially, they use familiar lab workhorses like *E. coli* or the yeast *Pichia pastoris* to grow the enzymes under perfectly controlled conditions. Beyond the lab, researchers are now mining DNA straight from the environment scouring spots like hot springs and compost piles. This metagenomic approach has uncovered extremophilic LPMOs that can survive brutal conditions that would normally shred a protein. Whether they are discovered in the wild or reengineered in a lab, these enzymes are built to be faster and much tougher against the chemical wear and tear of large-scale reactions (Jones *et al.*, 2026; Stepnov *et al.*, 2022).

Mechanism of action of LPMOs

The activity of LPMOs is based on a copper ion that is found in the active site of the LPMOs enzyme. This copper ion is kept in place by two histidine amino acids. They form a special arrangement that is called the histidine brace. When the LPMOs are not being used the copper is in the form of Cu(II) which is not active. For initiating the reaction , you must reduce Cu(II) to Cu(I) by things that give electrons, such as ascorbic acid, lignin compounds or other redox enzymes (Frandsen *et al.*, 2021; Wang et al., 2024). After the LPMOs are activated the Cu(I) center in the LPMOs reacts with oxygen or hydrogen peroxide. Forms molecules that are very reactive. These reactive molecules in the LPMOs take a hydrogen atom from the sugar unit of cellulose. Chitin and add oxygen to the bond that holds the sugar units together. This breaks the chain of sugar units into smaller pieces (Bissaro et al., 2020; Müller et al., 2022).

LPMOs use molecular oxygen or hydrogen peroxide as a co-substrate to launch an aggressive oxidative attack on glycosidic bonds, in contrast to conventional hydrolytic enzymes, which rely on water based cleavage. As the oxidative action snaps the sturdy, crystalline fibers of the plant cell wall, this functional role is essential for the degradation of highly recalcitrant biomass (Vandhana *et al.*, 2022).

Table 1: *Sources of LPMOs from diverse biological origins.*

Source (Organism)	Substrate Focus	Key Innovation	Reference
Aspergillus oryzae	Cellulose	Applied the CRISPER Cas9 gene editing to boost the native enzyme secretion by three times	Wang *et al.* (2021)
Thermomyces lanuginosus	Wood Pulp	Successfully produced highly heat stable enzymes using low cost agricultural waste	Li *et al.* (2024)
Bacillus licheniformis	Chitin	Found a specific calcium-binding site that keeps the enzyme stable even in alkaline settings	Zhao *et al.* (2023)
Vibrio campbellii	Marine Chitin	Identified a rare variant that continues to function under the intense pressure of the deep sea	Contreras *et al.* (2024)
Pichia pastoris	Crystalline Cellulose	Mastered a yeast based production method that protects the enzyme's copper site from damage	Kwon *et al.* (2022)
Compost Consortia	Hemicellulose	Used DNA mining to find enzymes that work perfectly in high pH (alkaline) environments	Smith *et al.* (2025)
Myceliophthora thermophila	Lignocellulose	Developed a precise feeding system for hydrogen peroxide to keep the enzyme running at top speed	Stepnov *et al.* (2022)
Lenzites betulina	Hardwood	Proved that natural plant based phenols are actually better boosters than synthetic chemicals	Bissaro *et al.* (2022)

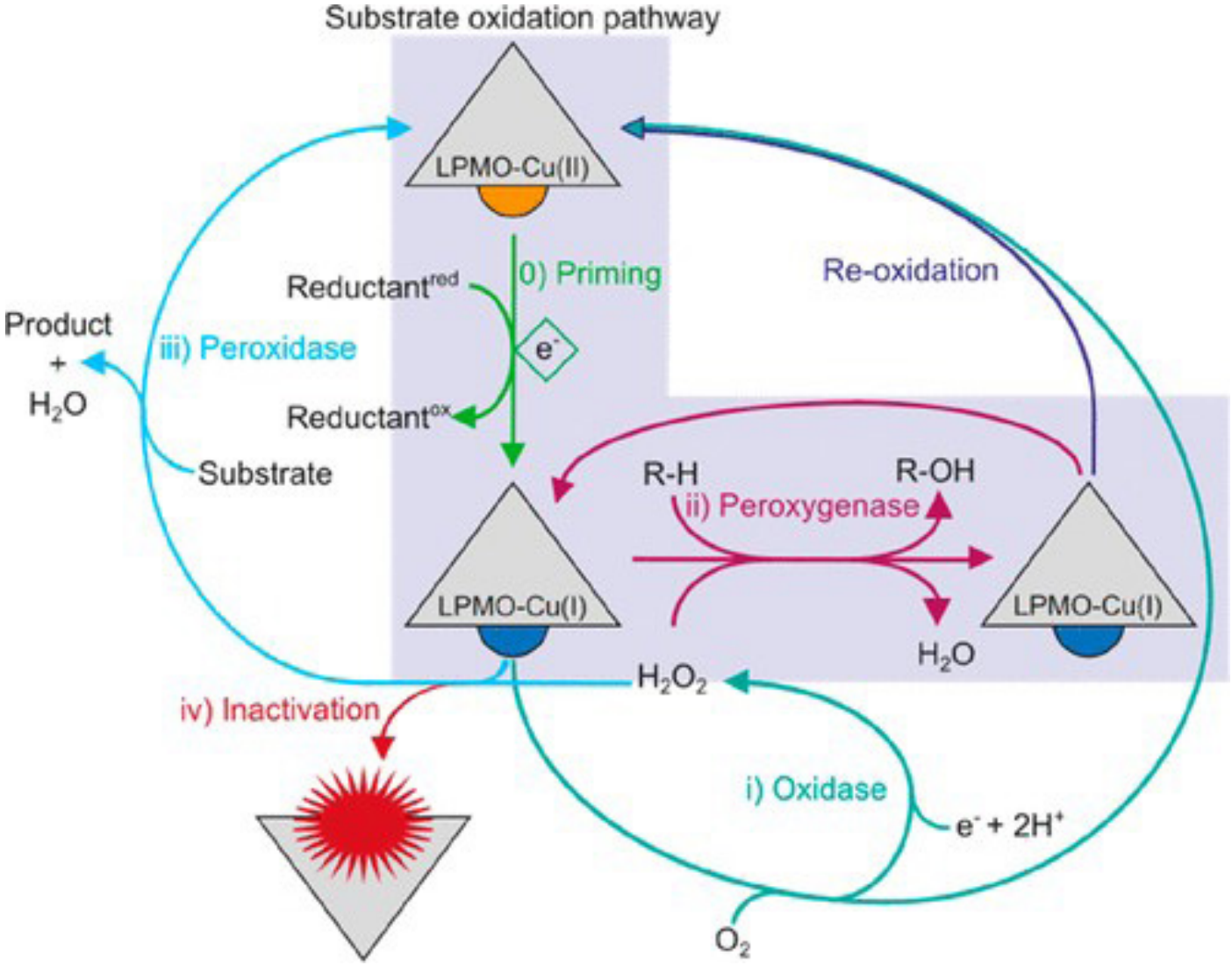

Figure 2: *A schematic representation of the interrelated LPMO reaction pathways. Priming (0), the one-electron reduction from the resting Cu(II) state to the active Cu(I) state, is essential to the LPMO reaction. Depending on the conditions of the reaction, four distinct pathways are thus possible. An oxidase reaction will reduce O_2 to H_2O_2 in the absence of a carbohydrate substrate. LPMOs catalyze a peroxygenase reaction that releases oxidized products when a carbohydrate substrate and H_2O_2 are present. Furthermore, LPMOs either inactivate as a result of autocatalytic oxidation of the active site or catalyze the oxidation of their reductant in a peroxidase reaction (Hedegard and Ryde, 2023; Wang et al., 2024; Muller et al., 2022; Bissaro et al., 2020).*

Traditional glycoside hydrolases are able to gain access to and more effectively break down the substrate thanks to the new entry points that LPMOs create on the surface of crystalline polymers (Zhu *et al*., 2023; Zerva *et al*., 2022). Because of their potent enzymatic synergy, LPMOs are essential components in contemporary industrial cocktails for the production of biofuel and sustainable waste processing.

For years, scientists believed molecular oxygen (O_2) was the main driver, that hydrogen peroxide (H_2O_2) is the true high speed fuel in industrial settings (Stepnov *et al*., 2022). While O_2 helps start the engine, H_2O_2 is what provides the rapid reaction speed needed for commercial production. However, there is a downside to this power: too much H_2O_2 can actually damage the protein's own structure and cause auto inactivation by burning out the enzyme (Paradisi *et al*., 2022; Bissaro *et al*., 2022). Currently, the primary focus of research is identifying superior electron donors to sustain these reactions more effectively (Monclaro *et al*., 2021; Cannella *et al*., 2023). Moving beyond standard laboratory reductants like ascorbic acid, scientists are now exploring bio inspired solutions. This includes utilizing lignin derived phenols or even harnessing plant pigments to drive the entire process through solar energy. The big goal is to get these enzymes fully integrated into the circular bioeconomy by 2026. This

isn't just about producing fuel, either; it's about using LPMOs to build super materials like nanocellulose and specialized chitin products. The main hurdle left is the factory floor. Figuring out how to control these sensitive, reactive enzymes so they don't break down in high density, oxygen heavy industrial settings is still a major challenge for the field (Tidke *et al.*, 2023; Smith *et al.*, 2025). The type of LPMOs determines where the oxidation happens on the sugar molecule in the LPMOs. It can happen at the C1 carbon, the C4 carbon or sometimes at both positions, in the sugar molecule of the LPMOs. This creates ends on the chain that can be broken down further by enzymes that break down cellulose and related enzymes. So, the LPMOs work with these enzymes and make it easier to break down biomass (Frandsen *et al.*, 2021).

Depending on enzyme type, oxidation may occur at the C1 position, C4 position, or both. This regioselectivity determines the nature of products released and affects synergy with cellulases and other biomass-degrading enzymes (Zhou and Zhu, 2020).

Classification and production of LPMO enzymes

The lytic polysaccharide monooxygenases (LPMOs) previously categorized based on sequence similarity are now classified into Auxiliary Activity (AA) families. Most studies have focused on the AA9 family, comprising predominantly fungal enzymes showing high specificity for conversion of cellulose and/or hemicellulose (Frandsen *et al.*, 2021). Enzymes in the AA10 family are mainly bacterial LPMOs (bLPMOs) exhibiting versatility by acting on chitin and/or cellulose (Vaaje-Kolstad *et al.*, 2024).

he newly classified AA11 family comprises fungal enzymes that are specifically active on chitin. (Courtade *et al.*, 2023). The starch-active LPMOs classified in the AA13 family are predominantly fungal enzymes that are active on resistant starch

Table 2: *Simplified catalytic cycle of LPMOs.*

Step	Catalytic Event	References
1	Cu(II)-LPMO reduced to Cu(I)	Bissaro *et al.*, 2021
2	Binding of O_2 or H_2O_2	Hedegard *et al.*, 2023
3	Formation of reactive oxygen intermediate	Joseph *et al.*, 2025
4	Hydrogen abstraction from substrate carbon	Hagemann *et al.*, 2024
5	Hydroxylation and bond cleavage	Zhou and Zhu, 2020
6	Release of oxidized oligosaccharides	Courtade *et al.*, 2023

Table 3: *Current classification and production of LPMO families (Modified for Fermentation Production).*

AA family	Major source	Main substrate	Production	References
AA9	Fungi	Cellulose, hemicellulose	Submerged fungal fermentation using *Trichoderma* and *Aspergillus* species under cellulase-inducing conditions	Frandsen *et al.*, 2021
AA10	Bacteria	Chitin, cellulose	Produced through bacterial fermentation, commonly recombinant expression in *E. coli* or *Streptomyces* strains	Vaaje-Kolstad *et al.*, 2024
AA11	Fungi	Chitin	Obtained from fungal cultures grown on chitin-rich media to enhance enzyme secretion	Courtade *et al.*, 2023
AA13	Fungi	Starch	Produced via fungal submerged fermentation using starch-containing substrates as inducers	Vu *et al.*, 2022
AA14	Fungi	Xylan-cellulose complex	Fermentation optimized with lignocellulosic biomass and xylan-rich agricultural residues	Couturier *et al.*, 2021
AA15	Insects / marine species	Chitin-like polymers	Mainly recombinant expression systems used for research-scale enzyme recovery	Sabbadin *et al.*, 2022
AA16	Fungi	Cellulose	Produced in fungal bioreactors under aerobic fermentation with cellulose inducers	Filiatrault-Chastel *et al.*, 2021
AA17	Oomycetes	Emerging substrates	Production still under development; heterologous fermentation systems being explored	Müller *et al.*, 2025

Note: *AA9 and AA10 remain the most commercially significant families due to easier large-scale fermentation and industrial biomass conversion applications.*

Table 4: *Structural components of LPMOs.*

Structural feature	Functional role	References
β-sandwich fold	Maintains structural stability	Frandsen *et al.*, 2021
Histidine brace	Coordinates catalytic copper ion	Hedegard *et al.*, 2023
Flat substrate-binding surface	Facilitates contact with insoluble polysaccharides	Courtade *et al.*, 2023
Surface loops	Determine substrate preference	Joseph *et al.*, 2025
Aromatic residues	Improve substrate adsorption	Bissaro *et al.*, 2021
N-terminal methylation	Enhances oxidative resistance	Frandsen *et al.*, 2021

Table 5: *Applications of LPMOs agriculture and industry.*

Fields	Applications	References
Agriculture	gene-silencing, The transgenic cotton plants showed resistance to both the cotton leaf curl virus which is spread by whiteflies, and the crop pest whitefly.	Askarian *et al.*, 2021
Environmental	the microbial degradation microbiota of pollutants and biomass, targeted enrichment of chitin-degrading bacteria, sequencing study of the macrogenome.	Park *et al.*, 2020; Wang *et al.*, 2021
Pharmaceutical	Applications for lignocellulose biomass (LCB) are many and include bioenergy, food, pharmaceuticals, and raw materials for value-added goods.	Hangyu Luo *et al.*, 2022
Food	transform plant lignocellulose into bioproducts, the physicochemical pretreatment is a crucial step. Both the soluble and insoluble biomass fractions produced by this technique may contain byproducts that prevent microbial fermentation and enzymatic biocatalysts.	World Journal of Microbiology and Biotechnology, 2020.
Industrial	Enzymes are thought of as nature's catalyst, and the fermentation process of biological materials produces the most enzymes possible today.	Ray Microbial biotechnology: 235-270, 2025.

Tstructures, retrograded starch or starch-based model substrates (Vu *et al.*, 2022). The AA14 family comprises fungal LPMOs targeting xylan associated with cellulose fibers. The recently identified AA15 family comprises enzymes from insects and marine organisms, which act on chitin-like polysaccharides, possibly participating in a wide variety of biological processes (Sabbadin *et al.*, 2022).

The predominantly fungal AA16 family consists of LPMOs that oxidize cellulose (Filiatrault-Chastel *et al.*, 2021). The recently assigned AA17 family comprises enzymes from oomycetes of which the biochemical properties and substrate range are unknown (Muller et al., 2025).

Applications

Industry: Enzymes are thought of as nature's catalyst and the fermentation process of biological materials produces the most enzymes possible today. These enzymes are frequently more beneficial than those derived from plants or animals because of their broad range of accessible catalytic activity, enormous yields that are achievable, ease of genetic manipulation, and quick microbial growth on inexpensive media. Microbial cellulases are an important class of enzymes with several industrial uses. COS are innovative prebiotic components with important uses in food science. The yields of sustainable COS synthesis are increased by developments in enzymatic hydrolysis. For use in food applications, short- and long-chain COS have different prebiotic and functional characteristics. Opportunities for advances in health-oriented food items are presented by unexplored COS functionalities. Cello oligosaccharides (COS) are novel oligomers made of short glucose chains that provide consumers health advantages in addition to other significant commercial.

Biofuels: A class of enzymes known as lytic polysaccharide monooxygenases (LPMOs) increases the release of oxidized products from plant biomass in a way that is more environmentally friendly than the conventional methods that use harsh chemicals. LPMOs may be exploited by immobilization on electrode surfaces because they are redox enzymes. Understanding the kinetic and thermodynamic details of the enzyme's interaction with the electrode surface is necessary for this method. In this work, an LPMO from the filamentous fungus *Thermothelomyces thermophile*, MtLPMO9H, is determined using a novel methodology.

A growing interest in producing clean, renewable fuel has given rise to a number of economical, effective, and environmentally friendly methods. Enzyme-mediated catalysis is one such method of biofuel production that has drawn a lot of attention worldwide. In comparison to its production using traditional methods, this chapter seeks to increase the overall yield in a less energy-intensive and more environmentally friendly manner. This chapter elaborates on the production of different clean fuels, the different enzymes that have been used thus far to produce biohydrogen and biodiesel, the importance of immobilization and improving the biofuel efficiency by identifying novel enzymes through metagenomics approach and enhancing the enzyme/metabolite production, and various challenges encountered and future perspectives.

Study on biofuels as alternative energy sources has increased due to the push for green energy and the desire to lessen reliance on the ever-depleting fossil fuel reserves. One of the most promising feed stocks for the production of advanced biofuels is lignocellulose. However, their use depends on the effective hydrolysis of polysaccharides, which depends in part on a safe and economical pretreatment of biomass to release or expose sugars to hydrolytic enzymes and remove or alter lignin. One of the enzymes under investigation is laccase, which is being used as a biotechnological tool to remove inhibitors (primarily phenolic) of subsequent enzymatic processes as well as a possible pretreatment agent in the production of biofuel, primarily as a delignifying enzyme. The present review addresses the key developments in the use of laccase as a possible pretreatment technique, the underlying ideas, and future research directions in the quest for improved enzyme-based technologies for the production of biofuel. Future prospects might include the adoption of the biorefinery concept in accordance with the shift towards the global implementation of the bioeconomy strategy and the synergy between enzymes that might be necessary for the best outcomes (Bangaru et al., 2022).

Recent advancements

Recent years have witnessed remarkable progress in the study of lytic polysaccharide monooxygenases (LPMOs) leading to a deeper understanding of their structure, catalytic mechanism, substrate specificity and biotechnological applications. LPMOs are copper-dependent oxidative enzymes that play a crucial role in the degradation of recalcitrant polysaccharides such as cellulose, chitin, hemicellulose, starch and other complex carbohydrates. Unlike conventional hydrolytic enzymes, LPMOs catalyze the oxidative cleavage of glycosidic bonds, thereby increasing the accessibility of polysaccharides to glycoside hydrolases and significantly enhancing the efficiency of biomass saccharification (Kumar *et al.*, 2024). Recent mechanistic studies have revealed that hydrogen peroxide serves as a highly efficient co-substrate and have provided detailed insights into electron transfer processes, oxygen activation and the formation of reactive intermediates involved in substrate oxidation (Hagemann and Hedegård, 2023). In addition, advanced structural investigations using X-ray crystallography, spectroscopy and computational modeling have improved understanding of the conserved copper-containing histidine brace, substrate-binding interfaces and the molecular determinants governing regioselectivity and substrate recognition (Yu *et al.*, 2023).

Another important advancement has been the discovery of protective electron-transfer or "hole-hopping" pathways mediated by aromatic amino acid residues such as tyrosine and tryptophan. These pathways help dissipate oxidative stress and protect the enzyme from self-inactivation thereby improving its stability under industrial conditions and providing valuable targets for protein engineering (Ayuso-Fernández *et al.*, 2024). Furthermore, the continuous identification of novel LPMO families and enzymes from fungi, bacteria, insects, plants and viruses has greatly expanded the known diversity of these enzymes and suggested biological roles extending beyond polysaccharide degradation (Munzone *et al.*, 2024). Advances in analytical methodologies including mass spectrometry, high-performance anion-exchange chromatography, fluorescence-based assays and spectroscopic techniques have enabled more accurate characterization of LPMO activity and facilitated high-throughput screening of enzyme variants (Wang *et al.*, 2021). Such developments have accelerated protein engineering and directed evolution approaches aimed at producing thermostable enzymes with enhanced catalytic efficiency and resistance to oxidative damage.

Moreover, recent studies have demonstrated strong synergistic interactions between LPMOs and glycoside hydrolases resulting in significantly

improved conversion of lignocellulosic biomass into fermentable sugars for the production of bioethanol, biochemicals, bioplastics and other renewable products (Kumar *et al*., 2024). Their application in sustainable biorefineries has therefore attracted considerable industrial interest. Emerging evidence has also revealed the involvement of certain microbial LPMOs in nutrient acquisition, host colonization and virulence highlighting their importance in microbial physiology and their potential as targets for antimicrobial drug development (Kracher *et al*., 2024). Collectively, these recent advancements have transformed LPMOs from auxiliary enzymes involved solely in biomass degradation into versatile metalloenzymes with broad applications in green chemistry, enzyme technology, environmental biotechnology and renewable energy production. Consequently, LPMOs represent one of the most dynamic and promising areas of contemporary enzyme research with continuing discoveries expected to further expand their scientific and industrial significance (Munzone *et al*., 2024).

Conclusion

Lytic polysaccharide monooxygenases have emerged as a transformative class of oxidative enzymes that significantly enhance the enzymatic degradation of recalcitrant polysaccharides such as cellulose and chitin. Their unique copper-dependent catalytic mechanism which introduces chain breaks through oxidative cleavage rather than hydrolysis alone has redefined the understanding of biomass deconstruction. The synergistic action of LPMOs with classical hydrolytic enzymes has demonstrated substantial improvements in lignocellulosic biomass conversion efficiency making them highly relevant for second-generation biofuel production and other biorefinery applications. Their widespread occurrence across fungi, bacteria and other microorganisms further highlights their ecological and biotechnological importance. Several limitations hinder their full-scale industrial application. LPMO activity is highly dependent on the availability of reducing agents and molecular oxygen making reaction conditions difficult to control and optimize at an industrial scale. Another major challenge is enzyme instability particularly susceptibility to oxidative self-inactivation which reduces catalytic efficiency over time. Additionally, the cost-effective large-scale production of active LPMOs with proper copper incorporation remains a significant bottleneck. Purification processes are often complex and yield loss during downstream processing further limits industrial feasibility. In conclusion, while LPMOs represent a major advancement in biomass conversion technology, overcoming current biochemical and industrial challenges will be essential for their full-scale deployment in bioenergy and other industrial applications.

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Novelty Statement

This review provides a critical synthesis of current advancements in the production and purification strategies for microbial Lytic Polysaccharide Monooxygenases, while uniquely bridging these technical optimizations with their transformative potential in sustainable bio-industrial applications.

Author's Contribution

Syeda Quratulain Gillani: Conceptualization, Methodology, Writing Original Draft, Administration, and Supervision.
Aliya Jabbar: Data Curation and Visualization.
Fareed Ahmed: Data Curation, Formal Analysis,
Asma Nadeem: Literature Search, Writing Original Draft.
Maham Sabir: Conceptualization, Supervision, Writing
Sheza Fatima Bajwa: Data Curation, Writing Review & Editing

Generative AI and AI assisted technology statement
The authors declare that no generative AI and AI assisted technology was used in the creation of this manuscript.

Conflict of interest
The authors have declared no conflict of interest.

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