

Research Article

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In silico* analysis of miR156-mediated post-transcriptional regulation of SPL genes involved in cell wall formation and cellulose biosynthesis in *Oryza sativa

Plant cell wall formation and cellulose biosynthesis are central processes determining plant growth, mechanical strength, and biomass quality. Rice (*Oryza sativa*), the second most important crop worldwide after maize, represents a well-established model system due to its fully sequenced and well-annotated genome. In this study, an *in silico* approach was applied to investigate microRNA (miRNA) mediated post-transcriptional regulation of genes involved in cell wall formation and cellulose biosynthesis in *Oryza sativa* (*O. sativa*). Using publicly available databases, including miRBase, TarDB, and NCBI, we systematically predicted miRNA — target gene interactions and reconstructed regulatory networks associated with structural, enzymatic, and signaling components of the plant cell wall. A total of 20 high-confidence miRNA — target gene pairs were identified, involving transcription factors (SPL, NAC, GRAS, AP2, TCP and HD-ZIP III), cell wall-related enzymes (laccases, redox- and copper-dependent proteins), and hormone-responsive regulators. The miR156 — SPL regulatory module emerged as a central and evolutionarily conserved node controlling secondary cell wall formation and cellulose microfibril organization. Additional regulatory layers included miR164 — NAC, miR397 laccase, and miR408/miR528-mediated redox pathways, as well as auxin-related miRNA networks. The results demonstrate that cellulose biosynthesis and cell wall formation in rice are governed by complex, multilevel miRNA-mediated regulatory systems. These findings provide a theoretical framework for future experimental validation and for biotechnological strategies aimed at improving agricultural biomass utilization and cellulose-based sustainable materials.

Keywords: *Oryza sativa*, miRNA, cell wall formation, cellulose biosynthesis, *in silico* analysis.

Introduction

The plant cell wall is a fundamental structural system that ensures the growth, development, and resistance of agricultural plants to environmental factors [1, 2]. Its main component, cellulose, not only provides mechanical strength to plant tissues but also plays a decisive role in maintaining cell shape, tissue differentiation, and morphogenesis [3, 4]. Therefore, investigating the molecular regulatory mechanisms that control cellulose biosynthesis and cell wall formation is a highly relevant topic in modern plant biology, agricultural biotechnology, and sustainable development [5]. In recent years, agricultural biomass has been widely considered a renewable and environmentally friendly source of raw materials. Plant-derived cellulose obtained from straw, rice husks, corn stalks, and other plant residues is regarded as a promising resource for the production of biodegradable and biocompatible materials [6, 7]. The high mechanical strength of cellulose, its processability, and its natural biodegradability make it a key component in the development of biodegradable packaging materials, eco-friendly composites, and sustainable polymer-based products [8]. In this context, a deep understanding of the genetic and post-transcriptional regulatory mechanisms that determine cellulose formation in plants provides a scientific basis for the efficient utilization of agricultural biomass and the development of environmentally friendly packaging technologies [9, 10]. The expression of genes involved in plant cell wall formation and cellulose biosynthesis is controlled by multilevel regulatory systems, among which post-transcriptional regulation plays a particularly important role [11, 12]. At this level, miRNAs act as key regulatory molecules. In plants, miRNA biogenesis begins with the transcription of MIR

genes in the nucleus, resulting in the formation of primary pri-miRNAs; these transcripts are sequentially processed by the DICER-LIKE1 (DCL1) enzyme and its cofactors to generate a mature miRNA duplex. The mature miRNA subsequently associates with Argonaute (AGO) proteins to form a functional complex that recognizes complementary mRNA sequences in the nucleus or cytoplasm. By binding to their target mRNAs, miRNAs promote transcript degradation or inhibit translation. In plants, such interactions are typically characterized by a high degree of complementarity and often lead to direct mRNA cleavage mediated by AGO-containing complexes. Consequently, miRNAs enable precise and efficient regulation of structural programs such as cell wall formation, cellulose synthesis, and cell wall remodeling (Fig. 1) [13–15]. *O. sativa* is not only one of the major crops ensuring global food security but also a model organism for plant genomics and molecular biology [16]. *In silico* analysis provides an efficient approach for predicting miRNA target gene interactions and reconstructing regulatory networks using genome-wide sequence information and curated bioinformatics databases [17, 18]. The complete sequencing of the rice genome, together with the availability of open bioinformatics resources such as miRBase, TarDB, and NCBI, enables comprehensive *in silico* analyses of miRNA–target gene interactions [19, 20]. These approaches facilitate the identification of key regulatory nodes, the characterization of gene network organization, and the formulation of functional hypotheses prior to experimental validation. The aim of this study is to analyze, using *in silico* approaches, the post-transcriptional regulation mediated by miRNAs of genes involved in cellulose biosynthesis and plant cell wall formation in *O. sativa*, including genes encoding SPL transcription factors. The results obtained provide deeper insight into the molecular mechanisms governing plant cell wall formation and establish a scientific foundation for future biotechnological and genetic engineering studies focused on the development of biodegradable materials and environmentally friendly packaging products derived from agricultural biomass.

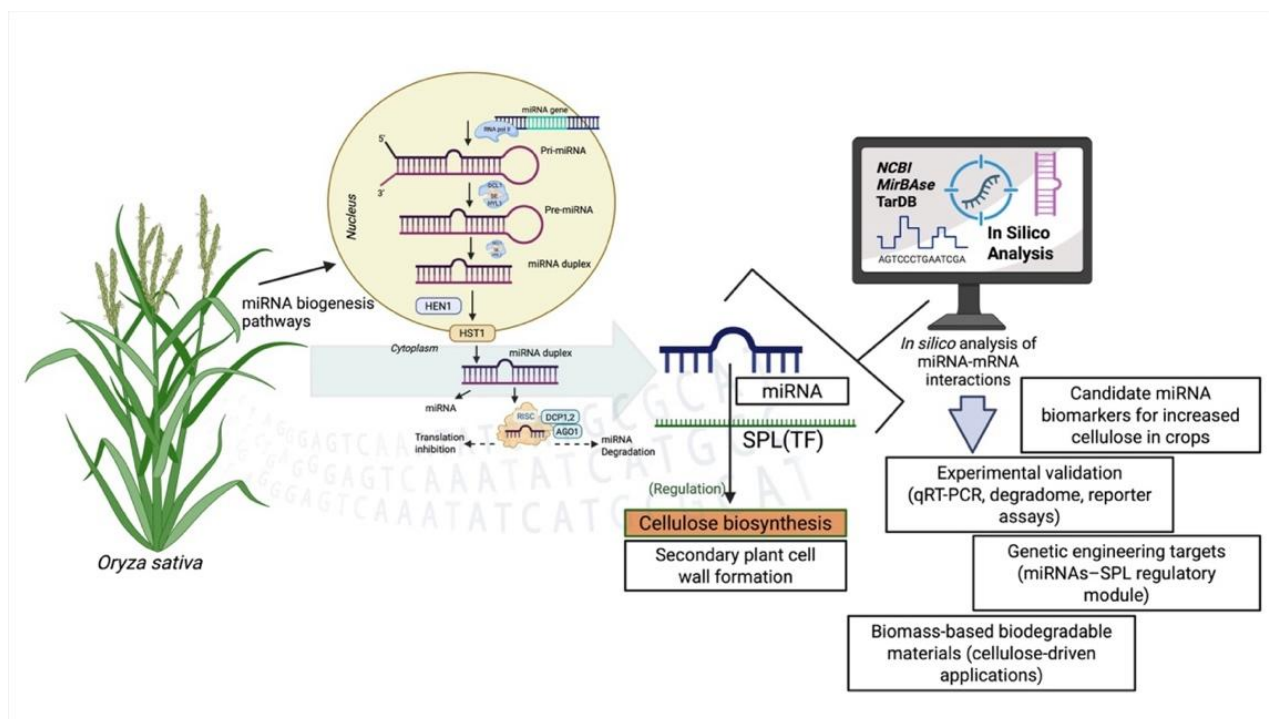


Figure 1. Schematic overview of miRNA biogenesis, miRNA–SPL interactions, and their role in the regulation of cellulose biosynthesis and plant cell wall formation in *O. sativa*.

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Experimental

Databases and retrieval of nucleotide sequences. In this study, all analyses were performed exclusively using *in silico* approaches based on publicly available bioinformatics databases. miRNA sequences specific to *O. sativa* were retrieved from the miRBase database (<https://www.mirbase.org>), which provides curated and experimentally validated annotations of plant miRNAs. Nucleotide sequences of candidate genes in-

volved in plant cell wall formation and cellulose biosynthesis, including transcripts encoding SPL transcription factors (LOC_Os08g39890.1 and LOC_Os09g31438.1), were obtained from the NCBI Gene and NCBI Nucleotide databases (<https://www.ncbi.nlm.nih.gov>). Functional annotations of these genes were additionally examined to confirm their involvement in cell wall development, secondary cell wall formation, and cellulose-related regulatory processes.

Prediction of miRNA target gene interactions. Prediction of miRNA — mRNA interactions was performed using the plant-adapted TarDB database (<http://www.biosequencing.cn/TarDB/>) [21]. This platform is specifically optimized for identifying plant miRNA interactions characterized by high sequence complementarity and predominantly cleavage-based regulatory mechanisms. For each candidate gene, all *O. sativa*-specific miRNAs were systematically screened. The following TarDB parameters were used to evaluate interaction confidence: TarHunter score, an indicator of interaction reliability; Total mismatch, the total number of mismatched nucleotides within the miRNA–mRNA duplex; Seed mismatch, the number of mismatches within the seed region; Predicted cleavage, the likelihood of Argonaute-mediated mRNA cleavage. This study was conducted entirely using computational methods, and the obtained results are proposed as a theoretical framework for future experimental validation.

Results and Discussion

Based on *in silico* analysis using the TarDB database, a multilevel regulatory network consisting of 20 miRNA target gene pairs was identified in *O. sativa*, which are directly or indirectly involved in plant cell wall formation and cellulose biosynthesis (Table 1). The identified network comprises miRNA families targeting transcription factors, structural and enzymatic proteins, as well as key components of phytohormone-dependent signaling pathways. These interactions indicate the presence of complex molecular mechanisms regulating cell wall formation and remodeling at the post-transcriptional level. The results demonstrate that miRNAs regulate the expression of cell wall-related genes not at a single level, but across multiple functional layers. This regulation is organized into interconnected modules involving transcriptional control, enzymatic activity, and hormonal signaling pathways, reflecting the integrative nature of cell wall biosynthesis regulation.

Table 1

Predicted miRNA target gene pairs involved in plant cell wall formation and cellulose biosynthesis in *O. Sativa* based on TarDB analysis

| No | miRNA | Target transcript | Gene function | References |
|----|---------------|-------------------|---|------------|
| 1 | miR156 family | LOC_Os08g39890.1 | SPL transcription factor (secondary cell wall regulation) | [22] |
| | | LOC_Os09g31438.1 | | |
| 2 | miR164 family | LOC_Os06g46270.1 | NAC transcription factor, regulation of cell wall formation and plant development | [23] |
| 3 | miR171 family | LOC_Os02g44360.1 | GRAS family transcription factor, regulation of plant growth and cell differentiation | [24] |
| | | LOC_Os06g01620.1 | | |
| 4 | miR172 family | LOC_Os06g43220.1 | AP2-like transcription factor | [25,26] |
| | | LOC_Os05g03040.1 | | |
| 5 | miR397 family | LOC_Os01g62490.1 | Laccase, a cell wall associated enzyme involved in lignin metabolism | [27] |
| | | LOC_Os01g63200.1 | | |
| 6 | miR394 family | LOC_Os01g69940.1 | F-box protein (auxin signaling) | [28] |
| 7 | miR395 family | LOC_Os03g53230.1 | ATP sulfurylase/sulfate metabolism regulator | [29] |
| 8 | miR414 | LOC_Os11g37990.1 | Regulatory protein (stress-responsive, rice-specific) | [30] |
| 9 | miR319 family | LOC_Os03g57190.1 | TCP transcription factor (growth and cell wall regulation) | [31, 32] |
| 10 | miR408-3p | LOC_Os01g03530.1 | Blue copper protein / oxidative stress and cell wall metabolism | [33] |
| 11 | miR169 family | LOC_Os10g26470.1 | NF-YA (Nuclear Factor Y, subunit A) drought/stress and development regulator | [34] |

| № | miRNA | Target transcript | Gene function | References |
|------------------|------------------|------------------------|--|------------|
| 12 | miR530 | LOC_Os01g56780.1 | Receptor-like regulatory protein (plant development and stress regulation) | [35] |
| 13 | miR393 family | LOC_Os01g53280.1 | TIR1/AFB auxin receptor pathway (auxin signaling) | [36] |
| 14 | miR396 family | LOC_Os01g53610.1 | GRF transcription factors (growth, leaf development; cell proliferation) | [37] |
| | | LOC_Os06g10310 | | |
| | | LOC_Os02g53690.1 | | |
| | | LOC_Os04g51190.1/.2/.3 | | |
| | | LOC_Os02g47280.1/.2 | | |
| | | LOC_Os06g02560.1/.2/.3 | | |
| | | LOC_Os03g51970.1 | | |
| | | LOC_Os03g47140.1 | | |
| | | LOC_Os12g29980.1/.2 | | |
| | | LOC_Os02g45570.1/.2 | | |
| LOC_Os04g48510.1 | | | | |
| 15 | miR167 family | LOC_Os04g57610.3 | ARF (Auxin Response Factor) auxin-mediated development | [38] |
| 16 | miR399e | LOC_Os11g03700.1 | PHO2/UBC24-related phosphate homeostasis (Pi starvation response) | [39] |
| 17 | miR166 family | LOC_Os02g45380.1 | HD-ZIP III transcription factors (vascular/cell wall patterning) | [40] |
| 18 | miR162a | LOC_Os03g01090.1 | DCL1 (miRNA biogenesis regulator) | [41] |
| 19 | miR164 family | LOC_Os02g36880.2 | NAC transcription factors (involved in plant development and stress responses; occasionally associated with cell wall-related regulatory networks) | [42] |
| 20 | miR528-5p family | LOC_Os12g36620.1 | Redox- and copper-dependent enzymes operating within cell wall-associated enzymatic networks | [43, 44] |
| | | LOC_Os03g03724.2 | | |

The miRNA families targeting transcription factors were identified as a major regulatory module associated with cell wall formation and cellulose biosynthesis. In particular, the miR156 family was predicted to interact with genes encoding SPL transcription factors, suggesting its involvement in regulating genes responsible for secondary cell wall formation and the organization of cellulose microfibrils. This miR156 — SPL module represents a central regulatory node controlling the structural program of the plant cell wall. The miR164 family targets NAC transcription factors and is associated with processes related to cell wall thickening, lignin biosynthesis, and tissue maturation. Regulation of NAC factors contributes not only to maintaining the mechanical strength of the cell wall, but also influences the plant's ability to adapt to external stress conditions during development [45]. These observations highlight the functional importance of the miR164 NAC regulatory interaction in ensuring cell wall stability. In addition, the miR171 and miR172 families were found to target GRAS and AP2-like transcription factors, respectively. These transcription factors indirectly affect cell wall formation through their roles in plant morphogenesis, cellular differentiation, and developmental programs [46]. Acting as components of higher-order transcriptional cascades, these miRNAs contribute to the temporal and spatial regulation of cell wall biosynthesis. Enzymatic components directly involved in determining the chemical composition of the plant cell wall were also found to be regulated by miRNAs. The targeting of laccase genes by the miR397 family is associated with lignin polymerization and the formation of the cellulose lignin matrix, representing one of the key enzymatic regulatory mechanisms governing cell wall rigidity and mechanical strength. Furthermore, miR408-3p and miR528-5p interact with genes encoding redox-active and copper-containing proteins, thereby regulating oxidation reduction processes linked to cell wall metabolism. These miRNAs constitute an additional regulatory layer contributing to the maintenance of energetic and metabolic balance during cell wall biosynthesis. Indirect regulation mediated through hormonal signaling pathways was also identified. The miR393, miR167, and miR394 families target key components of the auxin signaling pathway, coordinating cell expansion, cell wall remodeling, and de-

Predicted miR156 family binding sites in SPL-like transcripts involved in cell wall formation in *Z. mays*

| Species | miRNA | Target transcript | Pairing | Tar Hunter Score | Total mispair | Seed mispair |
|----------------|------------|--------------------|---|------------------|---------------|--------------|
| <i>Z. mays</i> | miR156a-5p | GRMZM2G126018_T02 | 5' GUGCUCUCUCUCUUCUGUCA 3' 3' CACGAGUGAGAGAAGACAGU 5' | 1 | 1 | 0 |
| | | GRMZM2G460544_T01 | 5' GUGCUCUCUCUCUUCUGUCA 3' 3' CACGAGUGAGAGAAGACAGU 5' | 1 | 1 | 0 |
| | | GRMZM2G307588_T01 | 5' GUGCUCUCUCUCUUCUGUCA 3' 3' CACGAGUGAGAGAAGACAGU 5' | 1 | 1 | 0 |
| | | GRMZM2G160917_T03 | 5' GUGCUCUCUCUCUUCUGUCA 3' 3' CACGAGUGAGAGAAGACAGU 5' | 1 | 1 | 0 |
| | | GRMZM2G371033_T01 | 5' GUGCUCUCUCUCUUCUGUCA 3' 3' CACGAGUGAGAGAAGACAGU 5' | 1 | 1 | 0 |
| | | GRMZM2G465165_T01 | 5' GUGGUCGUCUCUCUUCUGUCA 3' o 3' CACGAGUGAGAGAAGACAGU 5' | 3.5 | 3 | 0 |
| | | AC233751.1_FG T002 | 5' GUGCUCUCUCUCUUCUGUCA 3' 3' CACGAGUGAGAGAAGACAGU 5' | 1 | 1 | 0 |
| | | GRMZM5G806833_T01 | 5' GUGCUCUCUCUCUUCUGUCA 3' 3' CACGAGUGAGAGAAGACAGU 5' | 1 | 1 | 0 |
| | | GRMZM2G101511_T02 | 5' GUGCUCUCUCUCUUCUGUCA 3' 3' CACGAGUGAGAGAAGACAGU 5' | 1 | 1 | 0 |
| | | GRMZM2G052921_T01 | 5' GUGCUCUCUCUCUUCUGUCA 3' 3' CACGAGUGAGAGAAGACAGU 5' | 1 | 1 | 0 |
| | | GRMZM2G065451_T01 | 5' GUGCUCUCUCUCUUCUGUCA 3' 3' CACGAGUGAGAGAAGACAGU 5' | 1 | 1 | 0 |
| | | GRMZM2G414805_T07 | 5' GUGCUCUCUCUCUUCUGUCA 3' 3' CACGAGUGAGAGAAGACAGU 5' | 1 | 1 | 0 |
| | | GRMZM2G022489_T01 | 5' GUGCUCACCCUCUAUCUGUCA 3' 3' CACGAGUGAGAGA-AGACAGU 5' | 4 | 2 | 1 |
| | | GRMZM2G022489_T01 | 5' GUGCUCACUUCUCUCUCUGUCA 3' 3' CACGAGUG-AGAGA-AGACAGU 5' | 3 | 2 | 1 |
| | | GRMZM2G551565_T01 | 5' GUGCUCACUCUCUUCUGUCA 3' 3' CACGAGUGAGAGAAGACAGU 5' | 0 | 0 | 0 |
| | | GRMZM2G067624_T02 | 5' AUGCUCUCUCUCUUCUGUCA 3' 3' CACGAGUGAGAGAAGACAGU 5' | 2 | 2 | 0 |
| | | GRMZM2G113779_T01 | 5' AUGCUCUCUCUCUUCUGUCA 3' 3' CACGAGUGAGAGAAGACAGU 5' | 2 | 2 | 0 |
| | | GRMZM2G106798_T02 | 5' GUGCUCUCUCUCUUCUGUCA 3' 3' CACGAGUGAGAGAAGACAGU 5' | 1 | 1 | 0 |
| | | GRMZM2G146446_T02 | 5' GCCGUCGUUCUCUUCUGUCA 3' o 3' CACGAGUGAGAGAAGACAGU 5' | 4 | 5 | 0 |

Note. mRNA sequences are shown in green, miRNAs in blue; vertical bars indicate canonical base pairing, and “o” denotes a G: U wobble interaction.

These data demonstrate that the miR156 — SPL regulatory module represents an evolutionarily conserved, universal, and functionally significant molecular regulatory mechanism that governs gene networks involved in plant cell wall formation and cellulose biosynthesis. The identification of a conserved miR156 binding region shared by multiple SPL transcripts, together with the presence of numerous high-confidence miR156 isoforms targeting the same sites, indicates a robust and tightly controlled post-transcriptional regu-

latory system. The predominance of perfect or near-perfect complementarity within the seed region and the consistent prediction of cleavage-based regulation further support the functional relevance of these interactions. Importantly, the conservation of the miR156–SPL interaction across monocot species, including *O. sativa* and *Z. mays*, suggests that this regulatory module has been maintained during evolution due to its critical role in controlling structural and developmental programs of the plant cell wall. Such conservation implies selective pressure to preserve precise regulation of SPL transcription factors, which are known to orchestrate secondary cell wall formation, cellulose microfibril organization, and tissue maturation. These findings indicate that the miR156 — SPL axis functions as a central regulatory hub integrating developmental cues with structural gene expression, thereby ensuring coordinated control of cellulose biosynthesis and cell wall architecture.

Rice (*O. sativa*) is a crop of strategic importance in global agriculture and is considered one of the main food plants, ranking second after maize in terms of production volume [47]. In addition, the *O. sativa* genome has been fully sequenced, is well functionally annotated, and is widely used as a model species in molecular and genetic studies [16, 48]. These characteristics make rice a suitable model system for investigating the molecular regulation of cell wall formation and cellulose biosynthesis [49, 50]. Recent studies have shown that plant cell wall formation and cellulose synthesis are regulated through multilevel and dynamic regulatory networks [51]. These networks integrate transcription factors, enzymatic complexes, and phytohormone-dependent signaling pathways. Regulation at the post-transcriptional level, including the control of gene expression by miRNAs, has attracted increasing attention in recent years [13, 14, 52].

The *in silico* analysis conducted in this study demonstrated that miRNA-mediated regulation of genes involved in cell wall formation and cellulose biosynthesis in *O. sativa* represents a complex and integrated system. The results indicate that miRNA families targeting transcription factors act as dominant regulatory modules in this process. In particular, the miR156 — SPL regulatory module occupies a central position in controlling gene programs associated with secondary cell wall formation and the organization of cellulose microfibrils. Recent studies have shown that SPL transcription factors play a decisive role in regulating cell wall thickening and structural integrity [53, 54]. In addition, NAC transcription factors regulated by miR164 link cell wall formation and lignin accumulation with plant developmental stages and stress conditions. Recently, Xiong et al. (2025) demonstrated that NAC factors are key regulators of cell wall remodeling and stress tolerance [23]. This is fully consistent with our results and confirms the structural and physiological importance of the miR164 — NAC axis. At the enzymatic level, laccase genes regulated by miR397 play an important role in the formation of the cellulose lignin matrix. Laccases catalyze lignin polymerization, thereby enhancing the mechanical strength of the cell wall. Studies by Janusz et al. (2020) [55] and Chen et al. (2023) [44] have shown that copper-dependent redox enzymes coordinate cell wall formation through oxidation–reduction reactions in the apoplast. In this context, the redox/copper-dependent enzymes regulated by miR408-3p and miR528-5p identified in our study can be considered key components of enzyme networks associated with the cell wall. MiRNA networks associated with hormonal signaling also deserve special attention. Regulation of key components of the auxin signaling pathway by miR393, miR167, and miR394 is directly linked to cell elongation, cell wall remodeling, and morphogenetic processes. Recently, Prigge et al. (2020) [56] and Jing & Strader (2023) [57] highlighted the role of auxin signaling in regulating cell wall plasticity and emphasized the integrative function of miRNAs in this process. At the systemic level, the miR396 — GRF regulatory axis indirectly influences proper cell wall formation by determining cell proliferation and the rate of tissue growth. Recent genomic studies have shown that GRF factors contribute to structural development by regulating cell number and tissue architecture. [58, 59] In conclusion, this *in silico* study demonstrates that cell wall formation and cellulose biosynthesis in *O. sativa* are controlled by evolutionarily conserved, multilevel, and functionally significant miRNA-mediated regulatory networks. The obtained data provide a solid theoretical foundation for molecular-level control of cellulose properties derived from agricultural biomass and for the future development of applied biotechnological and genetic engineering based solutions.

Conclusion

This study provides a comprehensive *in silico* characterization of miRNA-mediated regulatory networks controlling cell wall formation and cellulose biosynthesis in *O. sativa*. The results demonstrate that these processes are regulated through interconnected and evolutionarily conserved miRNA — target gene modules that integrate transcriptional control, enzymatic activity, and hormone-dependent signaling pathways into a unified regulatory system. In particular, the miR156 — SPL axis represents a core regulatory module

governing secondary cell wall development and cellulose microfibril organization, highlighting its central role in determining structural properties of plant biomass. In parallel, miR164 — NAC and miR397 laccase interactions link cell wall reinforcement with developmental regulation and stress-responsive programs, underscoring the multifunctional nature of cell wall-associated regulatory networks. Furthermore, the involvement of redox- and copper-dependent enzymes regulated by miR408-3p and miR528-5p emphasizes the importance of apoplastic redox balance in coordinating enzymatic processes during cell wall assembly and remodeling. Together, these findings indicate that plant cell wall biosynthesis is governed by a multilayered post-transcriptional regulatory framework, rather than by isolated genetic pathways acting independently. The regulatory map generated in this study provides a solid theoretical foundation for future experimental validation and functional studies. Importantly, it also offers valuable perspectives for plant biotechnology, genetic engineering, and the rational improvement of cellulose-rich agricultural biomass aimed at the development of sustainable, biodegradable, and bio-based materials.

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Author Contributions

The manuscript was written through contributions of all authors. All authors have given approval to the final version of the manuscript. CRediT: **Belkozhayev A.M.** — conceptualization, methodology, investigation, bioinformatics analysis, data curation, formal analysis, writing — original draft, supervision; **Kossalbayev B.D. and Gizatullina N** — data curation, bioinformatic analysis, visualization, writing — review & editing; **Toleutay G.** — supervision, writing — review and editing.

Conflict of Interest

The authors declare no conflict of interest.

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***In silico* әдістерімен *Oryza sativa* өсімдігінде жасуша қабырғасының түзілуі мен целлюлоза биосинтезіне қатысатын SPL гендерінің miR156 арқылы посттранскрипциялық реттелуін талдау**

Өсімдік жасуша қабырғасының түзілуі мен целлюлоза биосинтезі өсімдіктің өсуін, механикалық беріктігін және биомассаның сапасын анықтайтын негізгі үдерістер. Күріш (*Oryza sativa*) жүгеріден кейінгі әлемдегі екінші маңызды дақыл толық секвенирленген және жақсы аннотацияланған геномы бар үлгілік жүйе ретінде кеңінен қолданылады. Бұл зерттеуде *Oryza sativa* (*O. sativa*) өсімдігінде жасуша қабырғасының түзілуі мен целлюлоза биосинтезіне қатысатын гендердің микроРНК (miRNA) арқылы посттранскрипциялық реттелуін зерттеу үшін *in silico* әдісі қолданылды. miRBase, TarDB және NCBI сияқты ашық дерекқорларды пайдалана отырып, miRNA таргет ген өзара әрекеттесулері жүйелі түрде болжанып, өсімдік жасуша қабырғасының құрылымдық, ферментативтік және сигналдық компоненттерімен байланысты реттеуші желілер қайта құрылды. Нәтижесінде транскрипциялық факторларды (SPL, NAC, GRAS, AP2, TCP және HD-ZIP III), жасуша қабырғасына қатысты ферменттерді (лакказалар, редокс- және мысқа тәуелді ақуыздар) және гормонға жауап беретін реттегіштерді қамтитын, жоғары сенімді 20 miRNA таргет ген жұбы анықталды. miR156 SPL реттеуші модулі екінші реттік жасуша қабырғасының түзілуі мен целлюлоза микрофибриллаларының ұйымдасуын бақылайтын орталық әрі эволюциялық тұрғыда консервацияланған түйін ретінде айқындалды. Қосымша реттеуші деңгейлерге miR164 NAC, miR397 лакказа, miR408/miR528 арқылы жүретін редокс жолдары, сондай-ақ ауксинге байланысты miRNA желілері кірді. Алынған нәтижелер күріште целлюлоза биосинтезі мен жасуша қабырғасының түзілуі күрделі, көпдеңгейлі miRNA-тәуелді реттеуші жүйелермен басқарылатынын көрсетеді. Бұл тұжырымдар болашақта эксперименттік валидация жүргізуге және ауыл шаруашылық биомассасын тиімді пайдалану мен целлюлоза негізіндегі орнықты материалдарды жетілдіруге бағытталған биотехнологиялық стратегияларды әзірлеуге теориялық негіз қалайды.

Кілт сөздер: *Oryza sativa*, miRNA, жасуша қабырғасының түзілуі, целлюлоза биосинтезі, *in silico* талдау.

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In silico* анализ посттранскрипционной регуляции генов SPL, участвующих в формировании клеточной стенки и биосинтезе целлюлозы, опосредованной miR156, у *Oryza sativa

Формирование клеточной стенки растений и биосинтез целлюлозы являются ключевыми процессами, определяющими рост растений, их механическую прочность и качество биомассы. Рис (*Oryza sativa*), вторая по значимости сельскохозяйственная культура в мире после кукурузы, широко используется как модельная система благодаря полностью секвенированному и хорошо аннотированному геному. В данном исследовании применён *in silico* метод для изучения посттранскрипционной регуляции генов, участвующих в формировании клеточной стенки и биосинтезе целлюлозы у *Oryza sativa* (*O. sativa*), опосредованной микроРНК (miRNA). С использованием открытых баз данных miRBase, TarDB и NCBI были систематически предсказаны взаимодействия miRNA с таргетными генами и реконструированы регуляторные сети, связанные со структурными, ферментативными и сигнальными компонентами клеточной стенки растений. В результате идентифицировано 20 высокодостоверных пар miRNA–таргетных генов, включающих транскрипционные факторы (SPL, NAC, GRAS, AP2, TCP и HD-ZIP III), ферменты, связанные с клеточной стенкой (лакказы, редокс- и медь-зависимые белки), а также гормон-чувствительные регуляторы. Регуляторный модуль miR156-SPL был выявлен как центральный и эволюционно консервативный узел, контролирующий формирование вторичной клеточной стенки и организацию микрофибрилл целлюлозы. Дополнительные уровни регуляции включали взаимодействия miR164-NAC, miR397-лакказа, редокс-пути, опосредованные miR408/miR528, а также miRNA-сети, связанные с ауксиновым сигналингом. Полученные результаты демонстрируют, что

биосинтез целлюлозы и формирование клеточной стенки у риса контролируются сложными многоуровневыми miRNA-опосредованными регуляторными системами. Эти выводы создают теоретическую основу для последующей экспериментальной валидации и разработки биотехнологических стратегий, направленных на эффективное использование сельскохозяйственной биомассы и совершенствование устойчивых материалов на основе целлюлозы.

Ключевые слова: *Oryza sativa*, miRNA, формирование клеточной стенки, биосинтез целлюлозы, *in silico* анализ.

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