
Enhancing Plant Nutritional Profile and Agronomic Performance: A Survey on α -Linolenic Acid, Genetic Engineering, and Metabolic Engineering

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Abstract

This survey paper explores the interdisciplinary approaches in plant biotechnology to enhance nutritional profiles and agronomic performance, focusing on α -linolenic acid (ALA). ALA, an essential n-3 polyunsaturated fatty acid, plays a crucial role in human health and plant resilience. The paper systematically reviews the integration of genetic and metabolic engineering techniques, including CRISPR-Cas9 and advanced delivery systems like carbon nanotubes, which have revolutionized genome modifications for improved agronomic traits. Metabolic engineering strategies have been pivotal in optimizing fatty acid biosynthesis pathways, enhancing ALA production. The paper also discusses the implications of enhanced fatty acid profiles on human health, particularly in reducing cardiovascular risks and chronic diseases. Challenges such as achieving multistress tolerance and addressing regulatory and ecological considerations are highlighted. The survey emphasizes the need for continued advancements in computational modeling and biosensor technologies to optimize metabolic pathways. Future directions include conducting randomized controlled trials for ALA intake guidelines, enhancing public acceptance of genetically engineered crops, and developing effective regulatory frameworks. Overall, this paper underscores the potential of interdisciplinary approaches in plant biotechnology to contribute to global food security and improved health outcomes.

1 Introduction

1.1 Significance of α -Linolenic Acid

α -Linolenic acid (ALA) is a crucial n-3 polyunsaturated fatty acid (PUFA) with significant implications in plant biotechnology and nutrition. As an essential fatty acid, ALA cannot be synthesized by humans and must be acquired through diet, where it plays vital roles in anti-inflammatory and antioxidant responses in mammalian cells [1]. Replacing linoleic acid with ALA may enhance dietary fatty acid profiles and provide protective benefits against conditions like nonalcoholic steatohepatitis (NASH) [2]. In plant biotechnology, ALA constitutes up to 45% of the total fatty acid content in certain species, such as tree peony seeds, underscoring its importance in plant-derived nutritional profiles [3].

Additionally, ALA serves as a precursor to longer-chain n-3 PUFAs, including docosahexaenoic acid (DHA), essential for cardiovascular health [4]. Incorporating ALA-rich plants, such as purslane, into diets enhances nutritional profiles due to their antioxidant properties [5]. Applications of synthetic biology in bioengineering further demonstrate ALA's potential to improve plant nutritional value [6]. Furthermore, understanding the digestion of galactolipids, which aids in ALA uptake, reveals important nutritional insights across various species [7]. The multifaceted role of ALA not only enhances plant nutritional profiles but also has broader implications for human health.

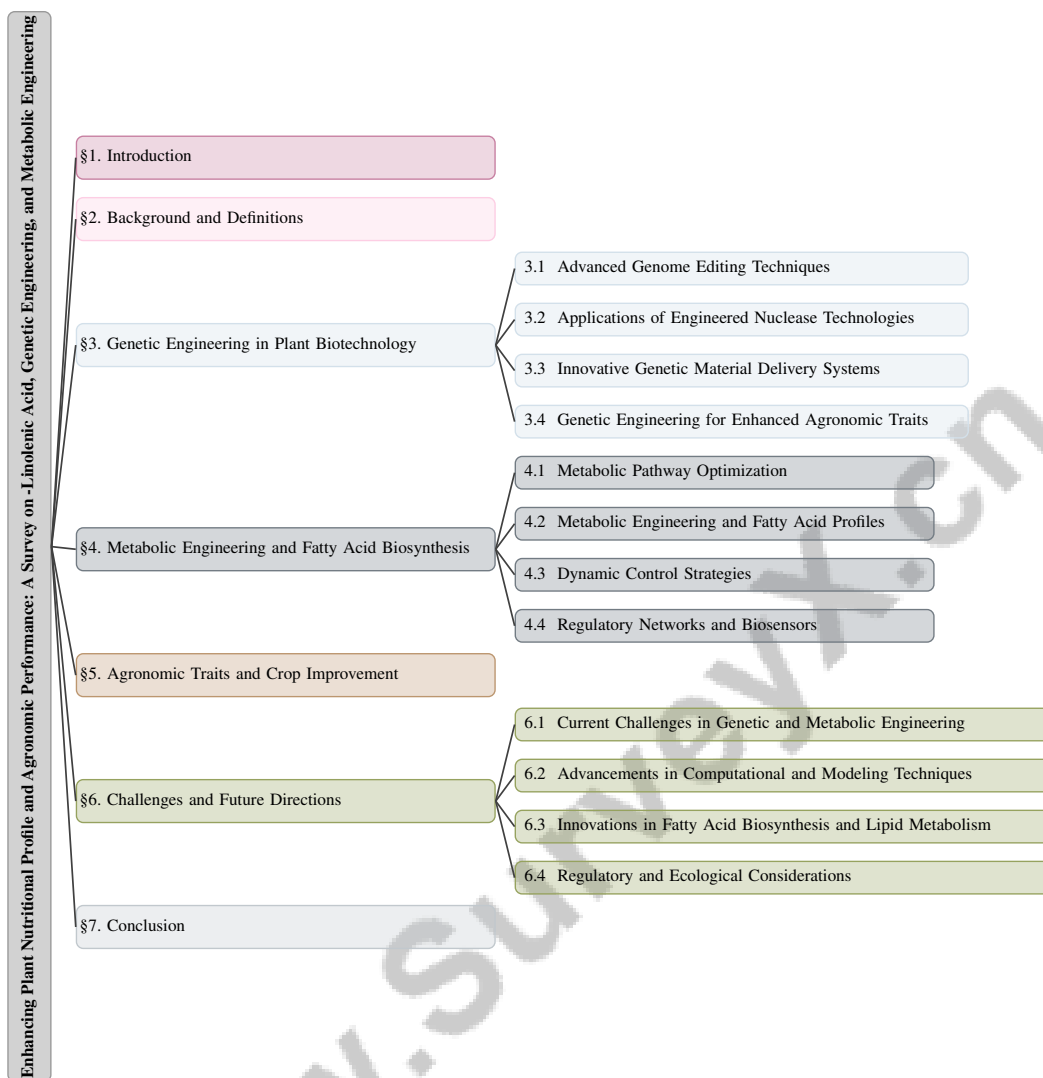


Figure 1: chapter structure

1.2 Structure of the Survey

This survey systematically presents a comprehensive overview of enhancing plant nutritional profiles and agronomic performance through genetic and metabolic engineering, focusing on -linolenic acid (ALA). The paper begins with an exploration of ALA's critical role in plant biotechnology, highlighting its nutritional and health benefits, including its potential as a dietary supplement due to its prevalence in various plant and animal tissues, such as silkworm larvae, and its bioactive properties in cancer prevention and treatment [8, 7, 9]. Following this, the survey defines core concepts such as genetic engineering, agronomic traits, plant biotechnology, fatty acid biosynthesis, and metabolic engineering, emphasizing their interconnections.

The subsequent section investigates the role of genetic engineering in plant biotechnology, detailing advanced genome editing techniques like CRISPR, engineered nuclease technologies, and innovative genetic material delivery systems. This section also discusses how genetic engineering enhances agronomic traits, including yield and stress tolerance.

Next, the survey focuses on metabolic engineering strategies aimed at optimizing fatty acid biosynthesis pathways, particularly for increasing ALA and other essential fatty acids. It examines metabolic pathway optimization techniques, the influence of metabolic engineering on microbial fatty acid profiles, and innovative dynamic control strategies—both open-loop and closed-loop systems—while

highlighting the roles of regulatory networks and biosensors in enhancing metabolic performance and product yields [10, 11, 12, 13, 14].

The paper thoroughly addresses the enhancement of agronomic traits through genetic and metabolic engineering, focusing on strategies for improving crop yield and resilience to abiotic stresses, the health benefits of optimized fatty acid profiles, and the challenges of developing multistress-tolerant crops in a changing environment. This analysis emphasizes the urgency of addressing micronutrient deficiencies and the potential of biofortification to combat global malnutrition, while also underscoring the importance of integrating traditional breeding methods with innovative engineering approaches for sustainable agricultural advancements [15, 11].

Finally, the survey examines the multifaceted challenges and prospective advancements in plant biotechnology, addressing significant issues in genetic and metabolic engineering, such as public concerns regarding the safety and environmental impact of genetically modified organisms. It also explores breakthroughs in computational and modeling techniques that enhance crop development, innovations in fatty acid biosynthesis and lipid metabolism that could improve oil yield and crop resilience, and the regulatory and ecological considerations shaping the future acceptance of biotechnological advancements in agriculture [8, 16]. The conclusion synthesizes key points and underscores the importance of interdisciplinary approaches in advancing plant biotechnology for improved nutritional profiles and agronomic performance. The following sections are organized as shown in Figure 1.

2 Background and Definitions

2.1 Interconnections and Relevance in Plant Biotechnology

Plant biotechnology integrates genetic engineering, metabolic pathway optimization, and agronomic trait enhancement to address nutrient deficiencies and food security challenges. Techniques such as transgenesis and genome editing facilitate the development of genetically modified crops with improved nutritional profiles, particularly those enriched with essential fatty acids like α -linolenic acid (ALA) [8]. These advancements are crucial given the high n-6:n-3 fatty acid ratio prevalent in Western diets, which is associated with inflammatory conditions and the progression of nonalcoholic fatty liver disease (NAFLD) and nonalcoholic steatohepatitis (NASH) [2].

Optimizing metabolic pathways is vital for enhancing ALA biosynthesis. Current methodologies often overlook the dynamic nature of phenotypic traits, which are essential for understanding genetic variability and improving crop performance [17]. Integrating genomic and metabolic data is necessary to identify genetic loci associated with desirable traits, as demonstrated in crops like peanuts [18]. Addressing missing reactions in genome-scale metabolic models (GEMs) is also essential for accurately simulating metabolic networks and optimizing pathways [19].

The digestion and metabolic fate of lipid classes, such as galactolipids, affect the bioavailability of essential fatty acids across species, including herbivores and insects [7]. Understanding these processes is crucial for enhancing the nutritional value of plant-based foods and tackling global hidden hunger, characterized by inadequate intake of essential nutrients [11].

2.2 α -Linolenic Acid and Fatty Acid Biosynthesis

The biosynthesis of α -linolenic acid (ALA) is a key component of plant metabolism, significantly enhancing the nutritional value of plant-derived foods. ALA is synthesized through desaturation and elongation reactions in plant cell plastids, primarily via the enzyme omega-3 fatty acid desaturase, which converts linoleic acid (LA) to ALA by introducing a double bond at the n-3 position [3]. This pathway is regulated by factors such as precursor fatty acid availability and the expression of desaturase genes, influenced by genetic and environmental conditions [9].

ALA serves as a precursor to long-chain polyunsaturated fatty acids (LCPUFAs) like eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA), essential for human health, particularly in preventing cardiovascular diseases and certain cancers. The conversion efficiency of ALA to DHA can be impacted by dietary factors, including the intake of competing fatty acids such as LA and hormonal influences like estrogen [4].

In plant nutrition, ALA enhances antioxidant capacity, improving resilience to oxidative stress and providing health benefits [5]. Its significant presence in species such as tree peonies highlights its importance in plant oils and seeds [3]. Genetic engineering to develop crops with elevated ALA content offers potential for improving dietary fatty acid profiles, addressing nutrient deficiencies, and mitigating chronic disease risks [1].

Research into fatty acid biosynthesis pathways, particularly ALA's role, reveals complex regulatory networks governing plant lipid metabolism. Advances in genomic and transcriptomic analyses have identified key genes in these pathways, offering opportunities for targeted manipulation to enhance ALA production [20]. Thus, ALA biosynthesis is a critical aspect of plant biotechnology, with significant implications for human nutrition and health.

In recent years, the field of plant biotechnology has witnessed significant advancements, particularly in the realm of genetic engineering. This review aims to elucidate these developments, particularly focusing on the innovative methodologies that have emerged. To provide a clearer understanding of the complex relationships among these methodologies, Figure 2 illustrates the hierarchical structure of genetic engineering in plant biotechnology. This figure delineates advanced genome editing techniques, applications of engineered nuclease technologies, and innovative genetic material delivery systems, alongside genetic engineering aimed at enhancing agronomic traits. Each section of the figure highlights key methodologies, delivery systems, and applications that collectively contribute to improving crop resilience, nutritional quality, and overall agronomic performance. By integrating these insights, this review seeks to present a comprehensive overview of the state-of-the-art practices in genetic engineering, paving the way for future research and application in the field.

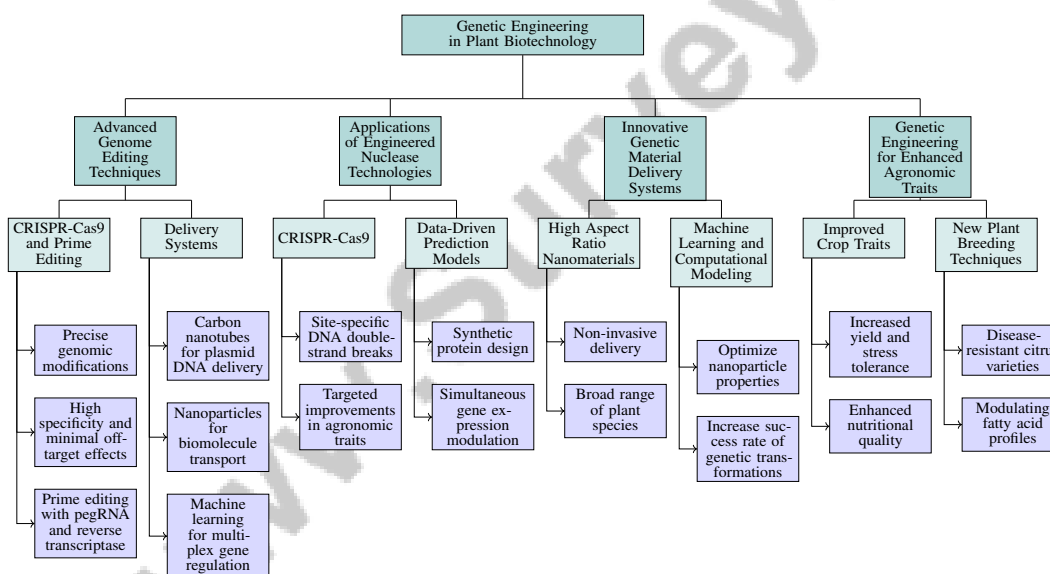


Figure 2: This figure illustrates the hierarchical structure of genetic engineering in plant biotechnology, focusing on advanced genome editing techniques, applications of engineered nuclease technologies, innovative genetic material delivery systems, and genetic engineering for enhanced agronomic traits. Each section highlights key methodologies, delivery systems, and applications that contribute to improving crop resilience, nutritional quality, and agronomic traits.

3 Genetic Engineering in Plant Biotechnology

3.1 Advanced Genome Editing Techniques

The advent of advanced genome editing techniques, notably the CRISPR-Cas9 system, has revolutionized plant biotechnology by enabling precise genomic modifications with high specificity and minimal off-target effects. Prime editing further enhances this capability by facilitating specific DNA sequence alterations through a prime editing guide RNA (pegRNA) and reverse transcriptase, expanding the scope for genetic modifications [21]. The integration of multiple gene prediction pipelines, such as

Method Name	Editing Precision	Delivery Systems	Application Enhancements
PE[21]	Improved Accuracy	Agrobacterium-mediated Transformation	Machine Learning
CNT-DNA[22]	Minimal Off-target Effects	Carbon Nanotubes	Machine Learning
dCas9-VP64[12]	Precise Control Transcription	Guide Rnas	Data-driven Model

Table 1: Overview of advanced genome editing methods, delivery systems, and application enhancements in plant biotechnology. The table highlights specific techniques, their precision in editing, the systems used for delivery, and the enhancements in application achieved through machine learning and data-driven models.

Seqping and FgenesH++, improves genome annotation accuracy and refines editing strategies beyond traditional single-method approaches [23]. New Plant Breeding Techniques (NPBTs), including genome editing and cisgenesis, allow for targeted modifications while preserving the elite cultivars' genetic background [24].

Innovative delivery systems have significantly advanced genome editing. Carbon nanotubes (CNTs) offer a non-mechanical, integration-free method for plasmid DNA delivery into plant cells [22], while nanoparticles facilitate biomolecule transport, enhancing genetic transformation across diverse species without external forces [25]. Machine learning and data-driven prediction models, employing nuclease-deficient Cas9 proteins fused with effectors like VP64, enhance multiplex gene regulation, broadening genome editing applications [12]. These advancements collectively underscore the transformative impact of genome editing in plant biotechnology, paving the way for improved agronomic traits and nutritional profiles. Table 1 provides a comprehensive overview of advanced genome editing techniques, detailing their precision, delivery systems, and application enhancements, as discussed in the context of plant biotechnology advancements.

As depicted in Figure 3, this figure illustrates the hierarchy of advanced genome editing techniques, categorizing them into genome editing methods, delivery systems, and application enhancements, each with specific examples from recent research. The transformative nature of genetic engineering in plant biotechnology is evident, enabling precise modifications to enhance desirable traits and improve crop resilience. The examples of metagenomics, bio-inspired nanoparticles for gene delivery, and bioprocess optimization illustrate the profound impact of advanced genome editing techniques in advancing plant biotechnology and fostering sustainable agricultural innovations [26, 25, 13].

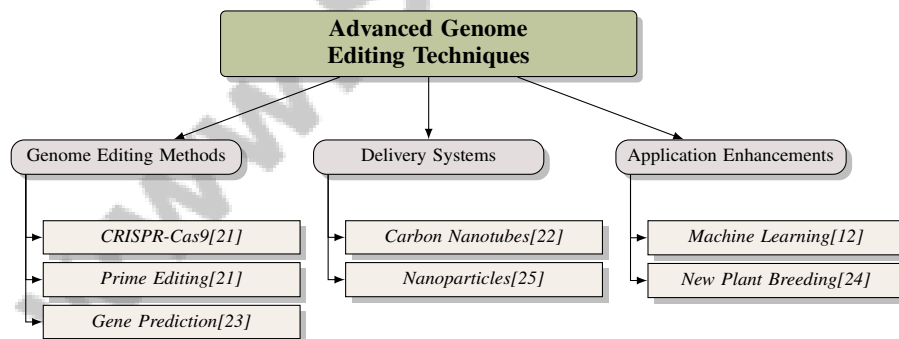


Figure 3: This figure illustrates the hierarchy of advanced genome editing techniques, categorizing them into genome editing methods, delivery systems, and application enhancements, each with specific examples from recent research.

3.2 Applications of Engineered Nuclease Technologies

Engineered nuclease technologies, especially CRISPR-Cas9, are pivotal for precise genetic modifications in plants, facilitating targeted improvements in agronomic traits and nutritional profiles. CRISPR-Cas9 induces site-specific DNA double-strand breaks, repaired by cellular mechanisms to introduce genetic changes, with prime editing allowing specific insertions and substitutions [21]. The effectiveness of these technologies hinges on delivery systems, with nanoparticles providing a promising alternative for transporting CRISPR-Cas9 and other genetic tools across cell membranes without external forces [25]. Integrating data-driven prediction models in synthetic protein design

refines engineered nucleases' application, enabling simultaneous gene expression modulation with a single synthetic protein [12]. This dynamic gene expression modulation is crucial for optimizing metabolic pathways and enhancing plant traits.

3.3 Innovative Genetic Material Delivery Systems

Method Name	Delivery Mechanisms	Efficiency and Precision	Technological Advancements
CNT-DNA[22] dCas9-VP64[12]	Carbon Nanotubes Guide Rnas	High Efficiency High Correlation	Machine Learning Data-driven Model

Table 2: Comparison of innovative genetic material delivery methods highlighting their delivery mechanisms, efficiency, precision, and technological advancements. The table emphasizes the role of carbon nanotubes and guide RNAs in improving genetic transformations in plant biotechnology.

Innovative genetic material delivery systems are crucial for advancing plant biotechnology, enabling efficient genetic construct introduction into plant cells. Traditional methods like *Agrobacterium*-mediated transformation and biolistic particle delivery face limitations in host range, transformation efficiency, and potential tissue damage. High aspect ratio nanomaterials offer a promising alternative, facilitating efficient, non-invasive delivery of genetic material into a broad range of plant species without DNA integration [8, 22, 11, 25]. Carbon nanotubes (CNTs) serve as a notable advancement, providing an integration-free method for plasmid DNA transport into plant cells [22]. Nanoparticle-based systems effectively transport biomolecules across plant cell membranes, overcoming physical barriers to genetic transformation [25]. Machine learning and computational modeling enhance delivery system design, optimizing nanoparticle properties for specific plant species and target tissues, increasing genetic transformations' success rate [12]. Table 2 presents a comparative analysis of cutting-edge genetic material delivery systems, illustrating their mechanisms, efficiency, and technological innovations in the context of plant biotechnology. These innovations represent significant advancements in plant biotechnology, enabling efficient and targeted crop trait enhancements while addressing traditional methods' challenges, such as tissue damage and unintended genetic integration [8, 22, 21, 25].

3.4 Genetic Engineering for Enhanced Agronomic Traits

Method Name	Techniques Used	Target Outcomes	Application Tools
CAFA-GE[3] PFACA[27] CNT-DNA[22] PE[21]	Real-time Rt-PCR Gas-liquid Chromatography Carbon Nanotubes Prime Editing	Improved Oil Quality Blood Pressure Regulation Strong Protein Expression Improved Accuracy	Ge-MS Fasting Blood Samples Carbon Nanotubes Reverse Transcriptase

Table 3: Overview of genetic engineering methods, techniques, target outcomes, and application tools used to enhance agronomic traits. The table highlights various methods such as CAFA-GE, PFACA, CNT-DNA, and PE, detailing their specific techniques and applications in improving crop quality and health outcomes.

Genetic engineering significantly enhances agronomic traits, offering solutions to improve crop yield, stress tolerance, and nutritional quality. Table 3 presents a comprehensive summary of the genetic engineering methods employed to enhance agronomic traits, illustrating the techniques, target outcomes, and application tools associated with each method. Precise genome editing targets specific genes responsible for desirable traits, such as those regulating -linolenic acid (ALA) levels in oil crops, crucial for enhancing ALA content and improving plant resilience and nutritional profiles [3]. New Plant Breeding Techniques (NPBTs), including cisgenesis and genome editing, have successfully developed disease-resistant citrus varieties with improved fruit quality and pathogen resistance [24]. Genetic engineering also modulates fatty acid profiles to improve health outcomes, with increased ALA and linoleic acid (LA) levels aiding in hypertension prevention [27]. Innovative delivery systems, such as carbon nanotubes (CNTs), enhance genetic engineering efficiency by enabling strong protein expression without DNA integration [22]. Genomic resources, like those for spinach, provide insights into disease resistance and nutritional quality traits, supporting targeted breeding programs [28]. Combined with precise genome editing, these resources facilitate accurate plant genome modifications, enhancing genetic engineering interventions' reliability and effectiveness [21].

4 Metabolic Engineering and Fatty Acid Biosynthesis

Metabolic engineering is pivotal in enhancing fatty acid biosynthesis, a key factor in improving nutritional quality and health benefits. This section explores strategies to optimize metabolic pathways, focusing on refining these pathways to boost yields of essential fatty acids like α -linolenic acid (ALA), crucial for human nutrition.

4.1 Metabolic Pathway Optimization

Optimizing metabolic pathways is essential for enhancing the biosynthesis of valuable compounds such as ALA. As illustrated in Figure 4, the hierarchical structure of metabolic pathway optimization strategies highlights key components including modular engineering, computational techniques, and genetic tools. Modular metabolic engineering (MME) divides complex pathways into modules, allowing for simultaneous optimization of each module's expression levels, reducing bottlenecks and increasing productivity [29]. Advanced computational techniques, such as the adjoint method, efficiently compute gradients in metabolic flux analysis, reducing complexity [30]. Neural networks further facilitate dynamic pathway optimization by correlating intracellular fluxes with extracellular exchange rates [14].

Genetically encoded small molecule biosensors provide essential feedback for fine-tuning metabolic pathways by accurately measuring metabolite concentrations [31]. CRISPR-based transcription regulators, like dCas9-VP64, exemplify precision tools for modulating gene expression in metabolic processes [12]. Despite advancements, challenges persist, including optimization difficulties during two-phase fermentation and limitations from autoregulated systems [13]. The scarcity of comprehensive experimental data for parameter estimation and the computational demands of dynamic simulations also pose hurdles [32].

Innovative dietary interventions further optimize fatty acid biosynthesis pathways, enhancing ALA conversion to long-chain polyunsaturated fatty acids (LCPUFAs) and improving the nutritional profile of plant-derived products [4]. These strategies underscore the importance of integrating computational tools, modular engineering, and dietary interventions to optimize metabolic pathways for enhanced fatty acid production.

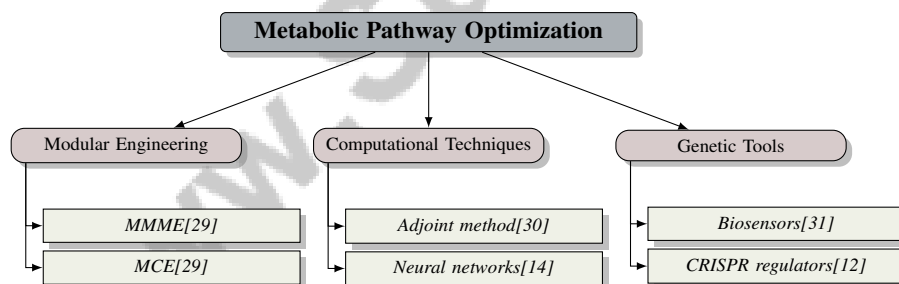


Figure 4: This figure illustrates the hierarchical structure of metabolic pathway optimization strategies, highlighting key components such as modular engineering, computational techniques, and genetic tools.

4.2 Metabolic Engineering and Fatty Acid Profiles

Metabolic engineering significantly influences fatty acid profiles in plants, affecting nutritional quality and health benefits. The integration of neural networks with constraint-based models has transformed process optimization, enabling the dynamic use of intracellular fluxes as optimization variables, enhancing precision in metabolic pathway manipulations [14].

Dietary ALA supplementation elevates levels of beneficial fatty acids like eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA) while reducing arachidonic acid, correlating with protective effects against prostate cancer, akin to fish oil consumption [33]. These findings highlight the health benefits of optimizing fatty acid biosynthesis pathways through metabolic engineering.

Advancements in biosensor technology further support fatty acid biosynthesis optimization. FRET-based, transcription factor-based, and riboswitch biosensors offer mechanisms for monitoring and

adjusting metabolic pathways to enhance desired fatty acid production [31]. These tools are crucial for achieving precise control over fatty acid profiles, ensuring the production of beneficial polyunsaturated fatty acids (PUFAs) with anti-inflammatory properties that mitigate cardiovascular disease risk [34].

The hybrid modeling approach, integrating kinetic and stoichiometric data, improves phenotype prediction accuracy and strain optimization, refining metabolic engineering strategies for desired fatty acid profiles [32]. Objective measurement of fatty acid composition in plasma phospholipids, as introduced by Tsukamoto et al., provides clearer insights into the relationship between dietary fats and hypertension [27].

Understanding very long-chain fatty acid (VLCFA) biosynthesis pathways, particularly through studies on centromeric regions dominated by LINE1 and Gypsy retrotransposons, is crucial for enhancing oil production in crops like yellowhorn [35]. This knowledge allows targeted interventions in metabolic pathways to improve oil yield and quality.

The impact of metabolic engineering on fatty acid profiles is profound, presenting opportunities to enhance plant nutritional value and address health concerns through strategic manipulation of biosynthetic pathways. These initiatives aim to improve the quality and nutritional profile of plant-derived food products, supporting human health by addressing dietary fat composition and enhancing micronutrient intake through biofortification, leveraging advanced agricultural technologies such as genetic modification and metabolic engineering [8, 11, 7, 34].

4.3 Dynamic Control Strategies

Dynamic control strategies are crucial in metabolic engineering for optimizing target compound production through real-time metabolic pathway adjustments. These strategies are particularly relevant in two-phase fermentation processes and autoregulation mechanisms, each offering distinct advantages and limitations [13].

Two-phase fermentation separates microbial culture growth and production phases, optimizing conditions to enhance growth initially and maximize biobased chemical yields during production. This method allows better management of metabolic pathways, improving production efficiency and addressing metabolic imbalances in recombinant strains [10, 29, 36]. However, managing phase transitions poses challenges that require precise control systems to maintain optimal conditions.

Autoregulation involves intrinsic mechanisms within metabolic networks that modulate pathway fluxes in response to metabolite concentration fluctuations or environmental changes. This process is vital for maintaining homeostasis and optimizing product formation, enabling organisms to adapt dynamically. Recent metabolic engineering advancements underscore the importance of understanding autoregulatory responses to enhance computational strain design accuracy and improve engineered pathway efficiency in microbial systems [13, 16, 14, 36]. While this self-regulating feature simplifies control processes, reliance on endogenous circuits may limit flexibility in achieving optimal production conditions.

Recent advancements in computational tools and biosensor technologies have significantly improved dynamic control strategies in metabolic engineering, enabling effective decoupling of growth from production and optimizing product formation through autoregulation and feedback control mechanisms. This progress supports using engineered microorganisms as biocatalysts for efficiently producing biofuels, pharmaceuticals, and other valuable compounds while addressing the challenges of maintaining cellular health during product generation [12, 14, 13]. Genetically encoded biosensors provide real-time feedback on metabolite levels, essential for fine-tuning enzyme activities and pathway fluxes, thereby maintaining homeostasis and optimizing production yields.

Additionally, integrating machine learning algorithms with dynamic control systems can refine these strategies by predicting optimal conditions and adjusting control parameters based on real-time data. This predictive capability enhances the reliability and efficiency of metabolic engineering processes, facilitating effective interventions for producing biofuels, pharmaceuticals, and other valuable compounds through precise regulation of gene expression and metabolic fluxes in engineered microorganisms. The synergy of biosensors and computer-assisted feedback mechanisms is set to revolutionize the field, enabling a better balance between cellular health and product yield [12, 14, 13].

4.4 Regulatory Networks and Biosensors

Regulatory networks and biosensors are crucial in metabolic engineering, enabling precise control and optimization of metabolic pathways essential for enhancing the yield of valuable products such as biofuels, chemicals, and pharmaceuticals. Recent advancements in synthetic biology, particularly the development of CRISPR-based transcriptional regulators and genetically encoded small molecule biosensors, allow for simultaneous activation and repression of gene expressions, providing measurable outputs linked to metabolite concentrations. These innovations facilitate dynamic control strategies, including open-loop and closed-loop feedback systems, significantly improving the efficiency of microbial cell factories in industrial biomanufacturing [31, 12, 13]. These systems offer necessary feedback mechanisms to monitor and adjust biochemical processes within cells, enhancing the production of desired metabolites like ALA and other essential fatty acids.

Regulatory networks consist of interconnected pathways governing gene expression and enzyme activity in metabolic processes. The complexity of these networks necessitates sophisticated tools for effective manipulation. Advances in computational modeling, integrating kinetic and stoichiometric data, have led to hybrid models that enhance phenotype prediction accuracy and strain optimization [32]. These models deepen the understanding of regulatory mechanisms governing fatty acid biosynthesis, allowing targeted interventions to optimize metabolic outputs.

Biosensors play a vital role in dynamic metabolic pathway control by providing real-time data on metabolite concentrations and environmental conditions. Genetically encoded biosensors, categorized into FRET-based, transcription factor-based, and riboswitches, offer distinct mechanisms for monitoring cellular processes [31]. These biosensors are essential for fine-tuning metabolic pathways, enabling precise regulation of enzyme activities and pathway fluxes to enhance target compound production.

Integrating biosensors with regulatory networks allows for feedback control strategies that maintain homeostasis and optimize production yields. For example, biosensors can trigger specific gene activations or repressions in response to metabolite level changes, ensuring balanced and efficient metabolic pathways. This feedback loop is vital for sustaining optimal conditions for synthesizing valuable compounds like ALA, crucial in plant metabolism, serving as a key component in membrane structures, and holding significant economic importance in oil crops. Understanding the regulatory mechanisms in this process can enhance ALA production efficiency and improve crop yields [16, 7, 29].

Integrating machine learning algorithms with biosensors and regulatory networks can significantly enhance metabolic engineering strategies by enabling more precise predictions and optimizations in biological system designs. Tools like the Automated Recommendation Tool (ART) utilize probabilistic modeling to guide strain engineering for producing valuable compounds, reducing development times. Additionally, deploying CRISPR-based transcriptional regulators allows multiplexed control of metabolic pathways, facilitating gene expression fine-tuning to improve product yields. Advanced computational methods, such as REMEP, enhance strain design accuracy by focusing on metabolite patterns reflecting cellular regulatory responses, providing deeper insights into metabolic dynamics and enabling more effective engineering approaches [6, 12, 26, 36]. These algorithms can predict optimal conditions and adjust control parameters in real-time, enhancing the robustness and efficiency of metabolic processes, particularly in dynamic environments where rapid adjustments are necessary to maintain optimal production levels.

5 Agronomic Traits and Crop Improvement

5.1 Enhancing Crop Yield and Resilience

Enhancing crop yield and resilience is pivotal in plant biotechnology to meet global food demands and ensure agricultural sustainability amid environmental challenges like climate change and abiotic stresses. Genetic engineering has enabled the development of genetically modified (GM) crops with traits such as herbicide tolerance, insect resistance, and multistress tolerance, significantly boosting agricultural productivity. Techniques like genome editing and biofortification are employed to improve nutritional quality and combat malnutrition affecting over two billion individuals globally. However, public concerns regarding safety and environmental impacts hinder the widespread adoption of these biotechnological solutions, prompting exploration of alternative methods to enhance consumer

acceptance and regulatory compliance [21, 15, 11, 25, 8]. Genetic and metabolic engineering techniques are vital for modifying plant genomes to enhance traits such as yield, stress tolerance, and nutritional quality.

Manipulating metabolic pathways to optimize the biosynthesis of essential compounds, like α -linolenic acid (ALA), is a primary strategy for improving crop yield. Increased ALA production enhances plants' antioxidant capacity, enabling better resilience against oxidative stress and environmental challenges [3, 5]. Advanced genome editing techniques, notably CRISPR-Cas9, allow precise modifications of genes associated with desirable agronomic traits, facilitating the development of crops with improved stress tolerance and yield potential. For instance, editing genes linked to stress response can yield crops more resilient to abiotic stresses such as drought and salinity [21].

Innovative delivery systems, including carbon nanotubes (CNTs) and nanoparticles, enhance genetic transformation efficiency by enabling precise genetic material introduction into plant cells without mechanical force. These systems broaden the scope of plant species eligible for genetic modification, fostering the development of crops with enhanced agronomic traits that can lead to increased yields, reduced chemical input reliance, and overall food production sustainability. This innovation addresses consumer concerns regarding foreign genes and facilitates faster regulatory approvals, promoting the adoption of GM crops [8, 21, 17, 28].

Integration of genomic resources, such as those developed for spinach, provides insights into the genetic basis of traits related to yield and stress tolerance [28]. These resources support targeted breeding programs and genetic engineering interventions for developing crops with enhanced performance and resilience.

The combination of genetic and metabolic engineering techniques, advanced genome editing tools, and innovative delivery systems presents a robust approach to enhancing crop yield and resilience. These advancements, including GM crop development and biofortification through metabolic engineering, are essential for increasing agricultural productivity, addressing global food security challenges, and fostering sustainable farming practices. By introducing beneficial traits like herbicide tolerance and nutritional enhancements, these technologies contribute directly to the United Nations' Sustainable Development Goal of eliminating hunger by 2030. Moreover, alternative genetic engineering methods, such as cisgenesis and genome editing, aim to alleviate public concerns regarding transgenic crops, potentially accelerating their acceptance and regulatory approval in the face of rising global food demand and environmental sustainability [8, 11, 7].

5.2 Impact of Enhanced Fatty Acid Profiles on Health

Enhancing fatty acid profiles in plants, particularly the increase of α -linolenic acid (ALA), carries significant implications for human health. ALA possesses anti-inflammatory properties and serves as a precursor to long-chain polyunsaturated fatty acids (LCPUFAs), essential for cardiovascular health and chronic disease prevention. Replacing linoleic acid with ALA has been shown to improve liver histology and reduce oxidative stress and inflammation, underscoring the therapeutic potential of optimizing fatty acid profiles in dietary sources [2].

Objective measurements of fatty acid composition clarify the dietary influences on health conditions such as hypertension. Tsukamoto et al. emphasize the importance of these measurements in understanding the health benefits linked to enhanced fatty acid profiles, especially in dietary interventions aimed at reducing cardiovascular disease risk [27]. Accurately assessing fatty acid composition in plant-derived foods is vital for evaluating their health impacts and guiding dietary recommendations.

Phenological growth stages and specific plant organs significantly influence the antioxidant activity, total phenolic content, and fatty acid profiles of plants like purslane. This variation highlights the need to consider plant developmental stages in nutritional enhancement and health benefits [5]. Purslane, rich in ALA and other beneficial fatty acids, exemplifies how targeted metabolic engineering can enhance plant nutritional value and improve health outcomes.

The nutritional benefits of galactolipids, which provide essential fatty acids for growth and development, are well-documented. These lipids play a crucial role in the nutrition of herbivores and other species, demonstrating the broader ecological and nutritional importance of enhancing fatty acid profiles in plants [7]. By improving the fatty acid composition of plant-derived foods, metabolic engineering can address nutrient deficiencies and support overall health and well-being.

Enhancing fatty acid profiles in plants presents a promising avenue for improving human health through dietary interventions. The application of advanced genetic and metabolic engineering techniques, particularly through biofortification strategies and synthetic biology, has the potential to significantly enhance the nutritional profiles of staple crops. This optimization not only addresses micronutrient deficiencies affecting over two billion people globally but also plays a crucial role in reducing chronic disease risks, ultimately promoting better health outcomes and food security worldwide [11, 26].

5.3 Challenges in Multistress Tolerance

Engineering plants for multistress tolerance presents significant challenges due to the complexity of plant responses to simultaneous abiotic stresses, including drought, salinity, extreme temperatures, and nutrient deficiencies. These stresses often occur concurrently in natural environments, complicating the development of effective tolerance strategies [15]. The primary challenge lies in the intricate network of signaling pathways and physiological responses that plants employ to cope with these stresses. Enhancing tolerance through genetic engineering may result in unintended trade-offs, such as reduced growth or yield under non-stress conditions.

Achieving multistress tolerance necessitates identifying key regulatory genes that confer broad-spectrum resistance to various abiotic stresses while maintaining essential agronomic traits like yield and quality. The complexity of this task arises from the intricate regulatory networks involving stress hormones, transcription factors, and signaling molecules that coordinate plant responses to multiple simultaneous stresses, emphasizing the importance of targeted genetic engineering approaches to enhance resilience without compromising overall plant performance [15, 8, 23, 18]. The pleiotropic effects of these genes can lead to undesirable phenotypes, necessitating a careful balance between stress tolerance and plant productivity. Additionally, the dynamic nature of stress responses, which can vary depending on the intensity, duration, and combination of stresses, complicates the development of stable and robust tolerance mechanisms.

Integrating advanced genomic and transcriptomic technologies offers potential solutions by enabling the identification of candidate genes and regulatory networks involved in multistress responses. As illustrated in Figure 5, this figure outlines the key challenges in engineering plants for multistress tolerance, highlighting the complexity of plant responses, the role of genetic engineering approaches, and the integration of genomic technologies. However, translating these findings into practical applications requires sophisticated genetic engineering techniques and a comprehensive understanding of plant physiology. Developing multistress-tolerant crops must consider ecological and environmental consequences to ensure that genetically engineered plants do not negatively impact biodiversity or disrupt ecosystem stability. This consideration is crucial, as abiotic stresses—such as extreme temperatures, water scarcity, high salinity, and heavy metal exposure—pose significant threats to plant growth and agricultural productivity. By integrating a robust understanding of plant defense mechanisms and regulatory networks, researchers can engineer crops that withstand multiple stresses while minimizing potential risks to surrounding ecosystems and non-target organisms. This approach is essential for addressing climate change challenges and meeting the increasing global food demand without compromising environmental integrity [15, 8, 11].

Engineering plants for multistress tolerance requires a comprehensive interdisciplinary approach that integrates knowledge from plant biology, genetics, and environmental science to effectively address the complex challenges posed by multiple abiotic stresses. This approach leverages insights into the intricate regulatory networks and defense mechanisms that plants have evolved, critical for developing robust strategies to enhance crop resilience in the face of environmental changes [8, 17, 15, 16, 28]. Addressing these challenges is crucial for enhancing crop resilience and ensuring agricultural sustainability in the context of global climate change and environmental variability.

6 Challenges and Future Directions

6.1 Current Challenges in Genetic and Metabolic Engineering

Genetic and metabolic engineering in plant biotechnology face substantial hurdles that limit their effectiveness. Efficiently delivering genetic material into plant cells remains challenging, as traditional methods like *Agrobacterium*-mediated transformation often show low efficiency in mature plants

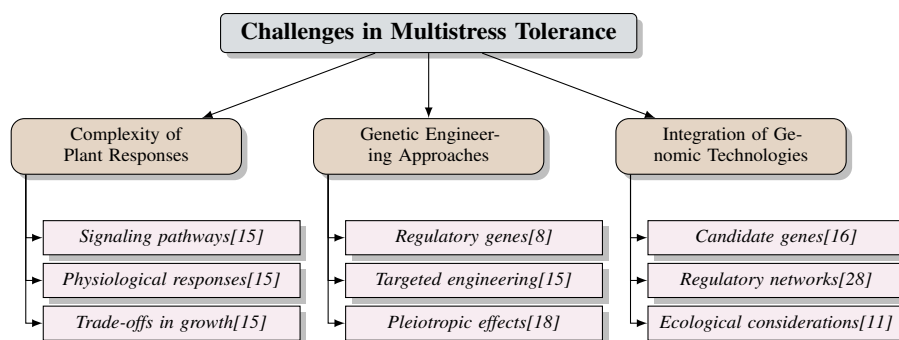


Figure 5: This figure outlines the key challenges in engineering plants for multistress tolerance, highlighting the complexity of plant responses, the role of genetic engineering approaches, and the integration of genomic technologies.

and may cause unintended DNA integration [22]. Novel delivery systems, such as carbon nanotubes, hold promise but require further refinement to achieve consistent transformation across various plant species.

In metabolic engineering, accurately modeling and optimizing metabolic pathways is difficult due to limitations in kinetic data and model scalability, which impede the prediction and enhancement of target metabolites like -linolenic acid (ALA) [32]. The development of real-time biosensing tools for monitoring metabolite levels is still emerging, restricting dynamic adjustments of metabolic pathways [31].

Genome assembly and functional analysis are complicated by the repetitive nature of centromere regions, particularly in polyploid species like peanuts, where the tetraploid structure complicates comprehensive genome coverage [35, 18]. Overproduction of target compounds can lead to growth defects and reduced cellular fitness, as resources are diverted from essential functions [13]. Additionally, competition between fatty acids, such as linoleic acid (LA) and ALA, may inhibit the conversion of ALA to long-chain polyunsaturated fatty acids (LCPUFAs) like docosahexaenoic acid (DHA) [4].

The extraction and utilization of complex biomolecules, such as galactolipids, are hindered by limited enzyme research and extraction challenges from biomass [7]. Tools like CLOSEgaps depend on the quality of initial genome-scale metabolic models (GEMs) and hypothetical reaction pools, limiting their applicability [19]. Moreover, reliance on well-characterized genetic parts and the metabolic costs of co-expressing effector proteins complicate precise regulation of gene expression and pathways [12]. Addressing these challenges requires a multidisciplinary approach, integrating advancements in delivery systems, computational modeling, and biosensor technology, alongside efforts to improve public perception and regulatory frameworks for genetically engineered crops.

6.2 Advancements in Computational and Modeling Techniques

Advancements in computational tools and modeling techniques have greatly enhanced plant biotechnology, aiding metabolic pathway optimization and trait improvement. Integrating computational models with experimental data allows for precise prediction and manipulation of plant metabolic processes. Techniques like constraint-based reconstruction and analysis (COBRA) and metabolite-centric methods such as REMEP reveal optimal intracellular flux trajectories and improve strain design by capturing intricate regulatory responses [14, 36].

Hybrid models combining kinetic and stoichiometric data improve phenotype predictions and strain optimization, providing a framework for understanding complex metabolic network interactions [32]. Machine learning and artificial intelligence analyze large-scale genomic and transcriptomic datasets, offering insights into gene expression patterns and regulatory networks, enhancing metabolic pathway optimization [12].

The integration of neural networks with constraint-based models has improved process optimization, allowing dynamic intracellular fluxes as optimization variables and enhancing precision in metabolic pathway manipulations [14]. Combining computational tools with biosensor technologies enables real-time monitoring and control of metabolic processes. Genetically encoded biosensors provide

feedback on metabolite levels, allowing for fine-tuning of enzyme activities and pathway fluxes to optimize production yields [31].

6.3 Innovations in Fatty Acid Biosynthesis and Lipid Metabolism

Advancements in fatty acid biosynthesis and lipid metabolism are driven by integrating cutting-edge technologies in metabolic engineering and synthetic biology. These innovations enable precise manipulation and understanding of fatty acid production processes. Functional characterization of genes involved in fatty acid biosynthesis, as seen in tree peonies, highlights genetic engineering's role in enhancing fatty acid profiles across crops [3].

Machine learning and automated reasoning technologies, like the ART framework, streamline bioengineering processes, improving fatty acid biosynthesis and lipid metabolism [6]. Biosensors, such as FRET-based sensors, transcription factor-based sensors, and riboswitches, are pivotal tools providing real-time feedback on metabolite levels, optimizing fatty acid production [31].

CRISPR-Cas systems enhance the precision of modifications in fatty acid biosynthesis pathways. Future research should focus on improving editing efficiencies by exploring alternative reverse transcriptases and optimizing pegRNA design [21]. Despite advancements, gaps remain in understanding ALA's specific effects compared to other polyunsaturated fatty acids (PUFAs) and optimal intake levels for health benefits [34]. Future research should elucidate ALA conversion mechanisms and its dietary implications [4].

The CNT-based delivery platform shows promise in enabling high-efficiency plasmid DNA delivery into multiple plant species, offering a versatile tool for enhancing fatty acid biosynthesis [22]. The study by Sheng et al. introduces a data-driven predictive model for designing CRISPR-based regulators, crucial for optimizing fatty acid biosynthesis [12]. Future research should validate identified SNPs and explore their functional roles in agronomic traits to enhance breeding strategies [18]. Integrating biochemical data and refining model predictions of enzyme functions could enhance metabolic network reconstruction [19].

Ongoing advancements in understanding fatty acid biosynthesis and lipid metabolism, particularly the enzymatic processes and regulatory networks involved in producing unsaturated fatty acids like oleic, linoleic, and ALA, underscore the potential for biotechnological innovations to enhance plant-derived foods' nutritional profiles. These innovations could address global food security challenges by improving oil content and nutritional quality through genetic and metabolic engineering, contributing to reducing malnutrition and promoting sustainable agricultural practices [8, 16, 11, 3].

6.4 Regulatory and Ecological Considerations

Regulatory and ecological dimensions are critical in advancing biotechnological innovations in agriculture. Deploying New Plant Breeding Techniques (NPBTs), like genome editing and cisgenesis, requires understanding regulatory frameworks for genetically engineered crops' release and commercialization. Future research should optimize transformation protocols and explore new NPBT methodologies to address regulatory challenges, facilitating technology adoption in citrus breeding and beyond [24].

Ecologically, introducing genetically modified organisms (GMOs) raises concerns about biodiversity and ecosystem stability. Developing synthetic promoters for targeted gene expression and employing high-throughput techniques can enhance understanding of stress tolerance mechanisms, allowing precise interventions that minimize ecological disruptions [15]. Exploring interactions between abiotic stress responses is essential for developing crops that withstand multiple environmental challenges without adverse ecological effects.

Biosensing technologies play a pivotal role in addressing regulatory and ecological considerations by providing real-time monitoring of metabolic processes. Integrating robust biosensors ensures engineered plants maintain homeostasis and do not produce unintended metabolites harmful to the environment [31]. Future research should focus on developing advanced biosensing technologies and optimizing integration for regulatory compliance and ecological safety.

Carbon nanotube (CNT)-based genetic material delivery offers advantages like high efficiency, non-toxicity, species independence, and avoiding DNA integration into the plant genome [22]. These

characteristics make CNT-based methods appealing from regulatory and ecological perspectives, mitigating unintended genetic modifications and potential ecological impacts.

7 Conclusion

The survey has provided an in-depth exploration of enhancing plant nutritional profiles and agronomic performance through genetic and metabolic engineering, with a particular focus on α -linolenic acid (ALA). By leveraging advanced genome editing techniques like CRISPR-Cas9 and innovative delivery methods such as carbon nanotubes, significant strides have been made in modifying plant genomes to enhance essential traits. Metabolic engineering has further refined fatty acid biosynthesis pathways, leading to increased production of ALA and other beneficial compounds, thereby improving plant resilience and nutritional quality.

The interdisciplinary approach of plant biotechnology, integrating genetic engineering, metabolic pathway optimization, and agronomic trait enhancement, is pivotal in addressing global food security and improving human health. Developments in computational modeling and biosensor technologies have empowered researchers to exercise precise control over metabolic pathways, enabling efficient production of target metabolites.

Future research directions should focus on conducting randomized controlled trials (RCTs) to establish definitive guidelines for ALA intake and explore personalized nutrition strategies to refine dietary recommendations. In vivo studies are necessary to confirm ALA's protective effects against colorectal cancer, providing further insights into enhancing nutritional profiles. Additionally, gaining public acceptance of genetically engineered crops, developing effective regulatory frameworks, and exploring innovative breeding technologies are essential for the successful application and acceptance of these biotechnological advancements.

References

- [1] Yimeng Lin, Jingping Ge, Yunye Zhang, Hongzhi Ling, Xiufeng Yan, and Wenxiang Ping. Monoraphidium sp. hdma-20 is a new potential source of α -linolenic acid and eicosatetraenoic acid. *Lipids in health and disease*, 18:1–10, 2019.
- [2] Sugeedha Jeyapal, Suryam Reddy Kona, Surekha Venkata Mullapudi, Uday Kumar Putcha, Puvaneswari Gurumurthy, and Ahamed Ibrahim. Substitution of linoleic acid with α -linolenic acid or long chain n-3 polyunsaturated fatty acid prevents western diet induced nonalcoholic steatohepatitis. *Scientific reports*, 8(1):10953, 2018.
- [3] Qing-Yu Zhang, Rui Yu, Li-Hang Xie, Md Mahbubur Rahman, Aruna Kilaru, Li-Xin Niu, and Yan-Long Zhang. Fatty acid and associated gene expression analyses of three tree peony species reveal key genes for α -linolenic acid synthesis in seeds. *Frontiers in plant science*, 9:106, 2018.
- [4] Donghee Kim, Jeong-Eun Choi, and Yongsoon Park. Low-linoleic acid diet and oestrogen enhance the conversion of α -linolenic acid into dha through modification of conversion enzymes and transcription factors. *British Journal of Nutrition*, 121(2):137–145, 2019.
- [5] Azadeh Saffaryazdi, Ali Ganjeali, Reza Farhoosh, and Monireh Cheniany. Variation in phenolic compounds, α -linolenic acid and linoleic acid contents and antioxidant activity of purslane (portulaca oleracea l.) during phenological growth stages. *Physiology and Molecular Biology of Plants*, 26:1519–1529, 2020.
- [6] Tijana Radivojević, Zak Costello, Kenneth Workman, and Hector Garcia Martin. Art: A machine learning automated recommendation tool for synthetic biology, 2020.
- [7] Moulay Sahaka, Sawsan Amara, Jutarat Wattanakul, Mohamed A Gedi, Noelia Aldai, Goetz Parsiegla, Jérôme Lecomte, John T Christeller, David Gray, Brigitte Gontero, et al. The digestion of galactolipids and its ubiquitous function in nature for the uptake of the essential α -linolenic acid. *Food & Function*, 11(8):6710–6744, 2020.
- [8] Krishan Kumar, Geetika Gambhir, Abhishek Dass, Amit Kumar Tripathi, Alla Singh, Abhishek Kumar Jha, Pranjal Yadava, Mukesh Choudhary, and Sujay Rakshit. Genetically modified crops: current status and future prospects. *Planta*, 251(4):91, 2020.
- [9] María José González-Fernández, Ignacio Ortea, and José Luis Guil-Guerrero. α -linolenic and γ -linolenic acids exercise differential antitumor effects on ht-29 human colorectal cancer cells. *Toxicology research*, 9(4):474–483, 2020.
- [10] José Montaña López, Lisset Duran, and José L Avalos. Physiological limitations and opportunities in microbial metabolic engineering. *Nature Reviews Microbiology*, 20(1):35–48, 2022.
- [11] Dominique Van Der Straeten, Navreet K Bhullar, Hans De Steur, Wilhelm Gruissem, Donald MacKenzie, Wolfgang Pfeiffer, Matin Qaim, Inez Slamet-Loedin, Simon Strobbe, Joe Tohme, et al. Multiplying the efficiency and impact of biofortification through metabolic engineering. *Nature communications*, 11(1):5203, 2020.
- [12] Jiayuan Sheng, Weihua Guo, Christine Ash, Brendan Freitas, Mitchell Paoletti, and Xueyang Feng. Data-driven prediction of crispr-based transcription regulation for programmable control of metabolic flux, 2017.
- [13] Makoto A Lalwani, Evan M Zhao, and José L Avalos. Current and future modalities of dynamic control in metabolic engineering. *Current Opinion in Biotechnology*, 52:56–65, 2018.
- [14] Sebastián Espinel-Ríos and José L. Avalos. Linking intra- and extra-cellular metabolic domains via neural-network surrogates for dynamic metabolic control, 2024.
- [15] Mei He, Cheng-Qiang He, and Nai-Zheng Ding. Abiotic stresses: general defenses of land plants and chances for engineering multistress tolerance. *Frontiers in plant science*, 9:1771, 2018.

-
- [16] Mei He, Chun-Xue Qin, Xu Wang, and Nai-Zheng Ding. Plant unsaturated fatty acids: biosynthesis and regulation. *Frontiers in Plant Science*, 11:390, 2020.
- [17] Hesam T. Dashti, Jernej Tonejc, Adel Ardalani, Alireza F. Siahpirani, Sabrina Guettes, Zohreh Sharif, Liya Wang, and Amir H. Assadi. Applications of machine learning methods to quantifying phenotypic traits that distinguish the wild type from the mutant *arabidopsis thaliana* seedlings during root gravitropism, 2010.
- [18] Xingguo Zhang, Jianhang Zhang, Xiaoyan He, Yun Wang, Xingli Ma, and Dongmei Yin. Genome-wide association study of major agronomic traits related to domestication in peanut. *Frontiers in Plant Science*, 8:1611, 2017.
- [19] Xiaoyi Liu, Hongpeng Yang, Chengwei Ai, Ruihan Dong, Yijie Ding, Qianqian Yuan, Jijun Tang, and Fei Guo. A generalizable framework for unlocking missing reactions in genome-scale metabolic networks using deep learning, 2024.
- [20] Yingfeng Niu, Guohua Li, Shubang Ni, Xiyong He, Cheng Zheng, Ziyang Liu, Lidan Gong, Guanghong Kong, Wei Li, and Jin Liu. The chromosome-scale reference genome of *macadamia tetraphylla* provides insights into fatty acid biosynthesis. *Frontiers in genetics*, 13:835363, 2022.
- [21] Kai Hua, Yuwei Jiang, Xiaoping Tao, and Jian-Kang Zhu. Precision genome engineering in rice using prime editing system. *Plant Biotechnology Journal*, 18(11):2167, 2020.
- [22] Gozde S Demirel, Huan Zhang, Juliana L Matos, Natalie S Goh, Francis J Cunningham, Younghun Sung, Roger Chang, Abhishek J Aditham, Linda Chio, Myeong-Je Cho, et al. High aspect ratio nanomaterials enable delivery of functional genetic material without dna integration in mature plants. *Nature nanotechnology*, 14(5):456–464, 2019.
- [23] Chan Kuang Lim, Tatiana V. Tatarinova, Rozana Rosli, Nadzirah Amiruddin, Norazah Azizi, Mohd Amin Ab Halim, Nik Shazana Nik Mohd Sanusi, Jayanthi Nagappan, Petr Ponomarenko, Martin Triska, Victor Soloviyev, Mohd Firdaus-Raih, Ravigadevi Sambanthamurthi, Denis Murphy, and Leslie Low Eng Ti. Evidence-based gene models for structural and functional annotations of the oil palm genome, 2017.
- [24] Fabrizio Salonia, Angelo Ciacciulli, Lara Poles, Helena Domenica Pappalardo, Stefano La Malfa, and Concetta Licciardello. New plant breeding techniques in citrus for the improvement of important agronomic traits. a review. *Frontiers in plant science*, 11:1234, 2020.
- [25] Francis J Cunningham, Natalie S Goh, Gozde S Demirel, Juliana L Matos, and Markita P Landry. Nanoparticle-mediated delivery towards advancing plant genetic engineering. *Trends in biotechnology*, 36(9):882–897, 2018.
- [26] Raúl García-Granados, Jordy Alexis Lerma-Escalera, and José R Morones-Ramírez. Metabolic engineering and synthetic biology: synergies, future, and challenges. *Frontiers in bioengineering and biotechnology*, 7:36, 2019.
- [27] Ikuyo Tsukamoto and Shiori Sugawara. Low levels of linoleic acid and α -linolenic acid and high levels of arachidonic acid in plasma phospholipids are associated with hypertension. *Biomedical reports*, 8(1):69–76, 2018.
- [28] Xiaofeng Cai, Xuepeng Sun, Chenxi Xu, Honghe Sun, Xiaoli Wang, Chenhui Ge, Zhonghua Zhang, Quanxi Wang, Zhangjun Fei, Chen Jiao, et al. Genomic analyses provide insights into spinach domestication and the genetic basis of agronomic traits. *Nature Communications*, 12(1):7246, 2021.
- [29] Hongyuan Lu, Juan C Villada, and Patrick KH Lee. Modular metabolic engineering for biobased chemical production. *Trends in biotechnology*, 37(2):152–166, 2019.
- [30] Stéphane Mottelet. Fast computation of gradient and sensitivity in ^{13}C metabolic flux analysis instantaneous experiments using the adjoint method, 2012.
- [31] Yang Liu, Ye Liu, and Meng Wang. Design, optimization and application of small molecule biosensor in metabolic engineering. *Frontiers in microbiology*, 8:2012, 2017.

-
- [32] Osvaldo D Kim, Miguel Rocha, and Paulo Maia. A review of dynamic modeling approaches and their application in computational strain optimization for metabolic engineering. *Frontiers in microbiology*, 9:1690, 2018.
- [33] Jingjing Li, Zhennan Gu, Yong Pan, Shunhe Wang, Haiqin Chen, Hao Zhang, Wei Chen, and Yong Q Chen. Dietary supplementation of α -linolenic acid induced conversion of n-3 lcpufas and reduced prostate cancer growth in a mouse model. *Lipids in Health and Disease*, 16:1–9, 2017.
- [34] Yvonne M Lenighan, Breige A McNulty, and Helen M Roche. Dietary fat composition: Replacement of saturated fatty acids with pufa as a public health strategy, with an emphasis on α -linolenic acid. *Proceedings of the Nutrition Society*, 78(2):234–245, 2019.
- [35] Hui Liu, Xue-Mei Yan, Xin-rui Wang, Dong-Xu Zhang, Qingyuan Zhou, Tian-Le Shi, Kai-Hua Jia, Xue-Chan Tian, Shan-Shan Zhou, Ren-Gang Zhang, et al. Centromere-specific retrotransposons and very-long-chain fatty acid biosynthesis in the genome of yellowhorn (*xanthoceras sorbifolium*, sapindaceae), an oil-producing tree with significant drought resistance. *Frontiers in Plant Science*, 12:766389, 2021.
- [36] Tolutola Oyetunde, Jeffrey Czajka, Gang Wu, Cynthia Lo, and Yinjie Tang. Metabolite patterns reveal regulatory responses to genetic perturbations, 2017.

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