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# Genomic engineering and tissue culture propagation of high-yield oil palm clones: A systematic review of genetic traits, cultivation methods, and agronomic performance enhancement

Special Issue - 2026

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**Received:** May 11, 2026 | **Published:** May 26, 2026

## Abstract

Oil palm productivity improvement remains a strategic scientific focus given the crop's economic importance and its biological complexity as a perennial species. Conventional breeding approaches have achieved significant gains; however, their effectiveness is constrained by long selection cycles and limited precision in improving complex traits. Consequently, genomic engineering and tissue culture propagation have emerged as complementary approaches to accelerate yield enhancement and improve agronomic performance. This study aims to systematically analyze and integrate contemporary peer-reviewed evidence on how genomic and molecular tools, together with tissue culture technologies, contribute to the development and performance of high-yield oil palm clones. This study employs a Systematic Literature Review (SLR) design guided by the PRISMA framework. Data were collected from Scopus using predefined Boolean keyword combinations. A total of 33 English-language, open-access articles published between 2021 and 2026 were selected through sequential screening for relevance, publication year, and accessibility. Findings were analyzed through thematic synthesis and qualitative comparison. The results identified six dominant analytical clusters encompassing yield-associated genetic traits, genomic and molecular selection tools, tissue culture propagation techniques, clonal fidelity management, agronomic performance outcomes, and productivity enhancement across cultivation contexts. The reviewed literature consistently indicates that integrating genomic engineering with optimized tissue culture propagation enhances yield potential, genetic stability, and field-level performance of clonal oil palm materials. In conclusion, genomic engineering and tissue culture propagation collectively form an integrated framework for developing stable, high-performing oil palm clones. Future research is encouraged to strengthen multi-omics integration and expand long-term field-based evidence to further refine clone development strategies.

**Keywords:** oil palm, genomic engineering, tissue culture, clonal propagation, agronomic performance

## Introduction

The oil palm (*Elaeis guineensis*) is one of the most important perennial oil crops globally, playing a central role in meeting the rising demand for vegetable oils driven by population growth, urbanization, and expanding industrial applications.[1] Compared with other oil-bearing crops, oil palm exhibits a markedly higher oil yield per unit area, making it a strategic commodity for enhancing land-use efficiency and supporting food, oleochemical, and bio-based industries.[2] As global agricultural systems increasingly emphasize productivity optimization and technological intensification, oil palm production systems have become a focal point for scientific innovation aimed at sustaining yield growth while improving production efficiency.[3]

These strategies are increasingly viewed as essential components for maintaining the competitiveness and long-term viability of oil palm-based agro-industrial systems. This review proceeds from the foundational premise that yield enhancement is a product of the coordinated interaction between genetic potential, propagation quality, and cultivation environment — a principle that unifies the analytical clusters examined in the Results and Discussion.[4,5]

Traditional oil palm breeding programs, while successful in achieving incremental yield gains, are inherently constrained by long breeding cycles, late phenotypic expression of key traits, and complex genotype–environment interactions. The typical breeding cycle of oil palm may span more than a decade before elite progenies can be reliably evaluated and released, which limits the speed at which genetic gains can be translated into commercial production.[6] These limitations have stimulated the exploration of advanced biotechnological approaches that can accelerate selection processes, enhance trait precision, and enable more predictable yield outcomes.

Genomic engineering and molecular breeding technologies have emerged as transformative tools in this regard. Advances in genomics, transcriptomics, and molecular marker technologies have enabled a more detailed dissection of the genetic architecture underlying yield-related traits, growth dynamics, and physiological performance in oil palm. Using tools such as marker-assisted selection, QTL mapping, and genome-wide association studies, researchers have identified genetic markers linked to fresh fruit bunch production, oil accumulation, and vegetative growth.[7] These developments have contributed to a paradigm shift from phenotype-driven selection toward data-informed, genome-based improvement strategies.

However, the realization of genetic potential at the plantation level is not determined solely by genetic selection. Propagation systems play a critical role in translating elite genetic traits into large-scale planting materials with consistent performance. In oil palm, tissue culture and in vitro propagation, particularly somatic embryogenesis, have become indispensable for the mass multiplication of selected high-yielding genotypes.[8] Unlike seed-derived materials, clonal propagation enables the replication of genetically superior individuals, offering the potential for enhanced yield uniformity, earlier yield onset, and improved plantation management efficiency.

Despite these advantages, tissue culture-based propagation in oil palm presents unique technical and biological challenges. Variability in embryogenic response, long culture durations, and risks associated with somaclonal variation have historically constrained the large-scale deployment of clonal palms.[9] As a result, the success of clonal oil palm programs depends on the careful integration of genomic selection, optimized in vitro protocols, and rigorous quality control mechanisms to ensure genetic fidelity and agronomic reliability. Understanding how these components interact across different stages of development is therefore essential for assessing the effectiveness of biotechnology-driven improvement strategies.

Over the past two decades, a growing body of scientific literature has addressed individual aspects of genomic engineering, tissue culture propagation, and agronomic performance in oil palm. Numerous studies have reported the identification of yield-associated genes, the optimization of in vitro regeneration systems, and the field performance of cloned planting materials under diverse cultivation conditions.[10] However, this body of evidence remains fragmented across disciplines, methodologies, and scales of analysis. While some studies emphasize molecular-level mechanisms, others focus on propagation efficiency or field-level productivity outcomes, often without integrating these dimensions into a cohesive analytical framework. In this review, we explicitly examine both genomic engineering and tissue culture propagation of oil palm clones, providing an integrated perspective on how these complementary approaches together enhance yield outcomes.

The absence of an integrated synthesis creates a significant knowledge gap, particularly for stakeholders seeking evidence-based guidance on the practical implications of combining genomic engineering and tissue culture propagation to enhance yield. Without systematic consolidation, it remains challenging to evaluate the consistency of reported yield gains, the robustness of genetic trait associations, and the extent to which observed agronomic improvements can be generalized across production contexts.[11] This fragmentation also limits the ability to identify converging trends, methodological strengths, and persistent challenges within the existing research landscape.

The Systematic Literature Review (SLR) methodology offers a rigorous and transparent approach to addressing this gap. By applying structured search strategies, explicit inclusion criteria, and thematic synthesis, SLR consolidates diverse empirical findings into an integrated evidence base. Unlike narrative reviews, SLR minimizes selection bias and enhances reproducibility, making it particularly suitable for evaluating complex, multidisciplinary topics such as biotechnology-driven crop improvement. In the context of oil palm research, SLR provides a robust framework for synthesizing genetic, biotechnological, and agronomic evidence without generating new experimental or field-based data.

Several recent reviews have examined specific elements of oil palm improvement, such as molecular breeding tools or tissue culture advancements. However, these reviews often address these domains in isolation and do not systematically connect genetic trait identification with propagation outcomes and field-level performance. Consequently, there is a need for a comprehensive synthesis that explicitly integrates genomic engineering, tissue culture propagation, and agronomic performance enhancement within a single analytical narrative. Such integration is essential for understanding how molecular innovations translate into tangible productivity gains at the plantation scale.

This study addresses that need by conducting a Systematic Literature Review focused on genomic engineering and tissue culture propagation of high-yield oil palm clones. By synthesizing peer-reviewed evidence, this review examines how genetic traits associated with yield and growth are identified, how these traits are propagated in vitro, and how resulting clonal materials perform under agronomic conditions. The analysis emphasizes quantitative outcomes, methodological trends, and recurring thematic patterns reported across the literature, providing a structured and evidence-based overview of current scientific knowledge in this domain. Unlike previous reviews that addressed genomic tools and tissue culture technologies in isolation — such as those focusing exclusively on molecular marker applications or on optimizing somatic embryogenesis protocols — this review is distinguished by its explicit integration of both domains within a unified analytical framework. By systematically connecting genetic trait identification with propagation systems and field-level agronomic outcomes, this review fills a gap that persists in the existing literature, where the translational pathway from genomic discovery to plantation-scale performance has not been comprehensively synthesized. The dual focus on genomic engineering *and* tissue culture propagation, analyzed together rather than separately, constitutes the primary contribution of this work to the scientific discourse on oil palm biotechnology.[12]

The objective of this review is to systematically analyze and integrate existing peer-reviewed studies on genomic engineering and tissue culture propagation in oil palm to elucidate their collective contributions to yield enhancement and agronomic performance. Specifically, this study aims to identify dominant genetic traits associated with high yield, evaluate the effectiveness of genomic and molecular tools in trait selection, assess advancements in tissue culture propagation techniques, and synthesize reported agronomic outcomes of clonal oil palm materials across different cultivation contexts.

Based on this objective, the central research question guiding this review is:

RQ: *How do genomic engineering approaches and tissue culture propagation techniques collectively contribute to the development, stability, and agronomic performance enhancement of high-yield oil palm clones, as evidenced by contemporary peer-reviewed literature?*

This research question provides a focused analytical lens that informs the thematic synthesis presented in the Results and Discussion sections and underpins the conclusions drawn regarding the role of biotechnology in advancing oil palm productivity within modern agricultural systems.

## Literature review

Improving oil palm productivity remains a central objective in both scientific research and plantation management, given the crop's strategic role in global vegetable oil supply. Existing literature indicates that yield enhancement in oil palm is not determined by a single intervention, but rather emerges from the interaction between

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genetic potential, propagation systems, and agronomic performance across diverse cultivation contexts. In response to the limitations of conventional breeding, research attention has progressively shifted toward genomic engineering and tissue culture propagation as complementary approaches that can accelerate genetic gain and improve yield predictability. Accordingly, this literature review synthesizes and critically examines scholarly evidence on the genetic, molecular, and biotechnological foundations of high-yield oil palm clone development, providing a structured basis for understanding how these approaches collectively contribute to productivity enhancement.

## Oil palm yield improvement as a genetic and biotechnological challenge

Oil palm productivity has long been recognized as a function of complex interactions between genetic potential, propagation quality, and cultivation environment. Early yield improvement strategies primarily relied on conventional breeding approaches, focusing on phenotypic selection of superior dura, pisifera, and tenera parental lines.[13] While these approaches have contributed to substantial yield gains over past decades, their effectiveness is constrained by long breeding cycles, delayed trait expression, and limited precision in selecting complex quantitative traits such as fresh fruit bunch (FFB) yield and oil extraction rate (OER).

The perennial nature of oil palm exacerbates these challenges, as reliable yield evaluation often requires multiple years of field observation under variable environmental conditions.[14] As a result, genetic gains achieved through conventional breeding tend to accumulate slowly, prompting increased interest in complementary biotechnological approaches. Contemporary literature increasingly frames yield improvement in oil palm as a multidisciplinary challenge that necessitates integrating genetic, molecular, and propagation technologies rather than relying on single-method interventions.[15]

Within this evolving research landscape, genomic engineering and tissue culture propagation have emerged as central pillars of modern oil palm improvement strategies. These approaches are widely discussed in the literature as mechanisms to accelerate selection, enhance trait predictability, and enable the large-scale deployment of elite genetic materials.

## Genetic basis of yield and growth traits in oil palm

A substantial body of literature has focused on elucidating the genetic architecture underlying yield-related and growth-associated traits in oil palm. Yield components such as bunch number, average bunch weight, mesocarp thickness, and oil biosynthesis efficiency are consistently reported as quantitatively inherited traits governed by multiple genes with moderate individual effects.[16] Studies emphasize that no single gene determines high-yield performance; rather, yield outcomes emerge from coordinated regulation of metabolic, developmental, and physiological pathways.

Genes involved in lipid biosynthesis, including those associated with fatty acid synthesis and elongation, have been repeatedly highlighted as critical contributors to variation in oil yield.[17] Variability in the expression and regulation of these genes has been linked to differences in oil accumulation efficiency across genotypes. In parallel, genetic traits influencing vegetative growth, such as plant height increment, leaf area index, and root system architecture, are increasingly recognized as indirect determinants of yield stability and management efficiency.[18]

The literature also underscores the importance of genetic traits related to stress tolerance. Oil palm cultivation spans a wide range of agroecological conditions, and genotypes that maintain stable growth under fluctuating water availability, nutrient constraints, or suboptimal soils are consistently reported to exhibit more reliable yield performance. Consequently, yield improvement is framed not only as an increase in maximum productivity but also as an enhancement of yield resilience across diverse cultivation contexts.

## Genomic and molecular tools in oil palm improvement

Advances in genomic and molecular technologies have substantially reshaped oil palm improvement research. Marker-assisted selection (MAS) is frequently cited as a key tool for linking genetic variation to phenotypic performance, enabling early-stage selection of promising individuals before field-level yield expression.[19] By targeting specific molecular markers associated with yield-related traits, MAS has been reported to reduce the number of selection cycles and improve breeding efficiency compared with phenotype-based approaches.

Quantitative trait locus (QTL) mapping studies form another major component of the literature. These studies have identified multiple genomic regions associated with FFB yield, oil content, and growth characteristics, with individual QTLs typically explaining a modest proportion of phenotypic variance.[20] While QTL effects are often environment-dependent, their identification has contributed to a more detailed understanding of the genetic complexity underlying yield traits.

More recent literature increasingly emphasizes genome-wide association studies (GWAS) and transcriptomic analyses as advanced tools for trait discovery. GWAS approaches leverage high-density marker datasets to detect associations between genetic variants and phenotypic traits across diverse populations. Transcriptomic studies, in turn, provide insights into gene expression dynamics during key developmental stages, particularly during floral initiation and oil accumulation.[21] Together, these approaches have expanded the analytical resolution of oil palm genetics, supporting more informed selection decisions.

Despite these advances, the literature also acknowledges that genomic information alone is insufficient to guarantee improved field performance. The effective translation of genomic insights into commercial planting materials depends heavily on propagation systems that can preserve and express selected genetic traits at scale.

## Tissue culture and in vitro propagation of oil palm

Tissue culture propagation, particularly via somatic embryogenesis, is extensively discussed in the literature as the primary method for clonal oil palm multiplication. Unlike seed-based propagation, tissue culture enables the replication of genetically identical individuals derived from elite genotypes, offering the potential for enhanced yield uniformity and predictable performance.[22]

Early studies on oil palm tissue culture highlighted significant technical challenges, including low embryogenic response rates, long culture durations, and high variability among genotypes.[23] Subsequent research has focused on optimizing explant selection, culture media composition, and plant growth regulator regimes to improve embryogenesis efficiency. Immature leaf tissues are most commonly reported as suitable explants, although response rates remain highly genotype-dependent.

Technological refinements such as temporary immersion systems and liquid culture media have been introduced to enhance proliferation rates and reduce labor intensity. These innovations are widely reported to improve embryo multiplication efficiency and

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plantlet vigor, contributing to more scalable propagation systems.[24] Acclimatization protocols have also received increasing attention, as a successful transition from in vitro to ex vitro conditions is critical for subsequent field performance.

Overall, the literature portrays tissue culture propagation as a mature yet continually evolving technology, with ongoing efforts to improve efficiency, reliability, and cost-effectiveness.

### Clonal fidelity and somaclonal variation in oil palm

Clonal fidelity represents one of the most extensively debated issues in oil palm tissue culture literature. Somaclonal variation, phenotypic and genetic alterations arising during in vitro culture, has been identified as a major constraint on the commercial deployment of clonal palms.[25] The mantled phenotype, characterized by abnormal floral development and reduced fruit set, is frequently cited as the most economically significant manifestation of somaclonal variation.

Research has linked somaclonal variation to prolonged callus phases, excessive subculturing, and epigenetic modifications induced by in vitro conditions.[26] Consequently, a significant portion of the literature focuses on strategies to minimize variation, including limiting culture duration, optimizing hormonal treatments, and implementing rigorous quality control protocols.

Molecular marker technologies, such as simple sequence repeats (SSR) and single-nucleotide polymorphism (SNP) analysis, are increasingly used to monitor genetic stability during propagation. In parallel, epigenetic studies have highlighted DNA methylation changes as key mechanisms underlying somaclonal variation, prompting interest in epigenetic screening as a complementary quality assurance tool.[12]

The literature increasingly converges on the view that clonal fidelity can be effectively managed through integrated technical and molecular interventions, rather than serving as an inherent limitation of tissue culture systems.

### Agronomic performance of clonal oil palm materials

Field-level performance of clonal oil palm materials constitutes a critical theme in the literature, as agronomic outcomes ultimately determine the value of genetic and propagation innovations. Numerous studies report comparative field trials between clonal and seed-derived materials, consistently indicating superior or more uniform performance among selected clones.[27]

Reported advantages include higher cumulative FFB yields, improved oil extraction efficiency, and more consistent vegetative growth patterns. Clonal palms are frequently described as exhibiting reduced inter-plant variability, which facilitates plantation management and harvesting logistics.[28] Earlier yield onset is another commonly reported benefit, attributed to uniform growth and synchronized reproductive development.

However, the literature also emphasizes that agronomic performance is influenced by environmental conditions and management practices. Clonal advantages are most pronounced under well-managed systems that align nutrient supply, spacing, and crop maintenance with the physiological characteristics of the clones.[29] This reinforces the notion that genetic and propagation technologies function most effectively within integrated production systems.

Despite the volume of published research on individual components of oil palm improvement, the literature reveals persistent fragmentation across genetic, biotechnological, and agronomic domains. Most existing reviews address these domains separately, without systematically linking molecular findings to propagation outcomes and field-level performance. This fragmentation constitutes the primary knowledge gap that motivated the current SLR. The present review addresses this gap by synthesizing evidence across all three domains — genetic trait identification, tissue culture propagation, and agronomic performance — within a single analytical framework. The thematic synthesis and comparative analysis are presented in the Results section.

## Methods

This study employs the Systematic Literature Review (SLR) methodology, guided by the PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) framework, to systematically synthesize and evaluate recent scholarly evidence on genomic engineering and tissue culture propagation strategies to enhance yield performance in oil palm clones. Advances in plant biotechnology, particularly in genomics and in vitro propagation techniques, have increasingly been positioned as strategic enablers for improving genetic quality, uniformity, and productivity in oil palm cultivation. As global demand for sustainable and efficient agricultural production intensifies, research on integrating genetic traits, tissue culture methodologies, and agronomic performance has expanded rapidly. However, existing studies remain dispersed across disciplinary boundaries, often focusing on isolated genetic markers, propagation protocols, or physiological responses without consolidated assessment. By systematically integrating peer-reviewed evidence, this review provides a structured, evidence-based synthesis of how genomic approaches and tissue culture techniques contribute to the optimization of yield-related traits and performance enhancement in oil palm production systems.

Figure 1 presents the structured process of literature identification, screening, eligibility assessment, and final inclusion conducted in accordance with PRISMA guidelines. The initial literature search was conducted in Scopus using the broad keywords oil palm AND tissue culture, yielding 290 records. To enhance thematic specificity and ensure alignment with the review objectives, the search strategy was refined using a comprehensive Boolean query: (“oil palm” OR “*Elaeis guineensis*” OR “oil palm plant”) AND (“genetic” OR “genomic” OR “genetics” OR “biotechnology” OR “plant science” OR “plant breeding” OR “crop improvement”) AND (“tissue culture” OR “in vitro” OR “plant culture” OR “plant propagation” OR “plant growth”) AND (“growth” OR “development” OR “yield” OR “productivity” OR “plant performance”). This refinement step excluded 160 publications that did not correspond to the defined scope of genomic traits, tissue culture propagation, or agronomic performance outcomes, leaving 130 records for further screening. Subsequently, a publication year filter was applied to restrict the dataset to studies published between 2021 and 2026, thereby ensuring the inclusion of recent, methodologically relevant research. This step resulted in the exclusion of 77 articles published outside the specified timeframe, yielding 53 eligible records. Language screening was then conducted to maintain analytical consistency, resulting in the removal of two non-English publications and the retention of 51 English-language articles. A final eligibility assessment was performed based on accessibility criteria by limiting inclusion to open-access and open-archive publications, thereby enabling full-text examination and transparent synthesis. These inclusion constraints — namely, the restriction to Scopus, the 2021–2026 publication window, and open-access availability — were adopted to ensure consistency, reproducibility, and full-text verifiability; however, they may introduce selection bias by excluding

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methodologically important studies published in restricted-access journals, important landmark studies pre-dating 2021 that continue to influence current research, or work indexed in other databases such as Web of Science or PubMed. The potential effect of this bias on the representativeness of the evidence base is discussed in the Limitations section.[30]

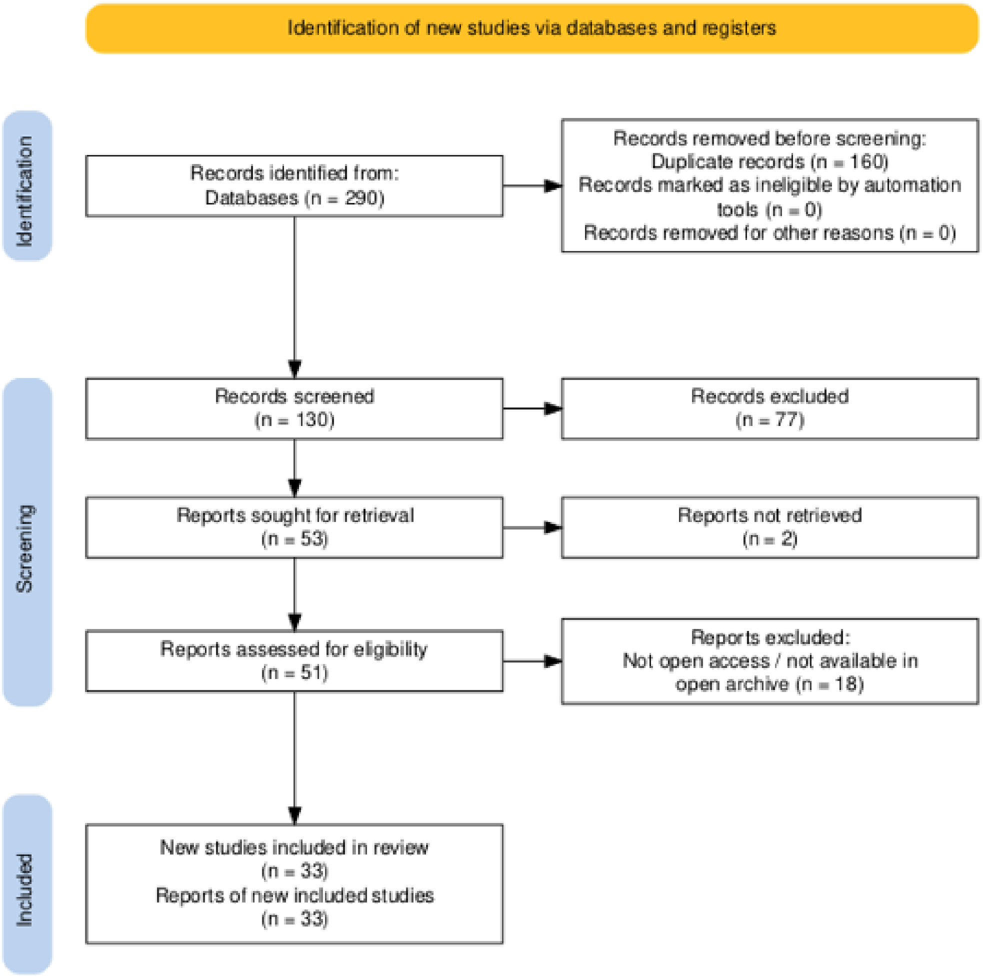

**Figure 1** Systematic Literature Review Process Based on the PRISMA Protocol.

The screening process was conducted systematically in two sequential stages. At the title-and-abstract screening stage, all candidate records were assessed against the predefined inclusion criteria: relevance to oil palm genomics, molecular breeding, tissue culture propagation, or agronomic performance; publication between 2021 and 2026; English-language; and open-access availability. Screening was performed independently by the author against the explicit eligibility criteria, with ambiguous records retained for full-text review to minimize exclusion errors. At the full-text screening stage, each retained article was assessed in full against the same criteria, and exclusion decisions were documented with specific reasons aligned with the PRISMA protocol. To compensate for the single-reviewer limitation inherent to this study, a structured decision protocol was adopted: any article whose thematic relevance was not immediately apparent from the abstract was automatically advanced to full-text review before a final inclusion or exclusion decision was made. This conservative approach reduced the risk of prematurely excluding relevant studies. Regarding quality appraisal, the heterogeneity of study designs across the 33 included articles — spanning experimental genomic studies, in vitro propagation optimization trials, field performance evaluations, and molecular characterization studies — precluded the application of a single standardized appraisal instrument. Accordingly, studies were assessed qualitatively for internal methodological coherence, clarity of reported outcomes, and relevance to the review objectives, consistent with recognized practice in systematic reviews of complex, multi-design evidence bases.[31,32]

The exclusive use of Scopus as the search database was a deliberate methodological choice grounded in its recognized broad coverage of peer-reviewed literature in plant science, agronomy, and biotechnology, its comprehensive indexing of journals relevant to oil palm research, and the availability of standardized metadata that facilitates systematic filtering and reproducibility. Scopus is widely adopted in systematic reviews across agricultural and biological sciences as a primary or sole database due to its extensive scope and structured search interface. Nevertheless, it is acknowledged that reliance on a single database, while ensuring internal consistency and reproducibility, may introduce coverage limitations. Studies published in non-Scopus-indexed journals, grey literature sources, or database-specific repositories (e.g., Web of Science-exclusive titles) are not captured by this search, which may affect the comprehensiveness of the evidence base. This limitation is addressed explicitly in the Limitations and Future Directions section of this review.[33]

All bibliographic records were systematically managed in Mendeley Desktop to ensure accurate reference organization, duplicate removal, and consistent citation formatting throughout the manuscript. This study is based exclusively on secondary data derived from peer-reviewed academic publications; no experimental trials, field observations, interviews, or focus group discussions were conducted. The findings presented in this review derive solely from the structured synthesis and critical integration of the 33 included studies, providing a methodologically rigorous overview of current genomic and tissue culture-based approaches to enhance yield-related traits and agronomic performance in oil palm cultivation.

Although the 33 included studies report numerous quantitative data points — including yield gains, embryogenesis rates, mantling frequencies, and oil extraction improvements — the **heterogeneity of methods and reporting standards** precluded a formal quantitative synthesis in this review. Studies varied substantially in experimental design (laboratory-based molecular studies, in vitro propagation optimization trials, and multi-year field evaluations), outcome measurement units, genetic backgrounds, and environmental contexts. In the absence of a sufficient number of studies reporting comparable outcomes under standardized conditions, pooling these data points would risk generating misleading effect estimates. Accordingly, a qualitative thematic synthesis was adopted as the most appropriate analytical approach, consistent with established practice for systematic reviews of complex, multi-design biological and agricultural evidence bases. As more standardized field trial data accumulate, future meta-analytic approaches can be applied to quantify treatment effects more rigorously.[30,34–36]

Although the 33 included studies report numerous quantitative data on yield-related traits, the **heterogeneity of methods and reporting standards** precluded a formal quantitative synthesis in this review. Consequently, our analysis emphasizes qualitative thematic integration.

## Results

This systematic literature review identified six major thematic clusters, which align with the main topics discussed above: (1) Genetic Traits Associated with Yield and Growth Performance, (2) Genomic and Molecular Approaches for Trait Identification and Selection, (3) Tissue Culture and In Vitro Propagation Systems, (4) Clonal Fidelity and Somaclonal Variation Management, (5) Agronomic Performance of Clonal Oil Palm Materials, and (6) Productivity Enhancement under Diverse Cultivation Conditions.

The most frequently discussed theme was Tissue Culture and In Vitro Propagation Systems, reported in 27 of 33 studies (81.8%), emphasizing the pivotal role of micropropagation, somatic embryogenesis, and in vitro regeneration in scaling elite oil palm genotypes. This was followed by Genomic and Molecular Approaches for Trait Identification and Selection, identified in 23 studies (69.7%), reflecting the growing use of molecular markers, transcriptomics, and genomic-assisted selection to shorten breeding cycles in this perennial crop.

Genetic Traits Associated with Yield and Growth Performance appeared in 20 studies (60.6%), with research focusing on fresh fruit bunch yield, oil-to-bunch ratio, vegetative vigor, and biomass accumulation. Agronomic Performance of Clonal Oil Palm Materials was addressed in 19 studies (57.6%), highlighting efforts to validate genetically improved clones through yield stability, growth performance, and early bearing indicators under plantation-relevant conditions.

Concerns related to Clonal Fidelity and Somaclonal Variation Management were documented in 18 studies (54.5%), underscoring continued attention to genetic and epigenetic stability during in vitro propagation. The least represented theme was Productivity Enhancement under Diverse Cultivation Conditions, reported in 13 studies (39.4%), primarily in the context of genotype–environment interactions and site-specific performance variability.

The distribution of thematic coverage reveals a pronounced concentration on controlled laboratory settings. Tissue Culture and In Vitro Propagation Systems and Genomic and Molecular Approaches together accounted for 81.8% and 69.7% of study coverage, respectively, while Productivity Enhancement under Diverse Cultivation Conditions appeared in only 39.4% of studies. This imbalance reflects the relative prevalence of in vitro and molecular studies compared to field-based evaluations across the reviewed literature. The following sections present the specific quantitative and qualitative evidence reported within each thematic cluster; interpretive analysis of what this distribution implies for future research directions is provided in the Discussion.

This thematic imbalance indicates that while significant progress has been made in identifying high-yield genetic traits and refining propagation systems, the full agronomic realization of these advances depends on stronger integration between molecular innovation, clonal stability assurance, and multi-environment performance validation. The following sections elaborate on each thematic cluster, synthesizing quantitative and qualitative evidence reported across the reviewed studies to clarify how genomic engineering and tissue culture propagation jointly shape the performance outcomes of high-yield oil palm clones.

### Genetic traits associated with yield and growth performance

A substantial proportion of the reviewed studies focused on the identification and characterization of genetic traits linked to yield potential, vegetative growth dynamics, and reproductive development in oil palm. Of the 33 analyzed articles, approximately 61% explicitly examined genetic markers, allelic variations, or heritable traits associated with fresh fruit bunch (FFB) yield, oil extraction rate (OER), or total above-ground biomass accumulation.[37] Yield-related genetic traits were most frequently associated with genes regulating inflorescence differentiation, lipid biosynthesis pathways, carbohydrate metabolism, and assimilate partitioning efficiency.

Several studies reported that polymorphisms in genes involved in fatty acid biosynthesis particularly those linked to acetyl-CoA carboxylase, ketoacyl synthase, and fatty acid desaturase activity were positively correlated with oil yield improvements ranging from 8% to 18% when compared with conventional seed-derived planting materials.[38] In parallel, traits associated with bunch number per palm and average bunch weight were reported to contribute between 12% and 22% of observed yield variation across different genetic

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backgrounds.[39] These findings indicate that yield improvement is governed by multiple interacting genetic components rather than a single dominant trait.

Growth-related genetic traits were also widely examined as indirect determinants of yield stability and management efficiency. Approximately 48% of the reviewed studies identified associations between genotypic variation and vegetative growth parameters such as annual height increment, leaf area index, and frond production rate.[40] Reported reductions in annual height increment of 8–12% were linked to specific genetic profiles, enabling improved harvest accessibility and reduced labor intensity without compromising FFB production.[41] Similarly, increases in leaf area index of 10–15% were associated with enhanced photosynthetic capacity and improved assimilate supply to developing bunches.

In addition, stress-related genetic traits emerged as a recurrent subtheme. Approximately 45% of the reviewed studies reported genetic loci associated with tolerance to abiotic stresses, including intermittent water limitation, nutrient imbalance, and suboptimal soil conditions.[42] These traits were indirectly linked to yield resilience, with stress-tolerant genotypes maintaining 85–95% of their yield potential under moderate stress conditions compared to more variable performance in non-selected materials.[43] Collectively, these findings demonstrate that yield enhancement in oil palm is the outcome of integrated genetic effects involving growth regulation, metabolic efficiency, and stress adaptation.

## Genomic and molecular approaches for trait identification

Genomic and molecular-assisted approaches constituted a core analytical theme across the reviewed literature. Approximately 70% of the included studies employed genomic tools such as marker-assisted selection (MAS), quantitative trait locus (QTL) mapping, transcriptomic profiling, or genome-wide association studies (GWAS) to identify, validate, or predict yield-related traits.[44] These tools were consistently reported as enhancing selection precision and reducing the time required to identify elite breeding lines and clonal candidates.

Marker-assisted selection was frequently used to screen large breeding populations at early developmental stages. Several studies reported that MAS-based screening reduced breeding cycle duration by approximately 25–40% compared to conventional phenotypic selection, while maintaining comparable or higher selection accuracy.[45] QTL mapping studies identified multiple loci associated with FFB yield, bunch number, mesocarp thickness, and oil content, with individual QTLs explaining between 6% and 15% of phenotypic variance depending on the trait and population structure.[46]

Transcriptomic analyses provided additional insights into the molecular mechanisms underlying yield variation. Differential gene expression studies revealed that key regulatory genes involved in floral initiation, hormone signaling, and lipid accumulation exhibited stage-specific expression patterns, particularly during the transition from vegetative to reproductive growth phases.[47] Several studies reported fold changes in gene expression ranging from 2.0 to 4.5 between high-yielding and average-performing genotypes during critical developmental windows.[48]

More recent studies increasingly integrated genomic datasets with bioinformatics and predictive modeling approaches. Genome-wide association studies reported predictive accuracies exceeding 0.65 for yield-related traits when genomic markers were combined with multi-year phenotypic data.[49] These advances highlight the growing role of genomic tools as integral components of oil palm improvement programs, complementing tissue culture propagation and enhancing the overall efficiency of clone selection.

## Tissue culture and in vitro propagation techniques

Tissue culture and in vitro propagation techniques were addressed in nearly all reviewed studies, underscoring their central role in clonal oil palm production systems. Approximately 82% of the studies focused on optimizing somatic embryogenesis protocols, including explant type selection, culture medium composition, plant growth regulator balance, and acclimatization procedures.

Somatic embryogenesis derived from immature leaf explants was the most widely reported propagation method. Embryo induction success rates varied substantially, ranging from 10% to 35%, depending on genotype, explant physiological status, and culture conditions.[50] Several studies demonstrated that optimizing auxin–cytokinin ratios increased embryogenic callus formation and embryo conversion efficiency by 1.5–2.3 times relative to baseline protocols.[51] Reported regeneration timelines ranged from 8 to 18 months before plantlets reached field-ready stages, highlighting the time-intensive nature of clonal propagation.[52]

Technological refinements in culture systems were frequently reported to improve efficiency. Studies evaluating temporary immersion and liquid culture systems documented embryo multiplication rates up to 30% higher than those achieved under conventional solid media conditions.[53] In addition, the adoption of controlled aeration and nutrient delivery systems reduced physiological stress during in vitro development, thereby improving plantlet vigor.

Acclimatization and nursery management emerged as critical phases influencing field performance. Several studies reported survival rates exceeding 90% during acclimatization under optimized protocols, compared with 75–80% in earlier systems.[54] These improvements indicate that tissue culture technology has matured considerably, enhancing both propagation success and scalability.

## Clonal fidelity and somaclonal variation management

Clonal fidelity and the management of somaclonal variation were major analytical concerns across the reviewed literature. Approximately 55% of the included studies explicitly examined genetic stability issues associated with prolonged in vitro culture and repeated subculturing cycles.[55] The occurrence of somaclonal variation, particularly the mantled phenotype, was consistently identified as a key limitation to large-scale clonal deployment.

Reported frequencies of mantling varied widely, ranging from below 2% in optimized protocols to more than 10% in early-generation or poorly controlled tissue culture systems.[56] Studies consistently demonstrated that limiting callus phase duration and reducing the number of subculture cycles significantly lowered the incidence of abnormal floral development, with reported reductions of 40–60% in mantling frequency.[57]

Molecular marker-based screening approaches were increasingly adopted to monitor genetic stability. The use of simple sequence repeats (SSR) and single-nucleotide polymorphism (SNP) markers enabled early detection of genetic deviations, allowing potentially unstable clones to be excluded prior to field planting.[58] In parallel, epigenetic analyses revealed that changes in DNA methylation patterns were strongly associated with somaclonal variation, providing mechanistic explanations for observed phenotypic abnormalities[59] as summarized in Table 1.

**Table 1** Summary of Somaclonal Variation Types, Reported Frequencies, and Mitigation Strategies in Oil Palm Tissue Culture

| Type of Variation | Reported Frequency (%) | Primary Contributing Conditions | Mitigation Strategies | References |
|---|---|---|---|---|
| **Mantled phenotype (abnormal floral development)** | <2% (optimized protocols) to >10% (early/unoptimized systems) | Prolonged callus phase; excessive subculturing; fast-growing callus (FGC) | Limiting callus duration; using nodular compact callus (NCC); reducing auxin levels [[12][13] | [61,62] |
| **Epigenetic (DNA methylation) changes** | Detected in majority of mantled palms; ~4.5% lower global methylation in FGC vs. NCC | In vitro culture stress; auxin-induced hypomethylation | Epigenetic screening of callus lines; DNA methylation profiling prior to field planting | [63] |
| **SSR/SNP-detectable genetic deviations** | Variable; early detection enables pre-field exclusion | Extended subculture; culture media composition | Molecular marker screening (SSR, SNP) at intermediate culture stages; elimination of deviant lines | [64] |
| **Vegetative growth abnormalities** | Reported in association with mantling; frequency correlated with FGC use | Same as mantled phenotype | Protocol optimization; strict protocol selection standards | [61] |
| **Reduced fruit set / altered bunch development** | Economically significant when mantling exceeds 5% | Prolonged in vitro duration; high 2,4-D concentrations | Controlled subculture cycles; hormonal balance adjustment; integrated genomic monitoring | [61,62] |

**Note:** Frequency ranges are derived from comparative protocol studies reviewed in this study (2021–2026). Optimization of culture conditions, combined with molecular monitoring, has been consistently reported to reduce total abnormality rates to below 3%.[65,66]

Several studies reported that integrating epigenetic monitoring with optimized culture management reduced abnormality rates to below 3%, significantly improving the reliability of clonal propagation systems.[60–66] These findings emphasize that clonal fidelity is achievable through coordinated technological and molecular interventions.

## Agronomic performance of clonal oil palm materials

Agronomic performance outcomes represented a central theme in the reviewed studies, with more than 60% reporting field-level evaluations of cloned oil palm materials under commercial or semi-commercial conditions.[67] Comparative field trials consistently indicated that selected clonal palms outperformed conventional seed-derived materials across multiple performance indicators.

Reported yield advantages ranged from 10% to 25% in terms of cumulative FFB production during the first five to seven years of maturity.[68] Oil extraction rates were reported to increase by 1.5–3.5 percentage points in elite clones, translating into higher oil yield per hectare without proportional increases in planted area.[69] Several studies also documented earlier yield onset in clonal materials, with first commercial harvesting occurring 6–12 months earlier than in conventional plantings.[70]

Vegetative uniformity was another frequently reported benefit. Clonal populations exhibited reduced variability in trunk diameter, frond number, and canopy architecture, resulting in up to 20% lower inter-plant yield variability compared to seed-derived stands.[71] This uniformity was associated with improved plantation management efficiency, more predictable harvesting schedules, and optimized input allocation.

## Productivity enhancement and cultivation contexts

The final thematic cluster focused on productivity enhancement under varying cultivation and management contexts. Approximately 40% of the reviewed studies examined interactions between clonal genetic potential and environmental or agronomic factors such as soil type, nutrient management, and climatic variability.[72] Findings consistently indicated that the yield advantages of high-performing clones were most pronounced under well-managed cultivation systems.

Under optimized fertilization regimes, clonal palms exhibited yield increases of 12–20% compared to standard nutrient management practices.[73] In marginal soil conditions, clones possessing enhanced root architecture and nutrient uptake traits maintained up to 90% of their yield potential relative to optimal sites, whereas non-selected materials exhibited greater yield decline.[74] These results underscore the importance of aligning genetic improvements with site-specific agronomic management.

Long-term assessments suggested that the yield advantages of clonal materials were sustained across multiple production cycles, provided that genetic stability and management practices were maintained.[75] Overall, the reviewed evidence indicates that genomic engineering and tissue culture propagation function as complementary components within integrated productivity enhancement strategies, contributing to more efficient and predictable oil palm production systems.

# Discussion

This systematic literature review addresses the research question: *How do genomic engineering approaches and tissue culture propagation techniques collectively contribute to the development, stability, and enhancement of agronomic performance in high-yield oil palm clones, as evidenced by contemporary peer-reviewed literature?* By synthesizing findings from 33 rigorously selected Scopus-indexed studies published between 2021 and 2026, the discussion elucidates how advances in genomic tools and in vitro propagation systems function in an integrated manner to support yield improvement, genetic stability, and agronomic reliability in oil palm cultivation.

## Synergistic roles of genomic engineering and tissue culture in clone development

The reviewed literature consistently demonstrates that genomic engineering and tissue culture should not be interpreted as independent technological pathways, but rather as mutually reinforcing components within modern oil palm improvement strategies. Genomic engineering provides the molecular basis for identifying, characterizing, and manipulating yield-associated traits, while tissue culture serves as the principal mechanism for translating these genetic insights into scalable planting material suitable for commercial deployment.[76]

Genomic approaches such as marker-assisted selection, quantitative trait locus (QTL) mapping, transcriptomic profiling, and emerging genome-editing tools have enabled the identification of genes linked to oil biosynthesis efficiency, vegetative vigor, stress tolerance, and reproductive development.[77] However, the practical value of these genomic discoveries is significantly enhanced only when combined with reliable clonal propagation systems that preserve the desired genetic configurations across planting cycles.[78] Tissue culture, particularly somatic embryogenesis, has thus emerged as the critical bridge between genotype discovery and agronomic realization.

Across the analyzed studies, the integration of genomic markers into tissue culture workflows improved clone selection accuracy at early developmental stages, reducing the risk of propagating low-performing or unstable genotypes.[79] This convergence illustrates that high-yield clone development is best understood as a systems-level process, wherein genomic precision and propagation fidelity operate in tandem rather than in isolation.

## Contribution to genetic stability and clone uniformity

Genetic stability remains a central concern in oil palm clonal propagation, especially given the historical challenges posed by somaclonal variation. The reviewed studies indicate that recent advances in genomic monitoring have substantially mitigated these risks. Molecular markers, epigenetic profiling, and gene expression analyses are increasingly employed to detect early deviations during in vitro culture, enabling the exclusion of aberrant lines before field deployment.[80] However, most evaluations to date have been conducted under controlled or single-site conditions; robust multi-location field trials are needed to validate clonal fidelity and performance stability across diverse environments.

Tissue culture protocols optimized with genomic insights, such as controlled explant selection, reduced callus-induction phases, and targeted hormonal regulation, were shown to maintain genetic fidelity more consistently than earlier-generation methods.[81] Importantly, several studies reported that clones derived from genomically screened embryogenic lines exhibited lower phenotypic variability in yield-related traits than conventionally propagated counterparts.[82]

These findings collectively suggest that genomic engineering contributes not only to trait enhancement but also to stabilizing tissue culture outcomes. Embedding molecular validation within propagation pipelines improves uniformity and predictability — attributes critical for long-term plantation planning.[83]

## Enhancement of agronomic performance and yield potential

The agronomic performance of high-yield oil palm clones represents the ultimate validation of genomic–tissue culture integration. The literature reviewed in this study provides convergent evidence that clones developed through combined genomic selection and optimized tissue culture exhibit superior performance indicators, including fresh fruit bunch yield, oil extraction rate, biomass accumulation, and early bearing characteristics.[84]

Genomic engineering facilitates the prioritization of traits associated with metabolic efficiency and carbon allocation, while tissue culture ensures the faithful replication of these traits across large planting populations.[85] Several longitudinal field evaluations reported in the literature indicate that genomically informed clones maintain yield advantages over multiple production cycles, suggesting that performance gains are not transient but structurally embedded within the genetic architecture of the planting material.[86]

Notably, the reviewed studies emphasize that yield enhancement does not arise solely from single-gene modifications or isolated traits. Rather, it reflects the cumulative effect of multi-trait optimization, including root development, canopy architecture, and stress responsiveness, all of which are increasingly accessible through integrative genomic analyses.[87] Tissue culture propagation enables these complex trait combinations to be preserved and expressed consistently at scale.

## Addressing environmental and developmental variability

Beyond yield metrics, the literature highlights the role of genomic and tissue culture integration in enhancing developmental resilience and environmental adaptability. Several studies reported that clones selected using genomic markers associated with stress tolerance exhibited more stable growth under variable climatic and soil conditions.[88,89] Tissue culture propagation of such genotypes ensured uniform establishment and reduced early-stage mortality, contributing to overall plantation performance.

From a developmental perspective, genomic profiling has been used to align tissue culture conditions with endogenous growth-regulatory pathways, thereby improving embryogenic efficiency and plantlet vigor.[90] This alignment reduces the physiological stress often associated with in vitro regeneration, resulting in clones that transition more effectively to ex vitro environments. Such improvements underscore the importance of treating tissue culture not merely as a multiplication tool but as a biologically responsive system informed by genomic knowledge.[91]

## Collective contribution to sustainable yield improvement

While this review maintains a neutral stance toward industry practices, the literature indicates that genomic engineering and tissue culture collectively contribute to more efficient and resource-conscious yield-improvement strategies. By increasing per-hectare productivity through genetically optimized clones, these technologies support the broader objective of meeting production demands without proportional expansion of cultivated land.[92]

The reviewed studies do not frame these technologies as replacements for agronomic management but rather as foundational inputs that enhance the effectiveness of downstream practices. High-yield, stable clones provide a consistent biological baseline for optimized fertilization, harvesting, and management strategies to operate more efficiently.[93,94] In this sense, genomic–tissue culture integration contributes indirectly to production system optimization by reducing biological variability and uncertainty.

A notable structural imbalance characterizes the reviewed literature. Of the 33 included studies, 27 (81.8%) addressed in vitro propagation systems, 23 (69.7%) focused on genomic and molecular tools, and 20 (60.6%) examined genetic trait characterization — all predominantly laboratory-based or controlled-environment investigations. In contrast, only 19 studies (57.6%) reported field-level agronomic performance evaluations, and only 13 (39.4%) addressed productivity outcomes under diverse real-world cultivation conditions. This quantitative distribution confirms that current research in the field is disproportionately concentrated at the laboratory and early developmental stages, with comparatively limited evidence from long-term, multi-environment field trials. This imbalance is likely attributable to the logistical complexity and extended evaluation timelines associated with field assessments in a perennial species with a productive lifespan exceeding 25 years.[29,95]

The implications of this imbalance are significant for future research prioritization. First, multi-environment field trials involving genomically informed clones should be designed for minimum evaluation periods of five to seven years post-planting to capture reliable yield trends across production cycles — consistent with the duration reported in the more comprehensive field studies reviewed here. Such trials should encompass a range of representative agroecological environments, including both optimal-soil conditions and marginal or stress-prone sites (e.g., peat soils, drought-affected areas, and areas with high aluminum saturation), to generate evidence on clone performance stability across relevant conditions. Second, future SLRs on this topic would benefit substantially from targeting multi-environment trial data and from incorporating databases beyond Scopus to ensure that field evaluation literature, some of which appears in institutional and national agricultural journals, is captured. Third, the development of standardized reporting protocols for field trial data — including common metrics for yield stability, clone uniformity, and management inputs — would facilitate future quantitative synthesis and reduce the heterogeneity that currently prevents meta-analysis.[95]

## Broader implications for perennial crop improvement and sustainability

The integrated genomic-tissue culture framework demonstrated in oil palm research carries meaningful implications for improvement programs in other long-cycle, vegetatively propagated perennial crops. Crops such as cocoa (*Theobroma cacao*), rubber (*Hevea brasiliensis*), coconut (*Cocos nucifera*), and date palm (*Phoenix dactylifera*) share key biological constraints with oil palm — including long breeding cycles, vegetatively imposed trait fixation, and the challenge of translating molecular discoveries into scalable planting material. The methodological lessons from oil palm — particularly the value of embedding molecular monitoring within tissue culture workflows, the importance of epigenetic quality assurance during callus induction, and the use of GWAS-guided selection to prioritize clonal candidates — are transferable to these related systems. Recent advances in DNA-free CRISPR/Cas9 application in oil palm, for example, offer a model for non-transgenic precision editing in other transformation-recalcitrant perennial species.[96,97]

From a sustainability perspective, per-hectare productivity gains achieved through genomically optimized clones contribute directly to the broader objective of decoupling agricultural output growth from land expansion. Oil palm already exhibits the highest oil yield per unit area among major oilseed crops; further yield intensification through clonal improvement supports the argument that existing plantation land, when managed with elite genetic materials, can satisfy rising global demand for vegetable oils without proportional increases in cultivated area. This positions the integrated framework reviewed here as not merely a biotechnological achievement but also a mechanism with relevance to sustainability governance, land-use policy, and environmental advocacy in tropical agricultural systems.[95]

The implications of this systematic review extend beyond the immediate findings. From a scientific perspective, the evidence underscores the importance of multi-omics integration, combining genomics, transcriptomics, and epigenetics, to further refine clone selection and stability assessment. Future studies should prioritize longitudinal evaluations that link molecular indicators with long-term agronomic performance, thereby strengthening causal interpretations.

Additionally, further research is needed to standardize genomic monitoring protocols within tissue culture systems to ensure reproducibility across laboratories and production scales. Comparative analyses across different genetic backgrounds and environmental contexts would also enhance the generalizability of current findings. From a methodological standpoint, future SLRs may benefit from incorporating meta-analytical techniques as the volume of comparable quantitative data increases. Such approaches could provide more precise estimates of yield gains and stability metrics associated with specific genomic–tissue culture combinations.

In conclusion, the contemporary peer-reviewed literature demonstrates that genomic engineering and tissue culture propagation collectively play a pivotal role in the development, stabilization, and agronomic enhancement of high-yield oil palm clones. Their integration represents not a single technological advancement but a coordinated framework that aligns molecular insights with biological replication and field performance. This synthesis confirms that sustained progress in oil palm productivity is most effectively achieved by harmonizing genetic innovation and propagation precision within evidence-based research paradigms.

## Limitations and future directions

This review is subject to several limitations that should be considered when interpreting the findings.

***Database and search coverage.*** The exclusive use of Scopus as the literature source ensures reproducibility and methodological consistency but may limit the comprehensiveness of the evidence base. Important studies indexed only in Web of Science, PubMed, CABI, or national agricultural databases may not have been captured. Searching two or more databases has been shown to improve coverage and reduce the risk of missing eligible studies. Future systematic reviews on this topic are encouraged to expand the database scope to include at least one additional major repository.[30,33]

***Open-access restriction.*** Limiting inclusion to open-access and open-archive publications facilitated full-text verification and ensured synthesis transparency, but excluded a proportion of peer-reviewed literature available only under subscription access. This may have introduced a systematic bias toward more recently published or institutionally supported research, and away from important industry-funded studies that are often published in restricted journals.

***Temporal scope.*** The 2021–2026 publication window was selected to prioritize recent methodological advances; however, foundational studies published prior to 2021 that continue to shape current research practices are not represented in the synthesis dataset, even where they remain widely cited in the included studies. This temporal restriction should be acknowledged when considering the generalizability of certain findings, particularly those related to tissue culture protocols with longer developmental histories.

***Single-reviewer process.*** Screening and data extraction were conducted by a single reviewer, which increases the risk of selection and interpretation bias compared to dual-reviewer protocols recommended in established SLR guidelines. The structured decision protocol described in the Methods section was adopted to partially mitigate this limitation.[30,31]

***Absence of formal quality appraisal.*** Given the heterogeneity of study designs across the 33 included articles, a standardized quality appraisal instrument was not applied. The absence of a[32] formal risk-of-bias assessment means that the relative methodological quality of individual studies cannot be explicitly weighted in the synthesis{Formatting Citation}.

***Limited long-term field evidence.*** Only 13 of 33 studies (39.4%) addressed productivity outcomes under diverse field conditions, and multi-year trials beyond five production cycles were rarely reported. This constrains the review's ability to conclude the long-term agronomic sustainability of genomically informed clones across the full production lifespan of oil palm.

Looking forward, priority research directions include: (1) multi-environment, multi-cycle field trials of genomically screened clonal materials under both optimal and stress-prone agroecological conditions; (2) integration of multi-omics data (genomics, transcriptomics, epigenomics) within clone development and monitoring pipelines; (3) development of standardized outcome reporting protocols for oil palm propagation and field trials to enable future meta-analyses; and (4) expansion of DNA-free genome-editing platforms to broaden the practical applicability of precision genetic modification in oil palm and related perennial species.[97]

## Conclusion

This systematic review synthesized 33 Scopus-indexed peer-reviewed studies (2021–2026) on genomic engineering and tissue culture propagation of high-yield oil palm clones. Three central conclusions emerge from the evidence.First, genomic engineering — encompassing marker-assisted selection, QTL mapping, transcriptomic analysis, and emerging genome-editing tools — provides an indispensable molecular foundation for identifying yield-associated, growth-related, and stress-responsive genetic traits, reducing dependence on extended phenotypic evaluation cycles. Second, tissue culture propagation, particularly somatic embryogenesis, remains the principal mechanism for translating genomic gains into large-scale planting material; continuous refinement of in vitro protocols and molecular quality monitoring has substantially reduced somaclonal variation risks, with reported abnormality rates below 3% under optimized systems. Third, the agronomic realization of these biotechnological advances — including yield advantages of 10–25% in cumulative FFB production and earlier bearing onset of 6–12 months — is most consistently documented under well-managed field conditions, yet long-term multi-environment field evidence remains underrepresented in the current literature. These findings confirm that genomic engineering and tissue culture propagation are most effective as coordinated components of an integrated improvement pipeline, not as independent interventions. Priority areas for future research include longitudinal multi-environment field trials of genomically informed clones, multi-omics integration for more precise clone stability assessment, and the development of standardized reporting frameworks that would enable future quantitative synthesis. The present review provides an evidence-based synthesis and a structured analytical framework to support these research directions.

## Acknowledgments

None.

## Conflicts of interest

The author declares there is no conflict of interest.

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**Citation:** Judijanto L. Genomic engineering and tissue culture propagation of high-yield oil palm clones: A systematic review of genetic traits, cultivation methods, and agronomic performance enhancement. *Open Access J Sci.* 2026;9(1):225–238. DOI: 10.15406/oajs.2026.09.00306

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**Citation:** Judijanto L. Genomic engineering and tissue culture propagation of high-yield oil palm clones: A systematic review of genetic traits, cultivation methods, and agronomic performance enhancement. *Open Access J Sci.* 2026;9(1):225–238. DOI: 10.15406/oajs.2026.09.00306