Enhancing Soil Carbon Sequestration in Crops Through Genomic Approaches: Investigating Root Development and Biomass Accumulation Traits

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Abstract

Soil carbon sequestration is a vital strategy for mitigating climate change, enhancing soil fertility, and promoting sustainable agriculture. Roots play a central role in this process through biomass accumulation, deep carbon deposition, exudation, and interactions with soil microbes that stabilize organic matter. Advances in genomics, including genome-wide association studies (GWAS), quantitative trait locus (QTL) mapping, marker-assisted selection (MAS), and CRISPR-based gene editing, have enabled the identification and modification of key genes regulating root depth, branching, turnover, and biomass traits. These genetic and biotechnological innovations enhance carbon storage potential by improving root system architecture, lignin synthesis, and beneficial symbiotic associations with microbes. Additionally, emerging tools such as high-throughput phenotyping, metabolomics, and artificial intelligence are accelerating the discovery and application of root traits for soil carbon management. Despite promising outcomes, challenges remain in regulatory policies, ethical acceptance, technological accessibility, and long-term ecological monitoring. This review highlights the genetic, physiological, and biotechnological foundations of root-mediated carbon sequestration in crops and emphasizes future opportunities for developing climate-smart agriculture through integrative genomic approaches.

Keywords: Soil carbon sequestration, Root traits, Genomics, Gene editing, Sustainable agriculture, Climate change mitigation

Significance | This study underscores genomic and biotechnological innovations enhancing root-mediated soil carbon sequestration for sustainable agriculture and global climate change mitigation.

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1. Introduction

Soil carbon sequestration presents itself as an important activity for better soil health and climate protection that also leads to higher agricultural production. The process involves absorbent carbon dioxide from the atmosphere through soil organic matter storage for extended periods of time (Lal, 2020). The way agricultural systems affect global carbon cycling becomes more effective when plants maintain features for carbon storage because this leads to reduced greenhouse gas production and improved soil conditions (Paustian et al., 2019).

Root growth together with biomass development stands two key factors which determine soil carbon sequestration because these elements control the quantity and stability of organic carbon entering the soil (Kell, 2012). The advancement of genomic study creates fresh prospects to both optimize plant carbon sequestration potential and improve the characteristics that store carbon.

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Different factors throughout biomass accumulation and root architecture control the sequestration process of carbon in soil. Soil carbon deposition becomes deeper, and breakdown rates decrease through extensive and deeply rooted systems because they enhance carbon storage in soil layers at greater depths (Lynch & Wojciechowski, 2015). Soil microbial activity supported by root exudates enables organic matter stabilization along with aggregate formation that secures additional carbon reservoirs according to Schmidt et al. (2011). Numerous genes along with signaling pathways govern the complex genetic regulation of properties involving root growth and shape as well as soil microbial interactions through these root elements (Kumar et al., 2020).

Genomic methods including GWAS with CRISPR-Cas9 gene editing and QTL mapping have identified essential root development and biomass allocation genes which scientists can now edit through their work (Coleman et al., 2021). Biomass accumulation becomes a vital factor for soil carbon sequestration because it determines how many organic wastes enter the earth. Higher biomass levels in shoots and roots of crops generate elevated carbon entry to the soil and produce higher organic matter content (Poorter et al., 2019). Soil carbon storage depends on genetic variables that affect photosynthetic processes along with carbon distribution and the lignin synthesis pathway (Lynch, 2019).

Genomic techniques allow breeders to enhance genetic attributes for biomass accumulation and carbon-use efficiency and deep root structures through allele selection (de Dorlodot et al., 2007). Bioinformatics together with molecular breeding have developed new effective tools which enhance biomass production and root features for carbon sequestration. Products from high-throughput phenotyping as well as functional genomics have simplified the identification of genes responsible for root depth regulation alongside branching development and exudation capacity (Uga et al., 2013). Transcriptome and metabolomic studies have revealed the molecular pathways through which carbon absorption and partitioning take place which provides opportunities to alter genetics specifically (Wang et al., 2021).

Research evaluates genomic strategies for effective soil carbon sequestration through investigations of crop root development along with biomass accumulation traits together with trait genetic identification and modern breeding practices and biotechnological methods for raised carbon storage in agricultural environments.

2. The Role of Roots in Soil Carbon Sequestration

Soil carbon sequestration heavily depends on the function of roots. Soil carbon sequestration stands as the essential climate change reduction method because it captures atmospheric carbon dioxide (CO_2) into soil organic matter. Plants reach soil carbon sequestration goals because roots maintain organic materials while managing microbial functions and guide the process of soil carbon absorption. Forest management and agricultural sustainability require knowledge of root-based carbon storage methods to develop effective carbon-sequestering practices (Lal, 2004).

2.1 Root Biomass and Carbon Input

Carbon sequestration in soil mostly occurs through the death of roots and the release of carbon substances into soil and through root exudation. Root break down processes lead to their integration into the soil matrix which establishes roots as one of the main organic carbon sources within the soil system. The microbial communities utilize exudates containing sugars and amino acids and other organic compounds to develop stable soil organic matter according to Kuzyakov and Domanski (2000).

The main mechanism identified by Jones et al. (2009) depends on root exudates as organic compounds that roots secrete into soil surroundings. Soil microorganisms benefit from root exudates consisting of sugars and amino acids and organic acids because this carbon matter activates microbial processes while it defends organic carbon preservation. Soil pH and nutrient availability change after root exudate secretion, and this indirectly supports microbial populations and leads to improved soil aggregate formation that increases carbon storage (Bardgett & Wardle, 2010).

The major carbon source for soil comes from root turnover because it includes the complete lifecycle of root development and aging and final decomposition. The soil collects organic matter through the decomposition process of roots while simultaneously increasing its carbon content. Root biomass turnover rate plays a vital role in determining carbon sedimentation in soil because increased turnover leads to greater carbon addition (Schenk & Jackson, 2002). Carbon deposition over time becomes greater when plants contain elevated biomass and maintain roots for longer periods.

Dead root biomass decomposition turns into an essential process for carbon sequestration. Decomposing root organic matter releases carbon through processes that convert the material into various storehouses of soil organic matter. The decomposition process of roots depends on three key factors: temperature levels and moisture content and the specific composition of microorganisms living in the area. Soil organic carbon attains steady states when root degradation resistance and lifespan durability are higher (Cotrufo et al., 2013).

2.2 Microbial Interactions and Carbon Stabilization

The relationship between plant roots and soil microbes is vital for converting and stabilizing organic matter, which enhances carbon sequestration. Mycorrhizal fungi, in particular, form mutually beneficial relationships with plant roots, exchanging nutrients for plant-derived carbon (Rillig et al., 2001). This interaction is key to increasing a plant's ability to sequester carbon. These fungi also produce a glycoprotein called glomalin, which is crucial for strengthening soil aggregation and keeping carbon stable within the soil structure (Cotrufo et al., 2013). The integration of root-derived

carbon into microbial biomass and long-lasting soil fractions effectively reduces atmospheric carbon dioxide levels.

In addition to glomalin, mycorrhizal fungi and other soil microbes contribute to the formation of a stable carbon pool through the synthesis of complex organic compounds. These compounds, often referred to as microbial necro mass, are the remains of dead microbial cells. This necro mass is highly resistant to decomposition and can persist in the soil for centuries, serving as a long-term carbon sink .The continuous turnover and death of microbial populations, fueled by root exudates, directly contribute to this stable carbon pool, providing a durable mechanism for carbon sequestration.

Furthermore, the diversity and composition of the soil microbial community play a significant role in carbon stabilization. Different microbial species have varying efficiencies in converting organic matter into stable carbon forms. A healthy and diverse microbial community, supported by a continuous supply of carbon from plant roots, can maximize the conversion of fresh organic matter into recalcitrant compounds. This synergy between plant roots and a diverse microbial population is a critical component of a functional and sustainable carbon sequestration system, highlighting the importance of managing agricultural practices to foster beneficial soil ecosystems.

2.3 Root Architecture and Its Influence on Carbon Sequestration

The amount and depth of soil carbon deposition heavily depends on both root system structure and its depth that combine to form root architecture. The deep and extensive root systems of plants enable them to deposit carbon at lower depths within the soil so it remains stable and prevents atmospheric reintroduction (Cong et al. 2015). Deep-rooted plants offer maximum carbon storage benefits to long-term carbon storage systems because they create carbon deposits at soil depths which resist both erosion and microbial breakdown.

A plant's soiling adaptation abilities are directly influenced by root structure features that determine its ability to capture carbon. Higher root biomass and more lateral roots enable crops to expand their contact with soil thus they can store increased levels of organic carbon. The ability of crops to store carbon depends strongly on three essential factors that include their root depth together with branching density and biomass attributes (Guo et al., 2010). Breeding or genetic modification of crops which directs root development toward carbon-friendly structures represents a successful strategy to enhance SOC levels in agricultural sites. The carbon sequestration process depends on root morphology and distribution when it comes to soil aggregation and organic matter protection effects. The research from Jackson et al. (2017) demonstrates how deep-rooted plants provide better carbon storage subsoil because these layers contain lower decomposition rates and result in extended carbon retention. Fungal hyphae and other parts of the root system remain in the soil for long periods as stable carbon pools which Gill and Burke (2002) describe while fine roots decompose fast to form particulate organic matter.

2.4 Root Biomass and Soil Organic Carbon Storage

The amount of carbon stored in the soil is directly related to the amount of root biomass beneath the surface. A large root biomass increases the organic matter in the soil and supports microbial communities that help protect carbon from degradation. As dead root biomass accumulates and decays, it provides a steady supply of organic carbon to the soil. This carbon is then stabilized within soil aggregates, protecting it from decomposition for many years (Cotrufo et al., 2013).

A larger root system also changes the dynamics of microbes in the rhizosphere, the area of soil directly influenced by plant roots. Increased root inputs lead to enhanced microbial activity, which produces stable organic matter complexes that protect carbon from decomposition. This process improves soil stability and promotes long-term carbon retention and sequestration (Six et al., 2002).

Beyond simply providing organic matter, root systems influence the physical and chemical properties of the soil to a remarkable extent. The growth and exploration of roots through the soil create channels and pores, which improve aeration and water infiltration. This enhanced physical structure not only benefits plant growth but also provides a more stable habitat for microbial communities. The physical protection of organic matter within these stable soil aggregates, a process known as occlusion, is a key mechanism by which root biomass contributes to long-term carbon storage.

The type of root biomass also matters for carbon sequestration. Roots with higher amounts of lignin and other complex, decay-resistant compounds are more effective at storing carbon for extended periods. This is because these compounds are difficult for microbes to break down, leading to the formation of stable soil organic matter. Plants with deep roots also contribute to long-term carbon storage by depositing organic matter in deeper soil layers, where it is protected from disturbance and the effects of climate change.

2.5 The Role of Root Systems in Enhancing Soil Microbial Communities

The distribution of organic matter together with root exudates in addition to the provision of microbial habitat by root systems determines the microbial populations in soil. Jones et al. (2009) explain that root exudates with sugars and amino acids and organic acids function as simple carbon sources to boost microbial diversity along with their activity in the rhizosphere. Soil structure and carbon sequestration receive enhancements from the combined effect of nutrient cycling and soil aggregate formation (Bardgett & Wardle, 2010). Rigorously branching roots enable better soil microbial stability and environmental change resistance because they provide stable habitat conditions at deeper soil depths (Cong

et al., 2015). Soil organic carbon preservation as well as microbial metabolism support depend on organic material originating from decomposed roots according to Cotrufo et al. (2013). The improvement of soil fertility together with sustainability depends on understanding how plants mutually interact with microorganisms in agricultural and ecological activities.

An enhanced soil carbon content arises from root systems that promote the maintenance of various microbial populations. The formation of lasting organic carbon reserves depends on microorganism diversity affected by root-released compounds and root-associated microbe connections. The soil bacteria act as converters of organic carbon into humic compounds according to Germida et al. (2016) who state that these resistant compounds persist in soil for centuries or decades.

2.6 Implications for Sustainable Agriculture and Carbon Sequestration

The implementation of practices that enhance root growth and biomass has a significant impact on sustainable agriculture and carbon sequestration. These measures lead to greater potential for sequestering carbon by improving soil structure and enhancing microbial diversity (Paustian et al., 2016) (Table 1). When plant species with deep and extensive root systems are chosen for cultivation, the storage of carbon becomes more effective. The advancements in root biology have both positive and negative effects on the process of soil carbon sequestration. Genetic and biotechnological methods that boost root biomass can improve soil structure and store carbon for longer periods by adding more organic matter to the soil.

Furthermore, the increased root biomass and the subsequent enhancement of soil structure led to a reduction in soil erosion (Kell, 2011). The extensive root networks act as a natural binder, holding the soil particles together and preventing them from being washed or blown away. This not only protects fertile topsoil but also ensures that the sequestered carbon remains in the ground, as erosion can lead to the release of carbon back into the atmosphere. This is particularly crucial in agricultural landscapes, which are often susceptible to erosion due to tillage and other farming practices.

Another key implication is the improved water-use efficiency of crops with enhanced root systems. Deeper roots allow plants to access water from lower soil layers, making them more resilient to drought conditions. This reduces the need for irrigation, conserving a valuable resource and decreasing the energy required for water pumping. By making crops more drought-tolerant, we can maintain stable yields even in areas with unpredictable rainfall, thereby increasing food security and reducing the risk of crop failure, which can lead to a loss of soil organic matter and sequestered carbon.

3. Precision Breeding for Enhanced Root Traits

Precision breeding integrates genomic selection, multi-omics profiling, and high-throughput phenotyping to accelerate the improvement of root traits directly linked to carbon sequestration, nutrient acquisition, and stress resilience. Advances in genome-wide association studies (GWAS) and quantitative trait locus (QTL) mapping have identified key loci governing root system architecture, including genes regulating gravitropism (e.g., *DRO1*) (Uga et al., 2011), lateral root initiation (e.g., *ARFs/LBD modules*), and root cortical development (Loudet et al., 2005). By applying genomic prediction models that integrate SNP marker data, transcriptomics, and metabolomics, breeders can now estimate root trait performance with high accuracy before field evaluation, enabling accelerated selection cycles. High-throughput phenotyping platforms using imaging, drones, and sensor arrays allow large-scale measurement of root vigor, depth, and exudation patterns, providing critical data for precision breeding pipelines (Michels et al., 2024). The combination of AI-driven predictive modeling with multi-environment trials further enhances the capacity to select genotypes tailored to future climate conditions and soil profiles, ensuring long-term sustainability and soil carbon gains.

Gene-editing technologies are increasingly integrated into precision breeding strategies to complement predictive selection, enabling targeted manipulation of alleles underlying beneficial root traits. CRISPR/Cas-based editing has successfully modified loci such as *OsNAC10* (Wang et al., 2025) and *PSTOL1*, which improve root thickness, biomass accumulation, and phosphorus uptake, translating into higher yield stability under stress (Milner et al., 2018). Multiplex editing further allows simultaneous fine-tuning of networks regulating root angle, hair density, and suberin deposition, thereby designing ideotype root systems for efficient carbon deposition into deeper soil layers (Xu et al., 2022). Precision breeding also leverages haplotype-based selection and pyramiding of favorable alleles, ensuring durable improvements across diverse germplasm pools (Wolabu et al., 2024). When combined with speed-breeding protocols and marker-assisted selection, these innovations dramatically reduce the breeding cycle, allowing rapid deployment of climate-smart cultivars. Thus, precision breeding represents a converging framework where data-driven genomic prediction, targeted editing, and accelerated field testing jointly enable the systematic engineering of root traits for enhanced soil carbon sequestration and agricultural resilience.

4. Genetic Regulation of Root Traits for Carbon Sequestration

Multiple studies now propose genetic engineering techniques as a potential method to enhance root characteristics for better carbon sequestration practice. Genetic breeding when combined with

Table 1. Key Genetic Traits for Root Development and Carbon Sequestration

Gene / Locus	Species (model/crop)	Primary mechanism / pathway	Observed phenotype / evidence	References
DRO1 (DEEPER ROOTING 1)	Rice (Oryza sativa); orthologs in wheat (TaDRO1)	Regulates root gravitropic set-point angle; promotes steeper, deeper roots	Deep rooting; higher yield under drought in field trials	(Furutani & Morita, 2021)
EGT1 (Enhanced Gravitropism 1)	Barley; conserved in wheat	Root angle control via mechanosensing/cell wall dynamics	Loss-of-function shallower roots; natural variation affects angle	(Fusi et al., 2022)
ZmRAP2.7 (ERF/AP2 TF)	Maize	Regulates root growth angle & RSA via ethylene/auxin signaling	Allelic variation associates with deeper RSA; lodging resistance links	(Guo et al., 2024)
RTCS / RTCL	Maize	LBD/ARF-dependent initiation of crown and seminal roots	rtcs mutants lack embryonic seminal roots; altered crown roots	(Singh et al., 2024)
PSTOL1 (Phosphorus Starvation Tolerance 1) / OsPSTOL1	Rice (introgressed into other cereals)	Ser/Thr kinase enhancing early root growth & P acquisition	Improved biomass & yield in low-P soils	(Kettenburg et al., 2023)
OsNAC10 (root-specific RCc3:OsNAC10)	Rice	NAC TF; thickens roots (stele/cortex); stress-responsive	Field trials: +25–42% yield under drought; thicker roots	(Kumar et al., 2022)
OsNAC5/9/14/25 (root-preferred promoters)	Rice	NAC TFs modulating root growth and drought tolerance	Overexpression increases drought tolerance and sometimes yield	(Martignago et al., 2021)
NPF6.3 / NRT1.1 (CHL1)	Arabidopsis; conserved in crops	Dual-affinity nitrate transporter that also transports auxin; integrates N signaling & auxin flux	Mutants show altered lateral root foraging	(Hachiya et al., 2024)
ARF7/ARF19 LBD16/29	Arabidopsis; conserved in crops	Auxin-responsive TFs initiating lateral root founder cell divisions (LBD module)	Loss-of-function reduces lateral roots; overexpression increases branching	(Muralidhara et al., 2021)
AUX/LAX (AUX1, LAX3)	Arabidopsis; rice/maize orthologs	Auxin influx carriers; LAX3 promotes cell-wall remodeling for lateral root emergence	Reduced emergence in mutants; enhanced emergence when overexpressed	(Bian et al., 2023; Yue et al., 2015)
RSL4 (bHLH TF)	Arabidopsis; conserved	Master regulator of root hair elongation; controls cell wall & tip-growth genes	Overexpression → very long root hairs; mutants short/absent hairs	(Hwang et al., 2017)
MYB41 → suberin pathway (GPAT5, CYP86A1, FARs, ABCG transporters)	Arabidopsis; translational to crops	Transcriptional activation of suberin biosynthesis in endodermis/periderm	Overexpression increases suberin lamellae deposition	(Shukla et al., 2021)
MYB36 / CASP1 / ESB1 (Casparian strip)	Arabidopsis; conserved	Endodermal differentiation & lignified Casparian strip assembly	Mutants show delayed/defective strips; altered nutrient uptake	(Xue et al., 2024)
MYB46 / MYB83 → SCW program (NAC-MYB cascade)	Arabidopsis; woody species orthologs	Master switches of secondary cell wall/lignin/cellulose/xylan biosynthesis	Overexpression increases lignin and SCW genes	(Yao et al., 2021)
RAM1 (GRAS TF; AM symbiosis)	Medicago, Brachypodium, tomato; cereals have orthologs	Master regulator of arbuscule development & nutrient exchange with AM fungi	ram1 mutants defective in arbuscules; overexpression increases colonization	(Ho-Plágaro et al., 2024)
OsADK1 (Adenylate kinase; AM symbiosis)	Rice	Promotes AM symbiosis efficiency; interacts with symbiotic signaling	osadk1 mutants reduce AM effectiveness	(Shi et al., 2022)
Suberin biosynthetic enzymes (GPAT5, CYP86A1/86B1, FAR1/4, ASFT, ABCG2/6/20)	Arabidopsis; crop orthologs	Polymer assembly/transport of aliphatic suberin monomers	Mutants reduce suberin; overexpression increases	(Gully et al., 2024; Ju et al., 2025; Teixeira, 2022; Venado, 2022)
SWEET11/12 (sucrose efflux)	Arabidopsis; cereals have SWEETs	Phloem-to-apoplast sucrose export; controls carbon allocation to roots & rhizosphere	double mutants reduce sucrose export to roots; altered exudation	(Shen et al., 2025)

genetic engineering functions to change genetically determined root architectural features that include depth distribution and branching and biomass allocation parameters. The size and depth of root systems determine the capacity for crops to store carbon deep in mineralization-resistant layers of soil (Jackson et al., 2008). Improved agricultural practices that enhance crop root functions

for carbon sequestration should become available through fundamental knowledge of root biomass genetic regulation and synthesis mechanisms. Research has identified important genes involved in root development notably the genes in Lateral Organ Boundaries (LOB) domain alongside genes in Auxin Response Factor (ARF) family which control biomass accumulation and root architecture (Huang et al., 2019). Genetic findings provide possible approaches to enhance root structures because they function as primary carbon sinks in the ground. The growth and operational activity of roots depend on hormone-mediated genetic signals to function properly.

4.1 Auxin and Cytokinin Signaling

The plant hormones auxin and cytokinin are critical regulators of root development, which in turn affects how carbon is stored in the soil (Lavenus et al., 2013). Auxin actively promotes the formation and elongation of roots, while cytokinin controls root branching. The combined action of these hormones shapes the root system's architecture, directly influencing the amount of carbon it can store. The balance between these two hormones is crucial; too much of one can inhibit the effects of the other, which is why their signaling pathways are finely tuned to ensure proper root development.

Beyond their direct effects on root architecture, auxin and cytokinin signaling also influence a plant's response to environmental cues. For example, in response to nutrient availability, the plant can alter the ratio of these hormones to adjust root growth, either favoring deep rooting to find water and nutrients or promoting a more extensive, shallow root system to absorb surface nutrients (Lynch et al., 2012). This dynamic regulation allows plants to optimize their root structures for a variety of soil conditions, making this hormonal pathway a prime target for genetic modification to improve carbon sequestration in diverse environments.

4.2 MYB and WRKY Transcription Factors

Transcription factors (TFs) are proteins that control the expression of genes related to plant growth, stress responses, and secondary metabolism. Plants use MYB and WRKY transcription factors to regulate root development and enhance the accumulation of biomass and carbon storage (Ambawat et al., 2013). By changing root morphology and root-hair development, these TFs control how plants absorb nutrients and release organic carbon into the soil.

The MYB family is the largest group of TFs in plants. They control various physiological processes, including secondary cell wall biosynthesis, lateral root formation, and root length expansion (Dubos et al., 2010). For instance, the functional interaction between AtMYB46 and AtMYB83 proteins is essential for lignin synthesis and secondary wall development in *Arabidopsis* roots. A study on rice showed that OsMYB30 successfully increased root growth and enhanced drought tolerance, making it a promising target for promoting below-ground carbon storage (Zhao & Bartley, 2014).

Further research into the MYB and WRKY families has revealed their roles in enhancing a plant's ability to withstand various abiotic stresses, such as drought, salinity, and extreme temperatures. By regulating the genes responsible for producing stress-response proteins and osmolytes, these transcription factors allow a plant to maintain root growth even under difficult conditions. This resilience is vital for consistent carbon sequestration, as stressed plants are less efficient at accumulating biomass and may shed their roots, releasing stored carbon (Zhang et al., 2022).

Additionally, the role of these TFs extends to regulating the composition of root exudates. MYB and WRKY TFs influence the genes that produce compounds released by roots into the soil (Li, Muneer Ahmed Khoso, et al., 2024). These exudates can influence the activity of soil microorganisms, promoting a microbiome that enhances nutrient cycling and the formation of stable soil organic matter. By genetically modifying these TFs to produce a more beneficial mix of exudates, we can create a positive feedback loop that not only increases carbon storage but also improves overall soil health.

4.3 Nodulation and Symbiotic Associations

Genes involved in symbiotic relationships, particularly those from legume-rhizobia partnerships, play an essential role in both nitrogen fixation and carbon sequestration. The NODULE INCEPTION (NIN) gene, for example, helps regulate these interactions. By enhancing these symbiotic associations, we can improve soil fertility and boost carbon sequestration through increased biomass production (Roy et al., 2021).

The establishment of a symbiotic relationship between a plant and nitrogen-fixing bacteria is a highly complex process that is tightly controlled by a series of genes. These genes govern everything from the initial signaling between the plant root and the bacteria to the development of the nodule structure where nitrogen fixation occurs. By optimizing these genetic pathways, we can improve the efficiency of nitrogen fixation, allowing plants to access a stable nitrogen source without the need for synthetic fertilizers (Soumare et al., 2020). This not only reduces the environmental impact of agriculture but also leads to more robust plant growth and, consequently, greater carbon sequestration.

Beyond nitrogen fixation, these symbiotic relationships also directly contribute to the accumulation of carbon in the soil. The carbon fixed by the plant through photosynthesis is transported to the roots, where a significant portion is used to support the growth and metabolism of the symbiotic bacteria (Udvardi & Poole, 2013). This process effectively transfers atmospheric carbon into the below-ground system. By genetically enhancing the plant's ability to form and maintain these associations, we can create a powerful, natural mechanism for long-term carbon storage.

5. Genetic Determinants of Root Development and Biomass Accumulation

The ability of plants to absorb water and nutrients and connect with soil microorganisms along with their carbon sequestration capacity depends strongly on how roots develop and the extent of biomass increase. Multiple environmental elements together with hormonal along with genetic factors determine how root systems grow and develop (Lynch, 2019). Root length together with branching patterns and biomass allocation receive their influence from genetic regulome through multiple signaling pathways that function in root growth regulation (Slovak et al., 2015). The comprehension of genetic factors remains vital for boosting carbon sequestration using organic matter inputs from roots along with bettering soil quality and increasing crop resistance.

5.1 Genetic Control of Root Architecture

Root system architecture (RSA) is primarily controlled by genetic elements that shape the main root, lateral root formation, and root hair development. Key transcription factors like NAC domain proteins and AUXIN RESPONSE FACTORS (ARFs) regulate root elongation and lateral root initiation (Li et al., 2022). The PIN-FORMED (PIN) transporters and the auxin signaling pathway are essential for root branching and gravitropic responses (Xie et al., 2021). Additionally, cytokinin signaling, which controls TYPE-A RESPONSE REGULATORS (ARRs), counteracts auxin signals to influence root characteristics like depth and lateral root numbers (Osugi et al., 2017). The distribution of biomass within the root system is also governed by these genetic processes, allowing plants to efficiently acquire nutrients and sequester carbon.

Specific genes are also crucial for root biomass development. WUSCHEL-RELATED HOMEOBOX (WOX) and ROOT MERISTEM GROWTH FACTORS (RGFs) are vital for maintaining root meristems and promoting biomass production. MYB and WRKY transcription factors influence root thickness and lignin production, which enhances carbon storage and extends root longevity (Rasheed et al., 2024). Furthermore, sugar-sensing genes like TARGET OF RAPAMYCIN (TOR) and HEXOKINASE (HXK) manage root biomass under fluctuating environmental conditions, and they affect how carbon reserves are distributed between the root and shoot systems.

Beyond the core regulatory genes, researchers are also identifying how certain gene families contribute to a plant's ability to adapt its root architecture to nutrient-poor soils. For instance, some genes enable plants to produce longer, deeper roots to reach water and nutrients in arid conditions, while others promote a more shallow, fibrous root system to efficiently absorb surface nutrients like phosphorus (Jarvensivu & Rajala, 2013). This genetic plasticity is a key target for breeding crops that can thrive in marginal lands, thereby expanding agricultural productivity without increasing the use of chemical fertilizers.

The intricate crosstalk between different signaling pathways further highlights the complexity of genetic control over root architecture. For example, the interaction between the auxin and cytokinin pathways is a finely tuned balance that determines the density and placement of lateral roots (ALONI et al., 2006). By genetically manipulating this balance, scientists can design root systems that are optimized for specific soil types, for example, a deeper root system for well-draining soils or a more expansive, shallow network for clay-heavy soils. This level of precision is unlocking new possibilities for sustainable agriculture.

5.2 Genetic Regulation of Root Biomass Accumulation

Secondary growth and cell proliferation along with differentiation depend on specific genes for root biomass development. The maintenance of root meristems and biomass production depends on WUSCHEL-RELATED HOMEOBOX (WOX) AS WELL AS ROOT MERISTEM GROWTH FACTORS (RGFs) according to Shimotohno et al. (2018). Changes in root thickness along with lignin production results from MYB and WRKY transcription factors which enhance carbon storage and extend root longevity (Zhao et al., 2018). Sugar-sensing genes TARGET OF RAPAMYCIN (TOR) and HEXOKINASE (HXK) together with TARGET OF RAPAMYCIN (TOR) manage root biomass under fluctuating environmental setups also affecting the distribution of carbon reserves between root and shoot systems (Sulpice et al., 2014).

Scientists have used quantitative trait locus (QTL) mapping and genome-wide association studies (GWAS) to identify crucial genetic regions for deep roots and high biomass in crops like maize and rice (Uga et al., 2013). The genomic modification tool CRISPR-Cas9 has been used to precisely alter genes, such as the DRO1 (*DEEPER ROOTING 1*) gene, to develop drought-tolerant rice varieties (Abe et al., 2019). These genetic methods provide efficient ways to create crops with ideal root systems that support carbon sequestration and sustainable farming.

The ability to manipulate specific genes is also helping to develop crops with enhanced symbiotic relationships with soil microorganisms. For example, genetic engineering can improve the efficiency of nodulation in legumes, leading to better nitrogen fixation and reduced need for synthetic nitrogen fertilizers (Asaye Demelash Limenie, 2024). By strengthening these natural partnerships, we can create more self-sufficient agricultural systems that improve soil health and reduce environmental impact.

5.3 Genetic implications for Soil Carbon Sequestration

The genetic factors that govern root development have a significant impact on how much carbon is stored in the soil. Plants with longer, deeper root systems can store carbon in deep soil layers, where it is less susceptible to microbial decomposition and erosion (Kell,

2011). This increased selection or design of crops with improved root conditions creates opportunities to build up organic carbon soil (SOC), enhance soil quality, and contribute to mitigating climate change.

Genetic control of root longevity and biomass quality is another critical aspect of carbon sequestration. Genes that promote the production of stable, decay-resistant root components, such as lignin, can increase the long-term storage of carbon in the soil. By breeding crops with roots that are not only large but also composed of more durable tissues, we can ensure that the sequestered carbon remains in the ground for longer periods, maximizing the environmental benefits.

Furthermore, genetic research is revealing how root exudates compounds released by roots can influence the soil microbiome. Some genes can be manipulated to increase the production of specific exudates that promote the growth of beneficial microbes, which in turn can enhance carbon storage and nutrient cycling (Huang et al., 2014). This understanding is paving the way for a holistic approach to crop improvement that considers not just the plant, but its entire underground ecosystem.

5.4 Gaining Genetic Basis of Root Development and Biomass Accumulation

Plant producers must understand root genetic elements for development alongside biomass increase and carbon storage capacity. Root structure together with biomass distribution exists as a controlled system which reacts to multiple genes alongside environmental stimuli and signaling processes. Knowledge about root development genetics improved significantly through molecular genetics and genomics research alongside biotechnological advancements (Lynch, 2019). Scientists develop breeding plans for crop roots with optimal characteristics to enhance nutrient intake and storage capabilities and resist droughts by locating essential genes and developmental regulatory networks (Uga et al., 2013).

The advancement of technology has generated modern methods for improving root system structure alongside biomass quantities in plants. Multiple plant production enhancements alongside stress resistance improvement and soil carbon sequestration occur because of the exact handling of roots through genomics and molecular breeding and gene editing and phenotyping methods (Lynch, 2019). Scientists employ these technologies to develop crops that have better root structure for sustainable agriculture practices and against climate change threats (Kell, 2011).

5.5 Genomics and Molecular Breeding

Genomic research has significantly advanced the study of root genetics. Tools like genome-wide association studies (GWAS) and quantitative trait locus (QTL) mapping have been used to identify the genetic loci responsible for biomass accumulation, branching, and root depths in crops like rice and wheat (Uga et al., 2013). Using marker-assisted selection (MAS), breeders can now identify beneficial root characteristics through genetic markers, leading to the faster development of high-yield and stress-tolerant crops.

Beyond trait identification, genomics is also enabling a deeper understanding of the entire gene regulatory network that controls root development (Li et al., 2022). By creating comprehensive genetic maps, researchers can see how different genes interact to control complex traits, allowing for more precise and effective breeding strategies. This system-level approach ensures that genetic modification for one trait doesn't negatively impact others, leading to more robust and resilient crop varieties.

5.6 Gene Editing and Biotechnology

Gene-editing tools like CRISPR-Cas9 are transforming plant breeding by allowing for precise modifications to root developmental genes. The targeted editing of the DRO1 gene, for example, has resulted in drought-tolerant rice cultivars (Abe and team.,2019). Researchers have also manipulated PIN-FORMED (PIN) transporters and auxin-related genes to improve lateral root formation and nutrient uptake in various crops (Xie et al., 2021). These biotechnological developments make it possible to optimize root system designs for enhanced biomass production and carbon sequestration.

The ability to create targeted mutations with gene editing is also being used to improve nutrient uptake from the soil. By modifying genes that control the expression of nutrient transporters, scientists are developing crops that can absorb essential elements like phosphorus and iron more efficiently (Chen & Liao, 2017). This not only improves the nutritional value of the crops but also reduces the need for costly and environmentally damaging fertilizers, promoting a more sustainable and economically viable farming model.

5.7 Advanced Phenotyping and Imaging Technologies

The study of root traits has been significantly improved by high-throughput phenotyping (HTP) platforms and advanced imaging technologies. Techniques like ground-penetrating radar, magnetic resonance imaging, and X-ray computed tomography allow for the non-invasive visualization of root structures in the soil (Atkinson et al., 2019). These instruments enable scientists to observe biomass growth, root-soil relationships, and developmental patterns under different environmental conditions, helping them breed crops with better root traits.

These technologies are also critical for bridging the gap between a plant's genetics and its visible traits. By collecting massive amounts of data on root growth patterns and correlating it with genomic information, scientists can build predictive models that forecast how a certain genetic modification will impact root architecture. This helps to streamline the research process and accelerates the development of new crop varieties.

5.8 Computational Modeling and Artificial Intelligence

Artificial intelligence (AI) and computational models are now essential for identifying root growth patterns and optimizing biomass allocation. Machine learning algorithms use large datasets from phenotyping, genomic research, and field trials to discover the key variables that influence root development (Lobet et al., 2017). These models allow researchers to virtually assess different breeding scenarios and select the optimal genotypes, which dramatically speeds up the crop development process.

AI-driven models are also being used to predict how climate change will impact root growth in different regions. By simulating future climate scenarios, researchers can identify the specific genetic traits that will be most beneficial for a crop in each environment (Srivastava & Maity, 2023). This predictive capability is helping to future-proof agriculture and ensure that new crop varieties are resilient to the challenges of a changing climate.

6. Integrating Genomic Approaches into Sustainable Agriculture

The implementation of genetic technologies in agricultural systems helps improve sustainable farming practices and establishes better global food security (Tester & Langridge, 2010). These technologies provide tools that enable breeders to efficiently select beneficial traits in crops.

6.1 Genomics in Crop Improvement

Research in crop breeding received industrial-scale improvements through genomic technologies because these tools help breeders detect and select beneficial genetic features. The fundamental method of traditional breeding techniques known as phenotypic selection requires extensive personnel labor while remaining vulnerable to environmental changes. Both genomic selection (GS) and genome-wide association studies (GWAS) allow breeders to locate genetic markers and genes which relate to critical characteristics including disease resistance along with nutrient efficiency and drought tolerance (Crossa et al., 2017).

6.2 Genome-Wide Association Studies (GWAS)

GWAS works by scanning large gene pools to find regulatory DNA sequences associated with key agricultural traits (Rodriguez et al., 2020). This helps researchers match genetic markers to specific features, simplifying the identification of genes vital for sustainable agriculture, such as those related to stress tolerance and root architecture (Wang et al., 2021). For example, the DRO1 (*Deeper Rooting 1*) gene in rice, which directs deep-root development, has been identified through GWAS and used to create drought-tolerant varieties (Uga et al., 2013). This precision allows for the development of crops with enhanced resilience to environmental challenges without the need for trial-and-error breeding. GWAS also plays a significant role in understanding the genetic basis of a plant's ability to absorb and utilize nutrients (Liang et al., 2025). By identifying genes that improve nitrogen-use efficiency (NUE) and phosphorus-use efficiency (PUE), researchers can breed crops that require less fertilizer. This not only reduces the cost for farmers but also minimizes environmental pollution from agricultural runoff. The identification of such genes is a critical step towards developing more sustainable and resource-efficient farming systems.

6.3 Genomic Selection (GS) and Marker-Assisted Breeding

Genomic selection (GS) and marker-assisted breeding (MAS) are powerful tools that reduce the time and resources needed to create new crop varieties. By using genetic markers, breeders can assess the potential value of plants before they reach maturity. This allows for the selection of desired plants earlier in the breeding process, which significantly shortens breeding cycles and boosts production efficiency (Varshney et al., 2019). These methods have been particularly effective in enhancing yield stability for crops like soybeans, wheat, and maize under variable climate conditions (Crossa et al., 2017).

Furthermore, GS and MAS are instrumental in combating new or evolving crop diseases. By screening genetic markers associated with disease resistance, breeders can quickly introduce these traits into new varieties, creating crops that are resilient to specific pathogens (Stuthman et al., 2007). This proactive approach helps to safeguard harvests and reduce reliance on chemical pesticides, thereby promoting more environmentally friendly agricultural practices. These techniques are essential for maintaining food security in a world where new threats to crops are constantly emerging.

6.4 Gene Editing for Sustainable Agriculture

Gene-editing systems, such as CRISPR-Cas9, allow for precise and targeted modifications to plant genomes, enabling the creation of sustainable traits that are difficult to achieve with traditional breeding methods. Unlike conventional breeding, which involves combining unknown genetic material, gene editing provides a level of control that can improve drought resistance, nutrient efficiency, and pest resistance (Zhang et al., 2020) (Figure 1).

6.5 Enhancing Stress Tolerance

Global food security is under constant threat from environmental stresses like drought and salinity. Gene-editing tools have proven effective in addressing these challenges. For instance, scientists have successfully enhanced drought tolerance in rice by editing the *OsNAC14* gene using a CRISPR-based approach (Miao et al., 2018). Similarly, the *AtHKT1* gene has been modified to enhance salt resistance in plants. These targeted genetic changes allow crops to thrive in harsh conditions, making previously non-arable land suitable for farming (Wang et al., 2021).

Another major area of focus for gene editing is improving a plant's ability to withstand extreme temperatures. Scientists are using gene-editing techniques to identify and modify genes that regulate a plant's response to both heat and cold stress. By creating crops that are more resilient to temperature fluctuations, gene editing can help

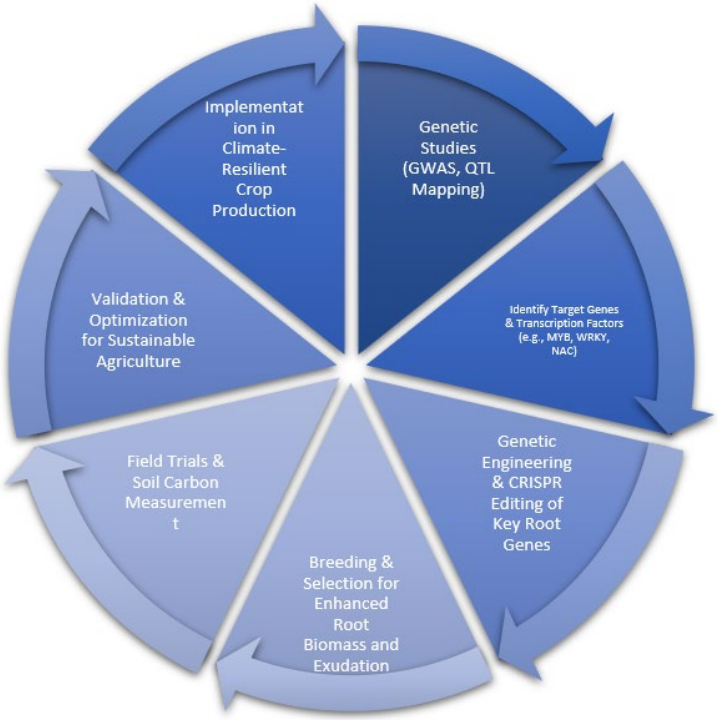

Figure 1. Flowchart: Genomic Approaches to Enhance Root Traits for Carbon Sequestration

ensure stable yields in regions impacted by climate change, reducing the risk of crop failure and food shortages.

6.6 Reducing Chemical Inputs

The overuse of fertilizers and pesticides contributes to soil erosion and environmental pollution. Gene-editing provides a solution by creating crops that are inherently more resistant to pests and more efficient at nutrient uptake Wang et al., 2018). For example, CRISPR-edited wheat has shown enhanced resistance to powdery mildew, a common fungal disease, which reduces the need for chemical fungicides. Similarly, by altering the OsNRT1.1B gene in rice, researchers have improved nitrogen-use efficiency, leading to a decreased reliance on synthetic fertilizers (Sun et al., 2014).

Also being explored to develop crops that can produce their own pest-deterrent compounds. This would provide a natural defense mechanism against insects and other pests, further reducing the need for chemical sprays. By harnessing a plant's natural genetic defenses, gene editing offers a pathway to a more self-sufficient and environmentally friendly agricultural system, moving away from high-input farming practices.

7. Future Prospects and Challenges of Integrating Genomic Approaches into Sustainable Agriculture

Sustainable agriculture encounters obstacles that hinder the adoption of genomic methods for future use. Certain regions face obstacles in gene-edited crop utilization because their laws control gene-edited crop usage differently (Zaidi et al., 2019). AI-driven agriculture needs to resolve the privacy-related ethical concerns and those related to gene modifications in genetic material. Biotechnology and genomic research continue to progress significantly which creates possibilities to decrease agricultural environmental burden alongside improving food security levels (Tester & Langridge, 2010).

The implementation of genomic technology in agriculture faces various barriers which must be solved to overcome ethical and regulatory issues and technical boundaries despite its current benefits.

7.1 Future Prospects of Genomic Approaches in Sustainable Agriculture

Climate-Resilient Crops

Beyond single gene modifications like the OsNAC14 gene, genomic applications are enabling more complex, multi-trait improvements (Miao et al., 2018). For instance, genomic selection (GS) leverages a vast database of genetic markers across an entire plant genome to predict the performance of new crop varieties without extensive field testing (Sinha et al., 2023). This accelerates the breeding process for climate-resilient traits, such as improved water-use efficiency, deeper root systems, and better heat and salinity tolerance, which are all controlled by many genes. By analyzing the genetic makeup of thousands of individuals, breeders can select the

most promising candidates for the next generation in a much shorter timeframe.

Furthermore, CRISPR-Cas9 is being used to make targeted changes to multiple genes simultaneously, a process known as multiplexing (Zhang et al. 2020). This allows scientists to address complex stress responses that involve multiple pathways. For example, researchers can edit genes that regulate stomatal opening to reduce water loss while also modifying genes that control the plant's hormonal responses to stress, like abscisic acid (ABA) production. This combined approach creates a more robust and comprehensive resistance to drought, heat, and salinity, which often occur together in the field. These precise, multi-gene edits can lead to crops that not only survive but also maintain high yields under challenging environmental conditions

7.2 Enhanced Nutrient Use Efficiency

Building on the success of single-gene modifications like OsNRT1.1B, researchers are now using genomic tools to tackle the complex, multi-gene nature of nutrient uptake (Sun et al., 2014). Gene stacking, for example, uses techniques like CRISPR-Cas9 to simultaneously introduce or modify multiple genes that control different aspects of nutrient efficiency. This might include genes that improve the plant's root architecture, allowing it to explore a larger volume of soil for nutrients, alongside genes that enhance the activity of nutrient transporters in the plant's cells (Aibara & Miwa, 2014). By combining these traits, scientists can create crops that are not just better at absorbing nutrients but also more effective at moving them throughout the plant, leading to a more comprehensive and robust improvement in NUE.

Furthermore, a future approach to enhancing NUE involves harnessing the plant's relationship with soil microbes. Metagenomics, the study of the collective genetic material from soil microbial communities, reveals the specific genes and pathways that enable microbes to convert atmospheric nitrogen into a form plant can use (Li et al., 2024). This knowledge is being used to develop bio-inoculants, which are microbial cocktails that can be applied to crops to boost their natural ability to fix nitrogen or solubilize phosphorus from the soil. By understanding the plant-microbe interaction at a genetic level, genomic research can reduce the plant's dependency on synthetic fertilizers and promote a more sustainable, biologically driven system of nutrient acquisition. This is a shift from pure genetic modification of the plant to a more holistic approach that supports a healthier soil ecosystem.

7.3 Disease and Pest Resistance

The CRISPR system allows researchers to modify genes like MLO in wheat which reduces plant susceptibility to powdery mildew and eliminates the need for chemical fungicides according to Wang et al. (2018). The breeding of pest-resistant maize and soybean varieties has become possible through genomic techniques according to Zaidi et al. (2019).

Another powerful genomic tool for enhancing disease and pest resistance is the use of genomic selection (GS). While CRISPR-Cas9 offers precise gene editing, GS accelerates the traditional breeding process. It leverages vast databases of genetic markers across an entire plant genome to predict which new crop varieties will have the strongest natural resistance to specific pathogens and pests (Biswal et al., 2024). Breeders can analyze the DNA of thousands of plant seedlings and select the most promising candidates for the next generation, all without having to wait for them to mature in the field and be exposed to disease. This significantly shortens the time it takes to develop and commercialize new, resistant crop varieties, allowing for a much faster response to evolving threats.

Furthermore, future applications will go beyond single-gene resistance to develop crops with more durable, broad-spectrum immunity. This involves identifying and stacking multiple resistance genes in a single plant, making it difficult for pathogens to overcome its defenses through simple mutation. For instance, researchers are using genomic data to find multiple genes that activate different parts of a plant's immune system. By combining these genes, they can create a "layered" defense. This approach, known as gene stacking or pyramid, ensures that even if a pathogen adapts to one defense mechanism, it will still be stopped by others. This creates a more sustainable and long-lasting form of resistance, reducing reliance on chemical pesticides and fungicides and safeguarding yields for a longer period.

7.4 Artificial Intelligence and Computational Biology

Artificial intelligence (AI) together with machine learning (ML) operates as sophisticated analytics platforms which analyze extensive genomic alongside phenotypic information. Predictive AI models allow breeders to identify top crop variations by processing genetic details with environmental factors (Hickey et al., 2017). Plant traits can be monitored precisely through automated phenotyping tools which consist of drones along with imaging sensors to speed up breeding programs (Araus & Cairns, 2014).

Artificial intelligence and computational biology are also being used to predict the function of unknown genes and to design entirely new proteins for specific agricultural applications (Biswas et al., 2023). By analyzing vast datasets of genetic sequences and protein structures, AI algorithms can infer the roles of uncharacterized genes, such as those involved in drought resistance or nutrient uptake. This accelerates the process of identifying new targets for gene editing. Similarly, AI can be used to design novel enzymes with enhanced efficiency, such as a more effective nitrogenase for nitrogen fixation in non-leguminous crops (Mahmud et al., 2020). This approach moves beyond simply modifying existing genes to creating custom-designed biological solutions for agricultural challenges.

Furthermore, AI and machine learning are revolutionizing pest and disease management by providing early warning systems and

optimizing treatment strategies. Predictive models can analyze real-time data from weather sensors, soil moisture probes, and satellite imagery to forecast the spread of pathogens or insect infestations (Aziz et al., 2025). For example, an AI model could predict the likelihood of a fungal outbreak based on a combination of high humidity and specific temperature ranges. This allows farmers to apply treatments proactively and precisely, reducing the overall number of pesticides and fungicides needed. This not only minimizes environmental impact but also lowers costs for farmers, representing a significant step towards more sustainable and efficient agriculture.

8. Challenges in Implementing Genomic Approaches

8.1 Regulatory and Policy Constraints

National governmental agencies apply divergent regulations to genetically modified (GM) and gene-edited crops in different jurisdictions. Gene-editing technologies operate within the United States and China as commercial entities while the EU maintains strict policies blocking commercial use (Zaidi et al., 2019). Genome-edited food production stands in serious jeopardy because there remain non-unified external rules about edited genome crops across the world.

The lack of a harmonized global regulatory framework is a major obstacle for the commercialization and international trade of gene-edited crops. While some nations, like Argentina, Japan, and Canada, have adopted a "product-based" approach, treating gene-edited crops similarly to conventionally bred ones if they don't contain foreign DNA, the European Union's "process-based" regulation classifies them as genetically modified organisms (GMOs) (Singer & Michaud, 2025). This strict classification imposes a lengthy and expensive approval process, which can take over a decade and cost millions of dollars. The resulting regulatory divide creates significant barriers for seed companies and farmers, limiting the global market and slowing down the adoption of these technologies, especially for crops important to developing countries.

8.2 Ethical and Societal Concerns

Widespread use of genetic modifications encounters barriers because the public and ethical opinions about such changes remain negative. Gene editing has led consumers and policy leaders to become doubtful because of biodiversity reduction and corporate genetic resource control and hidden impacts of gene editing (Kawall, 2021). Open communication with the public along with regulatory oversight are necessary for acceptance of such problems. Public perception and trust are critical for the adoption of genomic technologies in agriculture. Concerns often center on a lack of transparency regarding what is being changed and for what purpose. For instance, the public may view gene-edited crops as "unnatural" and worry about unintended health consequences, even when scientific consensus indicates they are safe (Macnaghten & Habets, 2020). A key challenge is the "perception gap" where the public's understanding of technology often lags scientific progress. Additionally, there are concerns that large multinational corporations will dominate the technology, creating a monopoly on genetic resources and marginalizing smallholder farmers. Building public confidence requires transparent communication, clear labeling, and inclusive governance models that involve all stakeholders, from farmers to consumers (Wilkes, 2022).

8.3 High Costs and Technological Gaps

Genomic research and breeding programs demand powerful investments in infrastructure knowledge and bioinformatics tools even though major progress has already occurred. Entities lacking both financial capacity and technological capability find it difficult to use genomic technology because they struggle with serious food safety challenges (Varshney et al., 2019). For sustainable agricultural breakthroughs to be accessible equally to all the technology gaps must be eliminated.

The significant investment required for genomic research and breeding programs creates a global divide in agricultural innovation. Advanced sequencing equipment, bioinformatics pipelines, and skilled personnel are often concentrated in well-funded institutions and private corporations in developed countries (Amer et al., 2024). This leaves many developing nations, which are often the most vulnerable to climate change and food insecurity, with limited access to these transformative tools. This technological and financial barrier means that crops vital to local food systems, such as cassava, millet, or sorghum, receive less research attention compared to staple crops like maize and rice. To bridge this gap, initiatives are needed to create open-source genomic resources and establish collaborative partnerships that make these technologies more affordable and accessible to researchers and farmers worldwide.

8.4 Long-Term Environmental and Ecological Risks

Scientists continue to research how genetic modifications of soil microbiomes and ecosystems impact them during extended periods. The advantages of editing genes in crops exist while ongoing monitoring must occur to prevent ecological disruptions along with undesired genetic reactions and gene transfers to wild species (Wolt et al., 2016). The risk assessment process provides structures to minimize possible ecological risks.

While the benefits of gene editing are clear, there is an ongoing need for rigorous, long-term ecological risk assessments. One primary concern is the potential for off-target effects, where unintended genetic changes occur at sites other than the intended ones, which could lead to unforeseen consequences. There is also the risk of gene flow, where a beneficial trait, such as herbicide resistance, could be transferred from a gene-edited crop to a wild relative (Hussain et al., 2021). This could create a "superweed" that is difficult to control

and could disrupt native ecosystems. While current methods for monitoring these risks are improving, continuous post-release monitoring is crucial to ensure that these technologies do not cause unintended ecological disruptions and to maintain biodiversity.

9. Conclusion

The sequestration of soil carbon depends on roots because they regulate the factors that cause carbon entry and microbial activity and stabilize organic matter. Land management practices aimed at reducing climate change will gain benefit by studying root system contributions together with their soil biota interdependencies. The essential focus for future research should be to determine root-based carbon storage levels and research new agricultural approaches for maximum sequestration potential. The improvement of root genetic control traits which enhance carbon sequestration represents a practical method to fight climate change. The main purpose of future scientific work must focus on developing plant species with suitable root structures for sustainable carbon storage through genetic and breeding and biotechnological advances.

Furthermore, the widespread adoption of these technologies hinges on the establishment of supportive policies and economic incentives. The widespread adoption of these innovations needs accessible and affordable approaches most especially for smallholder farmers because this will enable effective solutions to global agricultural and environmental problems.

The realization of advanced promises requires proper solutions to all current ethical and regulatory problems alongside technological obstacles. Agencies and research institutions and representative industry partners should constructively unite efforts to establish a dependable and sustainable worldwide food distribution network. Continued progress in research and support frameworks together with innovative approaches will convert agricultural systems into the effective delivery of both carbon sequestration strategies and environmental conservation measures.

Author contributions

Muhammad Ali, Hina Fatima, Maria, Rubab and Muhammad Anas reviewed literature and drafted the manuscript. Waqar and Anns contributed in figures and table. Raja Ahmad and Mujeeb managed references and formatting. Muhammad Sajad supervised and guided the work.

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