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Unraveling the genetic diversity and evolution of Arbuscular Mycorrhizal Fungi (AMF)

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Abstract

The analysis of genetic differences among arbuscular mycorrhizal fungi (AMF) species has shed light on the genetic diversity and evolution of these fascinating organisms. AMF are essential constituents of land ecosystems because of their mutualistic symbiotic associations with plant roots. Their capability to amplify nutrient absorption, enhance water assimilation, and stimulate overall plant development plays a pivotal function in sustaining thriving ecosystems. By extensively examining the genomes of various AMF classifications, researchers have uncovered their evolutionary connections and gained understanding of the impact of horizontal gene transfer (HGT) on their genetic makeup. This knowledge has not only upgraded our comprehension of the evolutionary past of AMF but has also furnished valuable insights into the mechanisms that govern the symbiotic interactions between fungi and plants. In future studies on AMF genome variance, it is crucial to prioritize functional characterization, understand co-evolutionary dynamics with host plants, uncover mechanisms and implications of HGT, and integrate metagenomic approaches. By identifying the specific genes and genetic variations that contribute to AMF's ability to form mutualistic associations with plants, scientists can gain insights into the underlying mechanisms of this important ecological relationship. Furthermore, through the analysis of genetic divergence in both AMF and their host plants, researchers can elucidate the co-evolutionary dynamics that have shaped their mutualistic symbiosis. Equally, understanding the contribution of horizontal gene transfer (HGT) to AMF genetic diversity can provide insights into the evolutionary history and adaptive abilities of these fungi. Ultimately, the incorporation of metagenomic techniques into future studies on AMF genetic diversity will facilitate a broader understanding of the microorganism populations associated with these fungi. By focusing on these domains, it is possible to advance our understanding of AMF biology and unlock novel opportunities for innovative applications in agriculture and ecosystem management.

Keywords: Arbuscular Mycorrhizal Fungi; Genetic Diversity; Genomic Variation; Horizontal Gene Transfer

1. Introduction

Arbuscular Mycorrhizal Fungi (AMF) are a cluster of advantageous soil fungi that establish mutualistic associations with plant roots. Their role is crucial in the soil ecosystem as they enhance the accessibility of nutrients to plants [1,2]. AMF possess the capability to retrieve nutrients, like phosphorus, from the soil and transfer them directly to the roots of plants. In return, plants provide AMF with carbohydrates, serving as an energy source [3,4]. This harmonious collaboration is advantageous for both parties, as it allows plants to obtain crucial nutrients while supplying AMF with necessary resources. Moreover, AMF have showcased their capacity to enhance plant growth by promoting root development and strengthening resistance against different stressors, such as water shortage and pathogens [5,6,7]. A key aspect of comprehending the ecological significance of AMF is understanding their genetic heredity. AMF species vary greatly in their capacity to absorb nutrients and enhance plant growth [8,9,10]. Furthermore, the intra-species genetic diversity can play a role in their interactions with different plant species [11,12]. The investigation of AMF genetic diversity can enable the identification of particular strains or species that are highly proficient in improving

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nutrient absorption or promoting plant growth in specific conditions. This knowledge can subsequently be applied in agriculture to optimize crop yield while reducing fertilizer usage.

1.1. Search strategy

The research incorporated English journals covering the period of 2003 to 2023. The search involved segmenting the research topic into different search terms, specifically “Arbuscular Mycorrhizal Fungi” and “Genetic Diversity.” Evolution of Arbuscular Mycorrhizal Fungi” Upon concluding the search, a total of 53 journal articles were discovered, with the exclusion of 5 duplicates, resulting in a final count of 48 individual articles. The abstracts of all these journals underwent scrutiny, and pertinent papers were marked for further assessment. The study employed a 20-year criterion to determine inclusion and exclusion. After meeting this condition, a thorough analysis of 45 journal articles was carried out to ascertain their relevance to the research theme. The study excluded 3 peer-reviewed journals and assessed 42 for inclusion, excluding two irrelevant ones that did not contribute to keyword identification. As a result, the research strategy generated 40 publications that were cited and referenced in this review (Figure 1).

2. The Genetic Diversity and Evolution of Arbuscular Mycorrhizal Fungi (AMF): Findings from Previous Studies

2.1. Genomic Variation among AMF Species

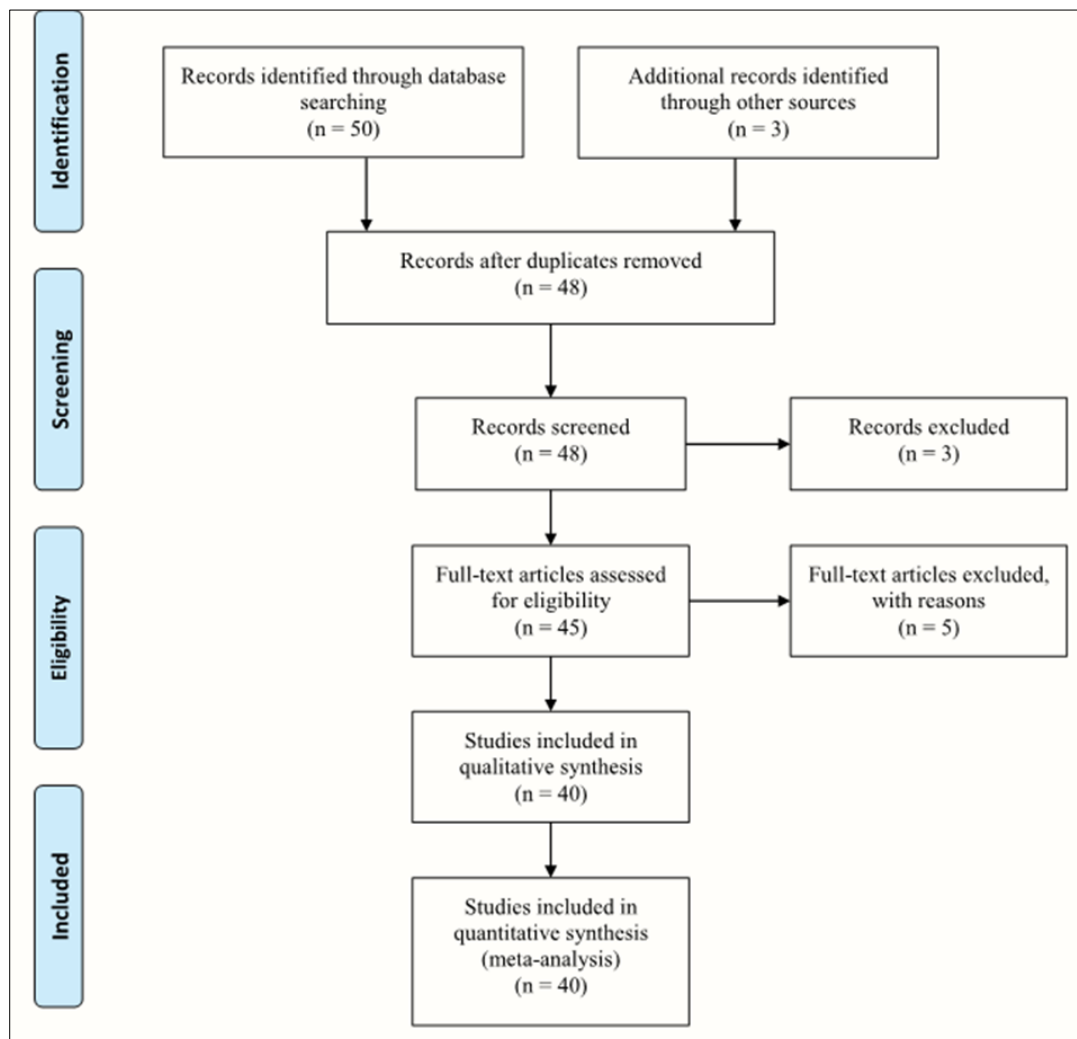


Figure 1 PRISMA diagram showing how papers were selected, excluded and included

In the study conducted by Sanders, it is revealed that genes, particularly the Bip gene, exhibit significant sequence variability, even within coding regions. The presence of considerable sequence variability in genes like Bip suggests the existence of diverse variants or alleles within the AMF population [13] [Table 1]. These variations have the potential to

influence gene expression and function, resulting in disparities in the fungus-host plant interaction. Understanding these variations is vital for accurately analyzing and manipulating AMF for agricultural utilization. Moreover, this study underscores the significance of employing a population genetic approach in AMF research [13]. Through the analysis of multiple individuals from a population instead of solely examining individual genes or isolates, researchers can acquire a more holistic comprehension of AMF genetics and evolution. This approach can also assist in the development of inoculum by identifying particular strains or variants that have a greater positive impact on promoting plant growth. Overall, Sanders's study underscores the necessity of considering genetic variability within AMF populations in gene expression and function studies. It also emphasizes the relevance of employing a population genetic approach to grasp AMF genetics and create potent inoculums. Additional research in this field will undeniably contribute to advancements in agriculture and the production of sustainable crops.

The study conducted by Tisserant et al. has raised doubts about the genomic organization of the 153-mb haploid genome of *Rhizophagus irregularis*. With a remarkable 28,232 genes, this fungus has enchanted scientists for years [14]. Nevertheless, recent research has brought to light some bewildering features of its genetic constitution. One striking observation is the low level of genome polymorphism found in *R. irregularis*. This hints at the possibility of intricate sex-related processes taking place in this organism. The limited genetic variability prompts inquiries into the fungus's reproductive and evolutionary mechanisms. Another captivating discovery is the lack of genes that encode enzymes capable of breaking down plant cell walls, as well as the absence of genes involved in toxin and thiamine synthesis in *R. irregularis* [14] [Table 1]. These enzymes are widely distributed in other fungi and have significant implications for their interactions with plants. The absence of these genes suggests that *R. irregularis* may have evolved unique mechanisms to interact with its plant hosts. Collectively, these findings challenge our prevailing comprehension of fungal genomics and emphasize the necessity for additional research on *R. irregularis*. Through unraveling the perplexities of its genomic arrangement, we can attain valuable discernment into the evolutionary narrative and ecological importance of this captivating fungus.

The study by Montoliu-Nerin et al. offers a comprehensive understanding of the evolutionary history of arbuscular mycorrhizal fungi (AMF) through the use of genomic data from single nuclei. One of the primary discoveries of this study is the investigation of phylogenetic connections within Glomeromycota, a phylum that includes AMF [15] [Table 1]. The researchers successfully provided support for family-level classification within Glomeromycota and additionally uncovered the polyphyletic nature of the order Glomerales. These findings elucidate the intricate evolutionary connections between different AMF species and offer valuable insights into their diversification over time. The successful sequencing of genomes from individual nuclei is a substantial achievement in and of itself [15]. This approach enables a more precise depiction of genetic information by eliminating potential biases caused by pooling multiple nuclei. By implementing this groundbreaking technique, [15] has opened doors for future explorations in phylogenomics and established a fresh benchmark for scrutinizing genomic data in AMF research. All in all, this study makes a substantial contribution to our knowledge of AMF's evolutionary history and underscores the importance of incorporating genomic data in phylogenetic analyses. The findings presented here not only deepen our understanding of these captivating fungi but also have broader implications for ecological and agricultural research, given the vital roles AMF play in nutrient cycling and plant health.

In the study conducted by Masclaux et al., it was determined that bi-allelic sites and frequencies exhibited a remarkable level of consistency across independent studies utilizing various methodologies [16]. This finding suggests the potential presence of genetic variation within the fungus. Nevertheless, there was minimal backing for the transcription of this variation in homokaryons. Homokaryons are fungal strains characterized by the presence of a single nucleus genotype [16] [Table 1]. The absence of transcription of genetic variation within fungi in homokaryons implies that this variation is not actively expressed or utilized in these strains. Conversely, it is postulated that intra-fungal diversity is partitioned between two nucleus genotypes in a heterokaryotic isolate. Heterokaryons are fungal strains characterized by the presence of multiple genetically distinct nuclei in a single cytoplasm [16]. The hypothesis suggests that the genetic variation found within fungi in previous research is upheld and displayed in heterokaryon isolates by virtue of the presence of multiple nucleus genotypes. This finding holds crucial implications for our knowledge of fungal genetics and evolution. It indicates that genetic diversity within a single fungus can be preserved and potentially exploited by forming heterokaryons. However, further exploration is needed to understand the mechanisms behind this phenomenon and its potential consequences for fungal biology [16]. Overall, Masclaux et al.'s study presents evidence supporting the existence of genetic variation within fungi, which can be divided among two nucleus genotypes in heterokaryon isolates. This finding emphasizes the need to take into account both homokaryotic and heterokaryotic states in the investigation of fungal genetics and evolution.

In the study conducted by Mathieu et al., it is unveiled that AMF display distinctive population biology, with conspecific strains exhibiting notable genetic and phenotypic diversity. This finding brings to light the extensive intraspecific

diversity observed in AMF, with phenotypes that differ depending on the host. One of the significant discoveries from this study is the existence of extensive and diverse pangenomes in a model AMF known as *Rhizophagus irregularis* [17]. Pangenomes encompass the entirety of genetic material within a species, comprising both universally shared core genes and strain-specific accessory genes. The presence of diverse pangenomes indicates the significance of intra-species genome diversity in AMF ecology. The variability seen in AMF populations can be ascribed to several factors [17] [Table 1]. Firstly, the preference for different host plants can lead to the selection of specific traits in AMF strains, resulting in phenotypic differences. This phenomenon exemplifies the mutually beneficial relationship between plants and their associated fungi. Furthermore, environmental factors, including soil conditions and nutrient availability, can exert an impact on the genetic and phenotypic diversity within AMF populations [17]. These findings highlight the adaptability of AMF to diverse ecological environments. Understanding the population biology of AMF is a fundamental aspect in comprehending their ecological roles and potential agricultural benefits. Through the clarification of the genetic and phenotypic variability within these fungi, scientists can develop methods to optimize their symbiotic interactions with plants, leading to improved nutrient uptake and stress tolerance. In summary, Mathieu et al.'s study demonstrates that AMF display distinct population biology, characterized by considerable genetic and phenotypic diversity among strains of the same species. The extensive intraspecific diversity observed in these fungi signifies the essential role of genome diversity in their ecology. Extensive exploration in this domain will advance our understanding of plant-fungal interactions and potentially shape sustainable agriculture practices.

In the study conducted by Koch et al., notable genetic and phenotypic diversity was noted among isolates of a *Glomus intraradices* population. Nonetheless, the total observed genetic diversity was discovered to be limited. This finding implies that natural selection has influenced the population's preservation of similar traits as a result of the multi-genomic characteristics of arbuscular mycorrhizal fungi (AMF) [18] [Table 1]. AMF are mutualistic symbionts that establish associations with the roots of the majority of terrestrial plants. They play a pivotal role in the absorption of nutrients and augment plant growth and productivity. The study concentrated on unraveling the genetic variation within a distinct population of *Glomus intraradices*, which is widely recognized as one of the most prevalent AMF species [18]. The researchers utilized molecular techniques to assess the genetic constitution of diverse isolates derived from this population. They established that despite considerable variations in certain genes and observable traits, the overall genetic diversity was minimal. This indicates that selection pressures have impacted this population to preserve particular traits. This phenomenon is influenced by the multigenomic nature of AMF. Within each individual, these fungi harbor multiple duplicates of their genome, which are called multinucleate cells or coenocytic hyphae. This enables rapid evolution and adaptation to ever-changing surroundings. The findings from this study carry substantial implications for the understanding of AMF population evolution and adaptation [18]. Through the determination of the factors that influence genetic diversity within these populations, we can glean insights into their ecological functions and potential applications in agriculture and ecosystem management. In summary, Koch et al.'s study underscores the substantial genetic and phenotypic variation within a population of *Glomus intraradices* isolates, while noting a limited total observed genetic diversity. The findings suggest that selection has influenced this population as a consequence of the multigenomic nature of AMF, leading to the preservation of analogous traits over time. Additional investigation is, however, required to delve into the potential applications of these findings in diverse fields like agriculture and ecosystem management.

In the study conducted by Savary et al., a high-resolution phylogeny of a single species of arbuscular mycorrhizal fungus (AMF) was utilized to investigate the correlation between fungal genetic variation and the control of the plant fatty acid pathway in cassava [19]. The results of this study illuminate the pivotal role of fungal genome variation in resource exchange and optimal cassava growth. Cassava, a staple crop in various regions, plays a dual role as a vital nutritional resource and a significant trade currency. Therefore, it is crucial to comprehend the factors that impact its growth and productivity for agricultural advancement. The study demonstrated that fungal genetic variability directly affects the regulation of the plant fatty acid pathway in cassava [19] [Table 1]. The AMF species investigated in this research cultivate mutualistic symbiosis with plants, thereby facilitating nutrient assimilation and augmenting plant growth. It was discovered that certain genetic variations within these fungi had an impact on their capacity to regulate the plant fatty acid pathway, thereby influencing cassava growth [19]. This study emphasizes the significance of taking into account fungal genome variation in the analysis of resource exchange and the enhancement of crop yield. Through an understanding of the influence of diverse genetic variations within AMF species on vital metabolic pathways in plants, such as the fatty acid pathway in cassava, we can formulate specific tactics to augment crop productivity. In general, this research offers valuable insights into the complex connection between fungi and plants, highlighting the crucial role of fungal genome variation in shaping agricultural systems.

Experimental studies have demonstrated substantial variation in plant performance across diverse AMF species. This variation proposes that the genetic heterogeneity within AMF could be pivotal in determining their influence on plant communities. In view of this, [20] puts forth a strategy to further explore the subject, aiming to pinpoint polymorphic

loci that define genetic diversity within AMF [Table 1]. Through the measurement of allele diversity in environmental DNA samples at the intraspecific level, researchers can gain insights into the pivotal levels of AMF diversity in plant communities. This approach carries significant potential due to several reasons. Firstly, it affords researchers the opportunity to identify distinct genetic markers correlated with variations in AMF performance. By understanding these markers, scientists can obtain insights into the mechanisms that facilitate the symbiotic interaction between plants and AMF. Secondly, this approach presents a technique for evaluating allele diversity within a population. This is of great importance as it provides researchers with insights into the influence of genetic variation within specific AMF species on their interactions with plants [20]. The examination of allele diversity in different environmental samples enables scientists to establish the dominance or utility of specific alleles in specific contexts. Lastly, this approach could advance the elucidation of the complex network of interactions between AMF and plant communities [20]. By elucidating AMF diversity at various levels, researchers can enhance their comprehension of the role these fungi play in ecosystem functioning and resilience.

2.2. Evolutionary Relationships between Different AMF Taxa

The study conducted by Dong et al. found that there is a positive correlation between the phylogenetic distances of plant species and the dissimilarity of AMF communities. This finding elucidates the relevance of plant phylogeny and plant-AMF networks in the coevolutionary dynamics of ecosystems [21]. The plant-AMF network is distinguished by its high connectance, nestedness, anti-modularity, and anti-specialization. Connectance is the measure of interactions between plants and AMF, whereas nestedness suggests that specialist AMF species interact with generalist plants. Anti-modularity suggests the absence of distinct modules within the network, implying that all plants have the potential for interactions with all AMF species. Lastly, anti-specialization suggests that no particular AMF species have exclusive associations with specific plant lineages [21] [Table 1].

Table 1 Summary of results from previous studies on the genetic diversity and evolution of AMF

The Genetic Diversity and Evolution of AMF	Study Findings	Reference
Genomic Variation among AMF Species	Bip gene, exhibit significant sequence variability in AMF	[13]
	Low level of genome polymorphism present in <i>R. irregularis</i>	[14]
	AMF exhibit polyphyletic nature in order Glomerales	[15]
	Presence of genetic variation within the AMF	[16]
	Presence of genetic and phenotypic diversity in AMF	[17]
	Presence of phenotypic in <i>Glomus</i> intraradices population	[18]
	Revealed a high-resolution phylogeny of a single species of AMF	[19]
	Established variation in plant performance across diverse AMF species	[20]
Evolutionary Relationships between Different AMF Taxa	Revealed positive correlation between the phylogenetic of AMF	[21]
	Established significant differences in the dispersal capacity among AMF taxa	[22]
	Revealed that nitrogen amendment does not significantly affect AMF diversity	[23]
Horizontal Gene Transfer in Shaping AMF Genomes	Found that a genetic exchange mechanism involves reciprocal recombination in AMF genomes	[24]
	Established 19 fungal genes transferred between fungi and bacterial plants	[25]

These network characteristics foster mutual reliance and equilibrium within ecosystems. The high level of connectance ensures the efficient exchange of nutrients between plants and AMF, thereby enhancing their mutualistic relationship.

The existence of nestedness permits redundancy in interactions, thereby guaranteeing ecosystem resilience in the event of disruptions or extinctions [21]. In addition, the absence of modularity inhibits the segregation of different plant groups or AMF species. Moreover, this study underscores the significance of taking plant phylogeny into account when examining these networks. The phylogenetic distances among plant species are critical factors in determining their associations with specific AMF communities. Acquiring an understanding of these relationships can offer valuable insights into how ecosystems operate and the dynamics of co-evolution. In general, Dong et al.'s study emphasizes the positive relationship between the phylogenetic distances of plant species and the dissimilarity of AMF communities. The distinct attributes of the plant-AMF network foster interdependency and resilience within ecosystems.

In the study conducted by Tipton et al., the researchers investigated the dispersal of arbuscular mycorrhizal fungi (AMF) taxa in four tallgrass prairie restorations. The research aimed to comprehend the varying abilities of different AMF taxa in spreading and modifying the growth of neighboring plants and community composition [22] [Table 1]. This study elucidates the intricate correlation between AMF and plant communities, emphasizing the necessity of grasping their dispersal patterns. The findings of this study underscored significant differences in the dispersal capacity and impact on neighboring plant growth among AMF taxa. Certain taxa exhibited a greater inclination to disseminate and modify non-inoculated plants, whereas others had minimal influence. This variation implies that specific AMF taxa may have a more significant impact on shaping plant communities compared to others [22]. Moreover, the study also showcased that AMF dispersal can lead to substantial implications for community composition. The presence or lack of particular AMF taxa had an impact on the abundance and variety of plant species in the restored prairies [22]. This emphasizes the potential role of AMF as promoters or deterrents of plant community formation. In summary, this research adds to our knowledge of the dispersal and interaction of AMF taxa with neighboring plants in tallgrass prairie restorations. It highlights the importance of delving deeper into specific AMF taxa and their ecological roles to augment restoration endeavors and advance biodiversity conservation.

The study conducted by Dirks and Jackson sheds light on the relationship between nitrogen amendment, arbuscular mycorrhizal fungi (AMF) diversity and community composition, as well as their impact on switchgrass yield [23]. The research findings indicate that nitrogen amendment does not significantly affect AMF diversity or community composition. However, a strong positive relationship is observed between AMF family richness and switchgrass yield. One of the key contributions of this study is the identification of core members of the switchgrass microbiome and novel AMF clades [23] [Table 1]. This discovery provides valuable insights into the intricate relationships between plants and their microbial partners. Understanding these interactions is crucial for developing sustainable agricultural practices that enhance crop productivity. The lack of significant effects of nitrogen amendment on AMF diversity and community composition challenges previous assumptions about the role of nitrogen in shaping belowground microbial communities. It suggests that other factors may play a more prominent role in determining AMF dynamics [23]. The positive relationship between AMF family richness and switchgrass yield highlights the importance of fostering diverse microbial communities for improved plant performance. This discovery corresponds with prior investigations stressing the advantageous impacts of AMF on the growth of plants, absorption of nutrients, and resilience against stress. In general, this exploration enhances our comprehension of the dynamics within subterranean microbial communities in reaction to the addition of nitrogen and their influence on the yield of switchgrass. The identification of core members within the switchgrass microbiome and novel AMF clades opens up new avenues for further research in harnessing these beneficial interactions for sustainable.

2.3. Role of Horizontal Gene Transfer in Shaping AMF Genomes

In the study conducted by Mateus et al., publicly accessible genome sequences were utilized to examine whether AMF (arbuscular mycorrhizal fungi) genomes demonstrate indications of sexual or parasexual reproduction. The study's findings showed a close relationship in the life-cycle of dikaryon and monokaryon isolates with the same putative mat-type, suggesting a genetic exchange mechanism involving reciprocal recombination in AMF genomes [24] [Table 1]. AMF consist of a range of fungi that form mutually beneficial relationships with the roots of most land-dwelling plants. They have a crucial function in acquiring nutrients and facilitating the growth and advancement of plants. Nevertheless, there remains limited knowledge concerning their reproductive mechanisms. This study sought to illuminate this aspect by examining publicly accessible genome sequences. The researchers conducted a comparison of various isolates of AMF with similar putative mat-types, which are genes responsible for mating compatibility. They observed that isolates sharing putative mat-types exhibited similarities in their life-cycle, implying the involvement of a genetic exchange mechanism [24]. The findings have substantial implications for our comprehension of AMF biology and evolution. Sexual reproduction is uncommonly observed in fungi, and this study offers evidence for its presence in AMF genomes. The existence of reciprocal recombination implies that these fungi have evolved mechanisms for genetic material exchange, potentially resulting in heightened genetic diversity. In summary, this study emphasizes the value of publicly accessible genomic data in expanding our understanding of understudied organisms like AMF. Further investigation is

necessary to decipher the complex mechanisms that govern sexual propagation in these fungi and its consequences for their ecological functions.

Li et al.'s study highlights the transfer of fungal genes between bacteria and plants, emphasizing the complex interaction among diverse organisms in genomics. The primary subject of this study was *Rhizophagus irregularis*, a prevalent soil fungus that establishes symbiotic associations with plant roots. The research findings indicated that a grand total of 19 fungal genes had been identified as having been transferred between fungi and bacterial plants [25] [Table 1]. Out of these, seven genes were derived from bacteria, whereas 18 were recently acquired. This discovery holds great importance as these external DNA segments play a vital role in diverse biological activities, including regulating the expression of genes, cell replication, and relaying messages. The consequences of revealing this fact are significant. It challenges the conventional notion of genetic transfer exclusively occurring within species boundaries [25]. The fact that genetic material can be shared among diverse organisms creates novel avenues for evolutionary adaptations and ecological interactions. A possible constituent that contributes to this occurrence is horizontal gene transmission (HGT), which includes the sideward transmission of hereditary material between unrelated living beings. HGT has been recognized as a significant catalyst for microorganism development for a long time, but its existence in eukaryotes, such as fungi and plants, has mostly remained unexplored until now. Comprehending the practical importance of these transferred genes is crucial in deciphering their influence on both the provider and receiver organisms [25]. For instance, the control of gene manifestation plays a vital part in molding an organism's reaction to its environment. By obtaining foreign genes related to this process, *Rhizophagus irregularis* may obtain new capabilities to adapt and flourish under different circumstances. Moreover, mitosis is of utmost importance in facilitating cell division and growth. The occurrence of foreign genes associated with mitosis indicates possible changes in cell division processes within *Rhizophagus irregularis* or its host organisms [25]. Signal transduction is another crucial biological process influenced by these transferred fungal genes. Signal transduction pathways facilitate intercellular communication and enable response to external stimuli. By acquiring foreign genes related to signal transduction, *Rhizophagus irregularis* may improve its capacity to detect and respond to environmental cues.

3. Potential for Future Research

3.1. Characterizing the Functional Significance of Genetic Variation

AMF serve as crucial constituents of terrestrial ecosystems, establishing mutualistic symbioses with the roots of the majority of land plants [26,27]. They play essential roles in nutrient cycling, formation of soil structure, and dynamics of plant communities. Nevertheless, despite their ecological significance, there is still a great deal of uncertainty surrounding AMF genetics and evolution. Investigating the genetic variability among AMF species can yield insights into their evolutionary past and reveal their adaptations to diverse environments. By conducting genome comparisons among different AMF species, researchers can pinpoint the genes responsible for particular traits or functions. This knowledge can facilitate our understanding of the dynamics between these fungi and plants, as well as other organisms in their ecological setting. Additionally, investigating the impact of genomic variability on AMF fitness can yield valuable insights into their adaptability in dynamic environments. Gaining insight into the genetic variations that enhance or hinder AMF fitness can facilitate predictions about their response to future environmental changes, such as climate change or habitat destruction. Apart from understanding the functional outcomes of genetic variation within AMF species, it is also important to study how this variability affects their symbiotic relationships with plants. Various genotypes may exhibit differing capacities to establish advantageous associations with particular plant hosts or contribute unequally to plant development and well-being [28,29,30]. Through the examination of these interactions at a molecular level, researchers can gain valuable insights into the intricate mechanisms that enable successful symbiosis between AMF and plants.

3.2. Elucidating Co-evolutionary Dynamics with Host Plants

Research on the genetic diversity of AMF has unveiled a wide variety of distinct species, each possessing distinctive traits and capacities to engage with host plants [31,32]. By examining the genetic constitution of these fungi, scientists can pinpoint the particular genes accountable for their symbiotic interactions and comprehend their evolutionary trajectory. Moreover, [33,34] state that examining the co-evolutionary processes between AMF and host plants can provide insight into the reciprocal selective pressures that govern their interactions. For instance, certain plant species may have undergone adaptations to selectively form associations with particular AMF species, whereas others may have devised tactics to manipulate fungal colonization for their own advantage. By enhancing our knowledge of these enthralling fungi and their ecological significance, we can unleash remarkable potential in various realms. For example, utilizing the knowledge acquired from studying AMF could potentially result in enhanced agricultural practices through the optimization of plant-fungal interactions to boost crop productivity. Furthermore, it could contribute to ecological

restoration efforts by fostering the establishment of beneficial mycorrhizal associations in degraded ecosystems. Through the exploration of co-evolutionary patterns between AMF and host plants, as well as the reciprocal selective pressures driving these processes, it becomes possible to uncover valuable insights that can be practically applied in agriculture and ecosystem management.

3.3. Uncovering the Mechanisms and Implications of Horizontal Gene Transfer

Exploring the mechanisms that govern their genetic diversity and evolution can offer insights into their ecological roles and potential agricultural applications. One potential avenue for research involves the investigation of horizontal gene transfer (HGT) within the genomes of AMF. HGT is the horizontal transfer of genetic material between disparate species, and it has been demonstrated to exert a substantial influence on the genomes of numerous organisms [35,36]. By analyzing HGT in AMF, researchers can gain valuable insights into the process of gene acquisition and the ability of these fungi to adapt to varying environments. Moreover, exploring the functional significance of horizontally acquired genes can enhance our comprehension of AMF adaptation and fitness. These genes may provide new traits that fortify fungal survival or optimize nutrient acquisition efficiency [37]. By recognizing these genes and investigating their effects, scientists can unveil fresh strategies for enhancing plant-fungal interactions or developing more potent mycorrhizal inoculants for agricultural purposes. By thoroughly examining the mechanisms that underlie HGT in AMF genomes and thoroughly exploring the functional implications of horizontally acquired genes, we can deepen our comprehension of these fascinating fungi and their ecological roles. This knowledge may act as a springboard for revolutionary applications in agriculture, fostering enhanced crop yields and the implementation of sustainable farming practices.

3.4. Incorporating Metagenomic Approaches for Holistic Understanding

The examination of hereditary diversity and evolution of arbuscular mycorrhizal fungi (AMF) showcases substantial potential for the future. Nonetheless, their genetic variability and evolutionary lineage remain elusive. [38,39] state that metagenomic techniques can be employed to investigate DNA that is uncultured and directly derived from environmental samples. This approach provides a thorough comprehension of the entire AMF community within a specific ecosystem. Through the application of genomic analysis, it becomes feasible to pinpoint critical genes correlated with nutrient absorption, stress tolerance, and other significant processes. Our knowledge can also be augmented through the incorporation of multi-omics approaches, amalgamating data from genomics, transcriptomics, proteomics, and metabolomics. According to [40], this integrated approach has the potential to reveal intricate connections among genes, proteins, and metabolites within AMF populations. By employing metagenomic techniques and multi-omics approaches, we can deepen our comprehension of AMF genetic diversity and functional traits, thereby expediting the realization of their full potential in sustainable agricultural practices. This knowledge can be employed to optimize interactions between plants and microorganisms, resulting in heightened crop productivity and diminished environmental footprints. Considering a comprehensive outlook, conducting research on the genetic variability and evolutionary dynamics of AMF through advanced methodologies presents promising prospects. This can yield valuable insights into the ecological roles of these intriguing fungi and empower us to exploit their advantages for sustainable agricultural practices.

4. Conclusion

Understanding the diversity in genes and the evolution of AMF is crucial for comprehending their strategies for adaptation and potential coevolution with host plants. The previous studies on gene variation, evolutionary relationships, and horizontal gene transfer in AMF genomes have laid the groundwork for future research in this field. By thoroughly investigating the functional importance of genetic variation, the dynamics of simultaneous evolution, methods of horizontal gene transfer, and embracing a comprehensive metagenomic approach, we can develop a profound understanding of the gene diversity and evolution of AMF, and their ecological significance.

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