Genomics and Applied Biology 2024, Vol.15, No.1, 54-63
http://bioscipublisher.com/index.php/gab

Research Analysis Open Access

Genomic Diversity and Evolutionary Mechanisms in the *Oryza* Genus: A Comparative Analysis

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Genomics and Applied Biology, 2024, Vol.15, No.1 doi: 10.5376/gab.2024.15.0008
Received: 02 Jan., 2024
Accepted: 06 Feb., 2024
Published: 18 Feb., 2024

Preferred citation for this article:
Li J.Q., and Jiong F., 2024, Genomic diversity and evolutionary mechanisms in the *Oryza* genus: a comparative analysis, Genomics and Applied Biology, 15(1): 54-63 (doi: 10.5376/gab.2024.15.0008)

Abstract The genus *Oryza* encompasses a diverse array of species that exhibit significant genomic variation and evolutionary complexity. This systematic study synthesizes current research on the genomic diversity and evolutionary mechanisms within the *Oryza* genus, providing a comprehensive comparative analysis. Studies have revealed that polyploidy plays a crucial role in the diversification and evolution of *Oryza*, with homoeologous genomic regions experiencing both independent and parallel evolution. Genetic diversity and phylogenetic relationships within the genus have been elucidated using various molecular markers, such as inter simple sequence repeat (ISSR) polymorphism and chloroplast DNA sequences, highlighting the polyphyletic evolution and extensive gene family expansions. Comparative genomic analyses have shown that different *Oryza* species have experienced dissimilar amplification histories of retrotransposons, leading to remarkable differences in genome sizes. Additionally, gene duplication events, including whole genome duplications and segmental duplications, have contributed to the structural and functional evolution of *Oryza* genomes. The rapid diversification of AA-genome species, driven by lineage-specific expansions and contractions of gene families, has facilitated adaptations to diverse ecological niches. The genomic diversity and evolutionary mechanisms in the *Oryza* genus are shaped by a complex interplay of polyploidy, transposable elements, gene duplications, and natural selection. This study underscores the importance of comparative genomic studies in understanding the evolutionary dynamics and potential for crop improvement within the *Oryza* genus.

Keywords Genus *Oryza*; Genomic diversity; Evolutionary mechanisms; Comparative genomics; Inter-species comparison

Rice (*Oryza sativa* L) is a staple food for over half of the world's population and serves as a model organism for plant biology research. The genus *Oryza* includes two domesticated species, *O. sativa* and *O. glaberrima*, and 22 wild species, representing a significant reservoir of genetic diversity that is crucial for crop improvement and food security (Zhang et al., 2014). The wild species of *Oryza*, with their untapped genetic potential, are essential for breeding programs aimed at enhancing disease resistance, stress tolerance, and yield.

The advent of genomics has revolutionized plant research, providing comprehensive insights into genome structure, function, and evolution. The sequencing of the rice genome, particularly the high-quality map-based sequence of *O. sativa* ssp. *japonica* 'Nipponbare', has been a landmark achievement, offering a valuable resource for comparative genomic studies and agricultural productivity improvements. Genomic tools such as bacterial artificial chromosome (BAC) libraries, genome-wide association studies (GWAS), and whole-genome sequencing have facilitated the identification of genetic variations and their association with important agronomic traits (Sakai et al., 2014). These advancements enable the exploration of genetic diversity and evolutionary mechanisms within the *Oryza* genus, providing a foundation for future crop improvement efforts.

This systematic study aims to explore the genomic diversity within the *Oryza* genus by analyzing various genomic resources and studies. By examining the genetic architecture of both cultivated and wild rice species, we seek to understand the extent of genetic variation and its implications for rice breeding and conservation. The research will cover the construction and analysis of BAC libraries, genome-wide association mapping, and the sequencing of multiple rice genomes to provide a comprehensive overview of the genetic diversity present in the *Oryza* genus.

In addition to exploring genomic diversity, this study will analyze the evolutionary mechanisms that have shaped the *Oryza* genus. By comparing the genomes of different *Oryza* species, we aim to identify specific genetic changes associated with adaptation, speciation, and domestication. The research will highlight the role of natural selection, gene duplication, and structural variations in driving the evolutionary processes within the genus. Understanding these mechanisms will provide insights into the evolutionary history of rice and inform strategies for utilizing wild genetic resources in rice improvement programs.

1 Literature Review

1.1 Classification and distribution of *Oryza* genus

The genus *Oryza* comprises approximately 24 species, including two cultivated species, *Oryza sativa* and *Oryza glaberrima*, and 22 wild species. These species are distributed across various geographical regions and ecological environments, reflecting a wide range of adaptations (Figure 1) (Stein et al., 2018). The genus is divided into ten distinct genome types, six diploid and four polyploid, with genome sizes varying significantly from 357 Mbp in *Oryza glaberrima* to 1283 Mbp in the polyploid *Oryza ridleyi*. The wild species of *Oryza* are particularly valuable as they harbor a reservoir of agriculturally important genes that can be utilized for crop improvemen.

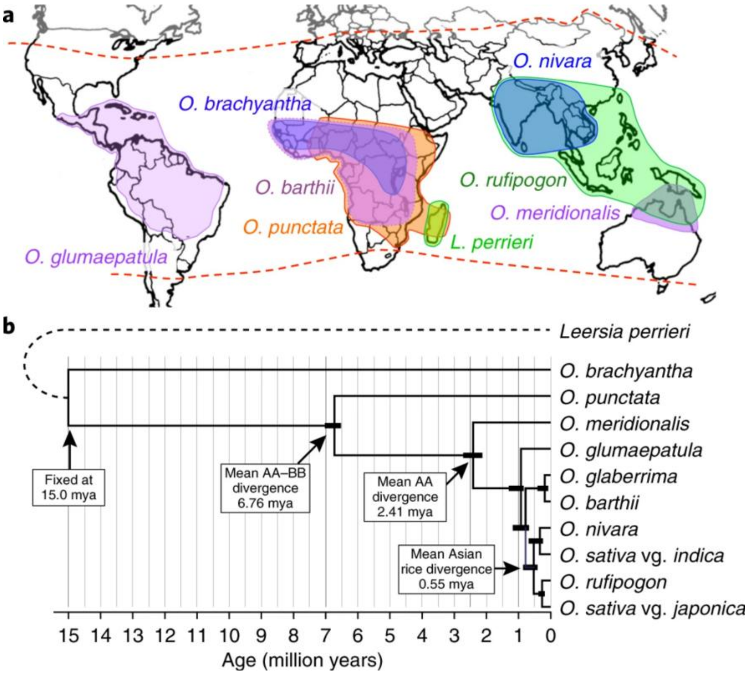

Figure 1 Geographic distribution and phylogenetic reconstruction of wild species of *Oryza* and *Leersia* (Adopted from Stein et al., 2018)

Image Caption: a, Geographic ranges of wild *Oryza* species and the outgroup species L. perrieri sequenced in this study. Dashed red lines show the limits of rice cultivation. Mapped ranges are adapted from IRRI’s Knowledge Bank (see URLs). b, Most frequently estimated species phylogeny in supermatrix and MP-EST analyses of each chromosome (inferred in 10 of 12 chromosomes and 11 of 12 chromosomes, respectively). Bootstrap proportions were obtained from 400 supermatrix bootstrap replicates, and MP-EST support values were obtained as described in the Methods. All clades were supported by both methods at 100%, except as indicated. Divergence times within the *Oryza* genus were estimated by PATHd8, assuming an age of 15 million years for the *Oryza* crown group. Bars on nodes represent the range of PATHd8 age estimates across all 12 chromosomes. Mya, million years ago (Adopted from Stein et al., 2018)

Stein et al. (2018) provides insights into the evolutionary timeline and biogeography of rice species, which is crucial for understanding genetic diversity and guiding rice breeding programs to enhance crop resilience and productivity. The figure presents a study on the evolutionary history and geographic distribution of *Oryza* species, the genus to which rice belongs. Panel (a) maps the distribution of various *Oryza* species and Leersia perrieri across the globe, highlighting distinct geographic regions for each species. For instance, O. glumaepatula is found in South America, while *O. nivara* and *O. rufipogon* are primarily located in Asia. Figure 1Panel (b) depicts a phylogenetic tree illustrating the evolutionary divergence among these species over time. Key divergence events are highlighted, such as the fixation of *Oryza* species at 15 million years ago (mya), the divergence between AA and BB genomes at approximately 6.76 mya, and the divergence within Asian rice species around 0.55 mya (Stein et al., 2018).

1.2 History and current status of rice genome research

Early genome research in rice focused on the sequencing of *Oryza* sativa, which has served as a model system for plant biology due to its relatively small genome size and economic importance. The completion of the rice genome sequence marked a significant milestone, enabling functional characterization and comparative genomic studies within the genus *Oryza*. Modern genomics technologies, such as single-molecule real-time (SMRT) sequencing, 10× Genomics, and Hi-C technologies, have further advanced our understanding of rice genomics. These technologies have facilitated high-quality de novo assemblies of wild rice genomes, revealing insights into the genomic basis of rice adaptation and domestication (Chen et al., 2019). Comparative genomic analyses have identified numerous genomic variants and structural variations that contribute to the diversity and evolution of rice species.

1.3 Current status of genomic diversity research

Genomic diversity research in the *Oryza* genus has employed various diversity indicators, such as single nucleotide polymorphisms (SNPs), simple sequence repeats (SSRs), and linkage disequilibrium (LD) patterns. These indicators have been used to assess genetic diversity within and between different rice populations. For instance, a study using 176 SSR markers revealed significant molecular diversity and polymorphism among three groups of rice germplasm accessions, including domesticated and wild relatives. The analysis of molecular variance and principal coordinates analysis further highlighted the genetic differentiation among these groups. Additionally, the study of transposable elements has shown that these elements play a crucial role in genome size variation and structural evolution within the *Oryza* genus. The identification of lineage-specific gene expansions and contractions has provided insights into the adaptive evolution of rice species to diverse ecological niches (Li et al., 2020).

The classification and distribution of the *Oryza* genus, the advancements in rice genome research, and the ongoing studies on genomic diversity collectively enhance our understanding of the evolutionary mechanisms and genetic diversity within this important genus. These insights are crucial for the continued improvement and conservation of rice as a vital global food resource.

2 The Structure and Function of the Rice Genome

2.1 Basic structure of rice genome

The rice genome, particularly that of *Oryza sativa*, is composed of 12 chromosomes, which collectively harbor a diverse array of genes essential for various biological functions (Stein et al., 2018). The genome structure is characterized by a high degree of conservation across different species within the *Oryza* genus, despite the presence of lineage-specific variations and chromosomal rearrangements. Gene distribution within the rice genome is not uniform; certain regions are densely packed with genes, while others are more sparsely populated. This distribution is influenced by evolutionary processes such as gene duplication and transposon activity, which contribute to the functional diversification of the genome. The rice genome also exhibits significant polymorphism and linkage disequilibrium, which are crucial for understanding the genetic basis of traits and for crop improvement.

2.2 Genomic annotation and functional prediction

Genomic annotation in rice involves the identification and characterization of genes and other functional elements within the genome. This process typically employs a combination of computational and experimental approaches. Methods such as comparative genomics, transcriptomics, and proteomics are used to predict gene functions and validate their roles. Comparative genomic analyses between different *Oryza* species have been particularly useful in identifying conserved and lineage-specific genes, as well as in understanding the evolutionary dynamics of gene families. Functional prediction often involves the use of databases like *Oryza*Genome, which integrates genotype and phenotype information to facilitate the analysis of gene function and structural evolution. Additionally, techniques such as BAC (Bacterial Artificial Chromosome) library construction and analysis provide valuable resources for functional characterization and comparative studies (Zhang et al., 2014).

2.3 Repeats and transposons

Repeats and transposons play a significant role in shaping the structure and function of the rice genome. The *Oryza* genome contains various types of repetitive elements, including LTR retrotransposons, which are the predominant class of repeats. These elements contribute to genome size variation and are involved in processes such as gene duplication and chromosomal rearrangement. Transposons, in particular, are classified into different families based on their structure and mode of transposition. They are known to drive genomic innovation by creating new gene combinations and regulatory elements. The activity of transposable elements is a key factor in the rapid diversification and adaptation of *Oryza* species, as they facilitate the emergence of novel genetic traits. Comparative analyses have shown that transposon activity and the removal of transposable elements through recombination are crucial mechanisms in the expansion and contraction of the rice genome (Wang and Han, 2022).

3 Comparative Analysis of Genomic Diversity in Three *Oryza* Genera

3.1 Genomic sequence alignment

Genomic sequence alignment is a critical method for comparing the genetic makeup of different rice species within the *Oryza* genus. Various techniques, such as whole-genome sequencing and the construction of bacterial artificial chromosome (BAC) libraries, have been employed to achieve high-resolution alignments. The construction and analysis of 12 deep-coverage large-insert BAC libraries representing the 10 genome types of the genus *Oryza* have provided a comprehensive resource for comparative genomic studies. These libraries facilitate the alignment of genomic sequences across different species, enabling the identification of conserved and divergent regions (Table 1) (Ohyanagi et al., 2015).

Ohyanagi et al. (2015) provides a detailed analysis of the mapping and detection of genome variants across various *Oryza* species and cultivars using deep next-generation sequencing (NGS). It covers several cultivars such as Os-japonica (Nipponbare), Os-indica (Guangluai-4), Os-aus (Kasalaath), and others, showcasing the number of read pairs, mapping rates, average depth, and genome coverage. Os-japonica and Os-indica demonstrate high mapping efficiency with significant genome coverage, highlighting their genomic stability. The SNP detection section reveals substantial genetic variability, especially in Os-indica and Os-aus, with over a million SNPs each. Homogeneous and heterogeneous SNP counts further elucidate genetic diversity, with Os-japonica displaying a high heterogeneous ratio. This extensive genomic data is pivotal for understanding genetic diversity within *Oryza* species, providing valuable insights for breeding programs aimed at enhancing crop resilience and productivity, thereby contributing to global food security and agricultural sustainability (Ohyanagi et al., 2015).

Additionally, the de novo assembly of genomes from five diploid AA-genome species closely related to *Oryza* sativa has revealed significant structural variations, including segmental duplications and rapid gene family turnover. These alignments help in understanding the evolutionary mechanisms driving genomic diversity and adaptation in different environments.

3.2 Genomic diversity measurement

Genomic diversity within the *Oryza* genus can be measured using various indicators such as single nucleotide polymorphisms (SNPs), insertions and deletions (Indels), and simple sequence repeats (SSRs). These markers provide insights into the genetic variation and evolutionary history of rice species.A detailed study using 176 SSR markers across three groups of rice germplasm accessions highlighted the molecular diversity and polymorphism within *Oryza* sativa and its wild relatives. The study reported a mean of 16 alleles per SSR marker and polymorphism information content values ranging from 0.43 to 0.91, indicating substantial genetic variation (Raza et al., 2023).

Table 1 Statistics of mapping analysis and detection of genome variants (SNPs) for deeper NGS genome sequences (Adopted from Ohyanagi et al., 2015)

Species/Ecotype	Cultivar name/NIG Wid Rice accession	Number of read pairs (original)	Number of read pairs (after preprocessing)	Mapping analysis					SNP detection			
				Mapping rate (%, average)	Mapping rate (%, read1)	Mapping rate (%, read2)	Average depth (x times reference genome)	Genome of coverage (%)	Number of SNPs(all)	Number of SNPs (homogeneous)	Number of SNPs (heterogeneous)	Heterogeneous ratio (%, hetero./all)
Os-japonica	Nipponbare (NIG stock)	27 163 585	21 977 537	85.28	94.17	76.39	9.131	89.75	12 376	4 937	7 439	60.11
	Nongken-58	68 213 581	60 824 534	98.50	98.65	98.36	12.69	96.54	46 422	38 261	8 161	17.58
Os-indica	Guangluai-4	54 309 982	45 105 225	92.86	93.02	92.70	15.13	90.21	1 231 216	1 145 128	86 088	6.992
Os-aus	Kasalath	206 469 104	199 240 404	91.53	91.54	91.51	92.39	92.84	2 020 481	1 865 985	154 496	7.646
Or-I	W0106	25 090 954	21 291 026	69.83	76.76	62.90	7.481	78.26	269 386	225 060	44 326	16.45
	W0630	79 734 147	70 417 961	90.13	90.31	89.94	32.37	89.10	2 201 911	2 053 089	148 822	6.759
	W1230	68 999 113	61 736 419	89.72	89.89	89.55	28.36	89.27	2 143 756	1 968 156	175 600	8.191
	W1921	24 756 280	21 323 134	70.03	77.36	62.69	7.086	77.87	191 542	155 355	36 187	18.89
Or-II	W0120	69 331 945	61 953 915	89.88	90.03	89.72	28.47	90.55	2 082 384	1 569 524	512 860	24.63
	W0180	63 097 081	56 313 044	88.89	89.11	88.68	25.61	89.44	1 984 170	1 629 437	354 733	17.88
	W1236	71 082 413	63 974 789	89.31	89.45	89.17	29.21	91.44	2 507 539	1 583 395	924 144	36.85
	W1715	59 688 661	53 023 455	89.84	90.03	89.64	24.36	95.20	2 776 086	974 774	1 801 312	64.89
	W1981	68 868 645	61 843 301	89.13	89.27	89.00	28.17	89.95	2 374 591	1 687 582	687 009	28.93
Or-III	W0593	72 006 505	63 695 769	88.68	88.86	88.50	28.94	88.44	2 117 072	1 963 157	153 915	7.270
	W1943	32 091 193	30 369 210	94.38	94.34	94.41	15.06	92.10	769 640	703 427	66 213	8.603
O. longistaminata	W1413	36 304 086	21 237 761	61.89	67.79	56.00	6.571	54.95	424 135	280 952	143 183	33.76
	W1508	15 768 341	11 679 929	66.15	68.95	63.34	3.766	51.07	305 631	198 973	106 658	34.90

Furthermore, the *Oryza*Genome database integrates SNP data and genomic variation information for wild *Oryza* species, offering a valuable resource for genotype-phenotype association studies. This database includes genotype information for 446 *O. rufipogon* accessions and provides tools for precise inspection of each variant.

3.3 Genomic structural variation

Structural variations, such as fragment duplications, deletions, and inversions, play a significant role in shaping the genomes of rice species. These variations can impact gene function and contribute to the evolutionary dynamics of the *Oryza* genus. Comparative genomic analyses have revealed the dynamic evolution of *Oryza* genomes, with transposable elements mediating massive replacement of intergenic space, gene disruption, and gene/gene fragment movement. Long Terminal Repeat (LTR) retrotransposons, in particular, have been identified as major contributors to genome size variation and structural changes (Qin et al., 2021).

Additionally, the rapid diversification of five *Oryza* AA genomes has been associated with significant structural variations, including segmental duplications and gene family turnover, particularly in defense-related genes (Qin et al., 2021). These structural changes are crucial for the adaptation of rice species to different ecological niches and environmental conditions. The comparative analysis of genomic diversity in the *Oryza* genus involves genomic sequence alignment, measurement of genetic diversity using various markers, and the study of structural variations. These approaches provide a comprehensive understanding of the evolutionary mechanisms driving the diversity and adaptation of rice species.

4 The Evolutionary Mechanism of the Rice Genus

4.1 Phylogenetic evolution of the rice genus

The phylogenetic evolution of the rice genus, *Oryza*, has been extensively studied using various molecular systematics methods, including the construction and analysis of phylogenetic trees. Whole chloroplast genome sequences have been utilized to elucidate the evolutionary and phylogenetic relationships within the AA genome *Oryza* species, providing a well-resolved and strongly supported phylogeny. Amplified fragment length polymorphism (AFLP) markers have also been employed to study species relationships, revealing a polyphyletic path of evolution within the genus *Oryza*. Additionally, simple sequence repeats (SSR) and their flanking regions in the mitochondrial and chloroplast genomes have been analyzed to gain new insights into phylogenetic relationships among *Oryza* species. These studies collectively contribute to a robust understanding of the phylogenetic evolution of the rice genus (Wambugu et al., 2015).

4.2 Genomic evolutionary dynamics

The genomic evolutionary dynamics of the *Oryza* genus involve processes such as genome replication, polyploidization, gene loss, and acquisition. The genus *Oryza* has experienced ancient whole genome duplications, common to all grasses, and more conserved segmental duplications, such as those between the distal regions of chromosomes 11 and 12. Comparative analyses of large genomic regions and whole-genome sequences have revealed molecular mechanisms involved in genome size variation, gene movement, and the transition of euchromatin to heterochromatin. The prevalence of transposon activity and the removal of transposable elements by unequal recombination or illegitimate recombination are significant factors contributing to the expansion or contraction of *Oryza* genomes (Liu et al., 2021). Furthermore, the genus *Oryza* consists of both recently formed and older allopolyploid species, providing insights into the process of diploidization and the temporal evolutionary dynamics of polyploid genomes.

4.3 Environmental adaptation and genomic variation

Environmental adaptation and genomic variation in the *Oryza* genus are driven by both natural and artificial selection. The rapid diversification of five *Oryza* AA genomes has been associated with rice adaptation to different environments across four continents, highlighting specific genetic changes related to defense against pathogens and reproductive diversification. This adaptation is reflected in the high instability of defense-related genes and the expansion or contraction of gene families, which have led to morphological and reproductive diversification. Additionally, the genus *Oryza* has been a model system for studying the impact of structural variation, lineage-specific genes, and the evolution of agriculturally important genes on phenotype diversity and adaptation. The identification of new haplotypes and functionally coupled disease resistance genes in domesticated and wild rice relatives further underscores the role of natural and artificial selection in shaping the genomic variation of cultivated rice (Yu et al., 2023).

5 Research Methods

5.1 Sample collection and genome sequencing

Sample collection and genome sequencing are fundamental steps in understanding the genomic diversity and evolutionary mechanisms in the *Oryza* genus. Various studies have employed different strategies to collect samples and sequence genomes. For instance, in the study by Stein et al. (2018), 13 reference genomes spanning the *Oryza* species tree were sequenced to explore genetic conservation and turnover across the genus. Similarly, another study utilized 42 genotypes, including wild and cultivated species, to determine genetic diversity using inter simple sequence repeat (ISSR) polymorphism. The collection of samples from diverse geographical locations and different species within the genus ensures a comprehensive analysis of genomic diversity.

5.2 Data analysis and processing

Data analysis and processing involve several computational and statistical methods to interpret the sequenced genomic data. Comparative genomics is a powerful tool used to decipher gene and genome evolution. For example, comparative sequence analysis of MONOCULM1-orthologous regions in 14 *Oryza* genomes revealed highly conserved gene colinearity and structure, providing insights into gene function and genome evolution. Additionally, studies have employed phylogenetic analyses to understand the evolutionary relationships among different *Oryza* species. The use of highly variable regions of chloroplast DNA has been particularly effective in elucidating these relationships with fine resolution. Advanced bioinformatics tools and software are crucial in processing large datasets and identifying significant genetic variations (Abdullah-Zawawi et al., 2021).

5.3 Gene function validation experiment

Gene function validation experiments are essential to confirm the roles of specific genes identified through genomic analyses. These experiments often involve functional genomics approaches such as gene knockouts, overexpression studies, and phenotypic analyses. For instance, the study on gene family expansion in the *Oryza* genus investigated the evolutionary dynamics of gene families like F-box and NB-ARC, showing that expansions resulted from both amplification and contraction by gene losses. Functional validation of these genes can be achieved through experimental approaches that assess their impact on plant traits and responses to environmental stresses (Sha et al., 2023). Such experiments provide a deeper understanding of the functional significance of genetic variations observed in the *Oryza* genus.

6 Discussion

The research findings on genomic diversity and evolutionary mechanisms in the *Oryza* genus have profound implications for understanding rice evolution and adaptability. The studies collectively highlight the significant contribution of genomic diversity to rice evolution. For instance, the analysis of molecular diversity and polymorphism in various *Oryza* species has revealed substantial genetic variation, which is crucial for the evolutionary processes at both population and genomic levels. The identification of genome-wide signatures of rice domestication and heterosis has provided insights into the genetic basis of rice adaptation and the origin of cultivated rice. Furthermore, the rapid species diversification and turnover of transposons and other genomic elements have been shown to play a pivotal role in the evolutionary dynamics of the *Oryza* genus.

The relationship between genomic variation and rice adaptability is also well-documented. Comparative genomic analyses have identified specific genetic changes responsible for adaptations to diverse ecological niches, such as defense against pathogens and reproductive diversification. The presence of functionally coupled disease resistance genes and the identification of new haplotypes offer potential for future crop protection and improvement. Additionally, the role of transposable elements in driving genome size variation and their correlation with genome sizes across different *Oryza* species further underscore the importance of genomic diversity in rice adaptability (Dai et al., 2022).

Despite the significant advancements, there are limitations and shortcomings in the current research. One major limitation is the sample size. Many studies have focused on a limited number of accessions or species, which may not fully capture the genomic diversity present within the entire *Oryza* genus. For example, the study on genome size variation included only 166 accessions from 16 non-AA genome *Oryza* species, which may not be representative of the entire genus.

Another limitation lies in the analysis methods. While advanced sequencing technologies have been employed, there are still challenges in accurately assembling and annotating complex genomes, particularly those with high levels of repetitive elements and structural variations. The reliance on single reference genomes for comparative analyses may also overlook the extensive genomic and allelic diversity within the genus. Additionally, the detection of linkage disequilibrium and marker-trait associations may be influenced by the choice of markers and the resolution of genome-wide scans (Li et al., 2020).

Future research should focus on addressing these limitations by leveraging the development of genomics technology and exploring new prospects for rice genome research. The integration of high-quality de novo assemblies and long-read sequencing technologies can provide more comprehensive and accurate genomic data, facilitating the discovery of novel genetic elements and structural variations. Expanding the sample size to include a broader range of *Oryza* species and accessions will enhance the understanding of genomic diversity and its role in rice evolution and adaptability.

Moreover, the establishment of comprehensive genomic databases, such as *Oryza*Genome, can serve as valuable resources for genotype-phenotype association studies and functional analyses. Future research should also focus on the functional characterization of identified genes and genomic elements, particularly those involved in stress responses, reproductive processes, and disease resistance. The application of integrated genomic approaches and comparative phylogenomics will further elucidate the molecular mechanisms underlying rice evolution and provide new opportunities for crop improvement and conservation of wild rice germplasm.

7 Concluding Remarks

The genus *Oryza*, encompassing both domesticated and wild rice species, has been extensively studied to understand its genomic diversity and evolutionary mechanisms. Key research achievements include the identification of significant genetic conservation, turnover, and innovation across the genus. For instance, the study of 13 reference genomes has highlighted rapid species diversification and the emergence of novel elements such as transposons and new coding and noncoding genes. Additionally, the analysis of molecular diversity and linkage disequilibrium patterns in various *Oryza* germplasm accessions has provided insights into the genetic structure and evolutionary processes within the genus.

The development of comprehensive genomic resources, such as the Rice TE database (RiTE-db), has facilitated the annotation and comparative analysis of transposable elements across multiple *Oryza* species. Furthermore, the sequencing and analysis of wild and cultivated rice genomes have shed light on the domestication processes and heterosis in rice, revealing genome-wide signatures and the origin of cultivated rice. The *Oryza* Map Alignment Project (OMAP) has also contributed significantly by establishing a genus-wide comparative framework, highlighting the impact of structural variations on genome diversity.

The application of genomic research in rice breeding has profound implications for the future of agriculture. The comprehensive genomic resources developed for the *Oryza* genus provide a valuable foundation for leveraging genetic diversity from wild relatives to improve cultivated rice varieties. For example, the construction of bacterial artificial chromosome (BAC) libraries representing the 10 genome types of *Oryza* has enabled the exploration of agriculturally important genes from wild species. These resources are crucial for maintaining a safe and secure food supply in the face of global challenges such as climate change and population growth.

Moreover, the integration of genomic and phenotypic data in databases like *Oryza*Genome facilitates genotype-phenotype association studies, which are essential for understanding the functional and structural evolution of rice genomes. The identification of positively selected genes involved in key traits such as flower development, ripening, and stress response further underscores the potential of genomic research to enhance rice breeding programs.

The advancements in genomic research within the *Oryza* genus have not only deepened our understanding of rice genome diversity and evolutionary mechanisms but also provided invaluable tools and insights for future rice research and breeding efforts. Continued exploration and conservation of wild *Oryza* species will be essential to harness their genetic potential for the development of resilient and high-yielding rice varieties, ultimately contributing to global food security.

Acknowledgments

We would like to express our gratitude to the two anonymous peer reviewers for their critical assessment and constructive suggestions on our manuscript.

Conflict of Interest Disclosure

The authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

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