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Genomic Evolution in *Oryza*: The Role of Novel Genetic Elements

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Abstract The genus *Oryza*, encompassing both domesticated and wild rice species, serves as a model system for studying genomic evolution due to its diverse genetic background and ecological adaptations. This study investigates the role of novel genetic elements in the genomic evolution of *Oryza*, focusing on the processes of diploidization, transposon activity, and *de novo* gene origination. By analyzing orthologous genomic sequences, chloroplast genomes, and structural variations across multiple *Oryza* species, the study uncovers the dynamics of genome size variation, the emergence of new protein-coding genes, and the adaptive evolution of chloroplast genes. The findings reveal that transposable elements, particularly LTR retrotransposons, significantly contribute to genome size variation and that *de novo* genes play a crucial role in protein diversity. Additionally, the adaptive evolution of chloroplast genes facilitates the adaptation of rice species to diverse ecological habitats. These insights enhance the understanding of the genomic mechanisms underlying the evolution and domestication of rice, providing valuable information for crop improvement strategies.

Keywords Rice (*Oryza sativa*); Genomic evolution; *Oryza*; Diploidization; Transposable elements; *De novo* gene

1 Introduction

The genus *Oryza* encompasses a diverse group of species, including the globally significant staple crops, Asian rice (*Oryza sativa*) and African rice (*Oryza glaberrima*). These species are not only crucial for feeding over half of the world's population but also serve as model organisms for genetic and evolutionary studies due to their well-characterized genomes and extensive genetic diversity (Wambugu et al., 2015; Wei and Huang, 2019; Kumar et al., 2020). The evolutionary history and domestication processes of *Oryza* species have profoundly influenced human civilization and agricultural practices, making them a focal point for research aimed at improving crop resilience and productivity (Veltman et al., 2018).

Studying genomic evolution in *Oryza* is essential for several reasons, it provides insights into the mechanisms of domestication and adaptation, which are critical for developing new rice varieties that can withstand biotic and abiotic stresses (Ahmad, 2022), understanding the genetic relationships and evolutionary history of wild and domesticated rice species can help in the conservation of genetic resources and the sustainable use of wild relatives in breeding programs (Jacquemin et al., 2013; Wambugu et al., 2015). Genomic studies can reveal the complex genetic architecture underlying important agronomic traits, thereby facilitating targeted breeding efforts to enhance yield, quality, and stress tolerance (Zhao et al., 2011; Li et al., 2018).

Novel genetic elements, such as transposable elements, gene duplications, and non-coding RNAs, play a significant role in the evolution of genomes by introducing genetic variability and enabling rapid adaptation to changing environments (Ammiraju et al., 2010). These elements can drive the evolution of new traits and contribute to the genetic diversity observed within and between *Oryza* species. Understanding the impact of these novel genetic elements on the genomic evolution of *Oryza* can provide valuable insights into the mechanisms of plant adaptation and speciation (Xu et al., 2021).

The objectives of this study are to explore the role of novel genetic elements in the genomic evolution of *Oryza* and to understand how these elements have contributed to the diversification and adaptation of rice species. The scope of the paper includes a comprehensive analysis of the genomic data from various *Oryz*a species, identification and characterization of novel genetic elements, and an assessment of their impact on the evolution of key agronomic traits.

2 Genomic Diversity in *Oryza*

2.1 Overview of the *Oryza* genus and its genetic diversity

The genus *Oryza*, which includes both wild and cultivated rice species, is a model system for studying plant genome structure, function, and evolution. The genetic diversity within this genus is vast, encompassing numerous species adapted to a wide range of environments across different continents. For instance, *Oryza sativa*, the most widely cultivated species, exhibits significant genetic variation across its subpopulations, such as indica and japonica, which have distinct evolutionary histories and adaptations (Zhao et al., 2011; Zhang et al., 2014). Wild relatives like *Oryza rufipogon* and *Oryza nivara* also contribute to the genetic pool, offering valuable alleles for crop improvement (Li et al., 2020). The genetic diversity within *Oryza* is not only crucial for understanding evolutionary processes but also for enhancing rice breeding programs aimed at improving yield, quality, and stress resistance (Wang et al., 2018).

2.2 Comparative genomics

Comparative genomic studies have provided deep insights into the genomic variations across different *Oryza* species. For example, the *de novo* sequencing of five diploid AA-genome species revealed extensive structural variations, including segmental duplications and rapid gene family turnover, particularly in defense-related genes (Zhang et al., 2014). These variations are indicative of the adaptive strategies employed by different species to thrive in diverse ecological niches. Additionally, the analysis of 13 reference genomes spanning the *Oryza* species tree highlighted the rapid species diversification and the emergence of novel genetic elements, such as transposons and new coding genes, which play a significant role in the evolutionary process. Such comparative studies underscore the importance of genomic innovations in the adaptation and speciation of *Oryza* species.

2.3 Role of whole genome duplications and their impact on diversity

Whole genome duplications (WGDs) have been pivotal in shaping the genomic landscape of *Oryza* species. These duplications have led to the expansion of gene families, providing raw material for evolutionary innovation and adaptation. For instance, the lineage-specific expansion of gene families in *Oryza* has been linked to reproductive isolation mechanisms and the evolution of mating systems (Li et al., 2020). Moreover, WGDs have contributed to the high levels of genetic diversity observed in *Oryza*, facilitating the development of new traits and enhancing the species' ability to adapt to changing environments (Zhang et al., 2014; Stein et al., 2018). The impact of WGDs is also evident in the presence of numerous positively selected genes involved in critical processes such as flower development, reproduction, and stress responses, which are essential for the survival and success of *Oryza* species in various habitats (Li et al., 2020).

3 Classification and Types of Novel Genetic Elements in *Oryza*

3.1 Definition and categorization of novel genetic elements

Novel genetic elements in the genus *Oryza* encompass a variety of sequences that contribute to genomic diversity and evolution. These elements include transposons, non-coding RNAs, gene duplications, and other repetitive sequences. Transposons, or transposable elements (TEs), are DNA sequences that can change their position within the genome, thereby creating or reversing mutations and altering the cell's genetic identity. Non-coding RNAs (ncRNAs) are RNA molecules that are not translated into proteins but play crucial roles in regulating gene expression. Gene duplications involve the creation of an extra copy of a gene, which can lead to new functions or regulatory mechanisms (Stein et al., 2018).

3.2 Examples of novel genetic elements identified in *Oryza* genomes

Several studies have identified various novel genetic elements in *Oryza* genomes. For instance, Long Terminal Repeat (LTR) retrotransposons, such as the Ty3-gypsy elements RIRE2 and Atlantys, have been shown to significantly contribute to genome size variation across different *Oryza* species (Zuccolo et al., 2007). Miniature

Inverted-Repeat Transposable Elements (MITEs) are another class of TEs that have been extensively studied in rice (*Oryza sativa*). These elements have been found to be associated with a large number of genes and are involved in gene expression and species diversity (Lu et al., 2011). Additionally, whole-genome duplications (WGDs) have been observed in *Oryza*, leading to the duplication of nearly all subunits of protein complexes associated with essential cellular functions (Ma et al., 2009).

3.3 Mechanisms of how these elements arise and propagate

The mechanisms by which these novel genetic elements arise and propagate are diverse. Transposons, for example, can move within the genome through a “cut and paste” or “"copy and paste” mechanism, facilitated by transposase enzymes (Böhne et al., 2012). LTR retrotransposons replicate through an RNA intermediate, which is reverse-transcribed and inserted back into the genome, leading to genome expansion (Ammiraju et al., 2007). MITEs proliferate through *Amplification bursts*, where multiple rounds of replication occur, leading to their widespread presence in the genome (Lu et al., 2011). Whole-genome duplications result from errors during cell division, leading to the duplication of the entire genome, which can then undergo diploidization and functional divergence over time (Figure 1) (Zou et al., 2020).

4 Functional Roles of Novel Genetic Elements in *Oryza* Genomes

4.1 Impact on gene regulation and expression

Novel genetic elements, such as microRNAs (miRNAs) and transposable elements, play crucial roles in the regulation of gene expression in *Oryza* species. miRNAs, for instance, are non-coding RNAs that modulate post-transcriptional gene regulation. Studies have shown that miRNAs in *Oryza* species exhibit significant evolutionary changes, with some miRNA families expanding differently across species. These miRNAs are involved in regulating responses to environmental stresses, such as salinity, by differentially expressing in various *Oryza* species (Ganie et al., 2017). Similarly, Miniature Inverted-Repeat Transposable Elements (MITEs) have been found to be associated with a large number of genes in the rice genome, influencing their expression. MITEs generate a substantial portion of small RNAs in rice, which can regulate gene expression by forming natural sense/antisense transcripts (Lu et al., 2011).

4.2 Role in adaptive evolution and environmental stress response

Novel genetic elements contribute significantly to the adaptive evolution of *Oryza* species, enabling them to thrive in diverse environments. The *Dof* transcription factor family, for example, has been shown to regulate various stress responses and developmental processes in rice. These genes have undergone strong purifying selection and segmental duplications, which have expanded their family members in *Oryza* genomes. The miR2927, targeting the *Dof* domain, regulates gene expression under different climatic conditions, aiding in the adaptation to changing environments (Tabassum et al., 2022). Additionally, the rapid diversification of *Oryza* genomes, particularly in defense-related genes, highlights the role of novel genetic elements in adaptation to different ecological niches.

4.3 Contribution to genome structure and stability

Novel genetic elements also play a pivotal role in shaping the genome structure and maintaining its stability. The *Oryza* genus has experienced lineage-specific emergence and turnover of many novel elements, including transposons and new coding and noncoding genes. These elements contribute to the structural variation observed in *Oryza* genomes, such as segmental duplications and gene family turnover, which are crucial for the evolutionary process of speciation and adaptation (Figure 2) (Stein et al., 2018). Furthermore, the presence of MITEs in the rice genome has been linked to the generation of small RNAs, which can influence genome stability by regulating gene expression and maintaining genomic integrity (Lu et al., 2011).

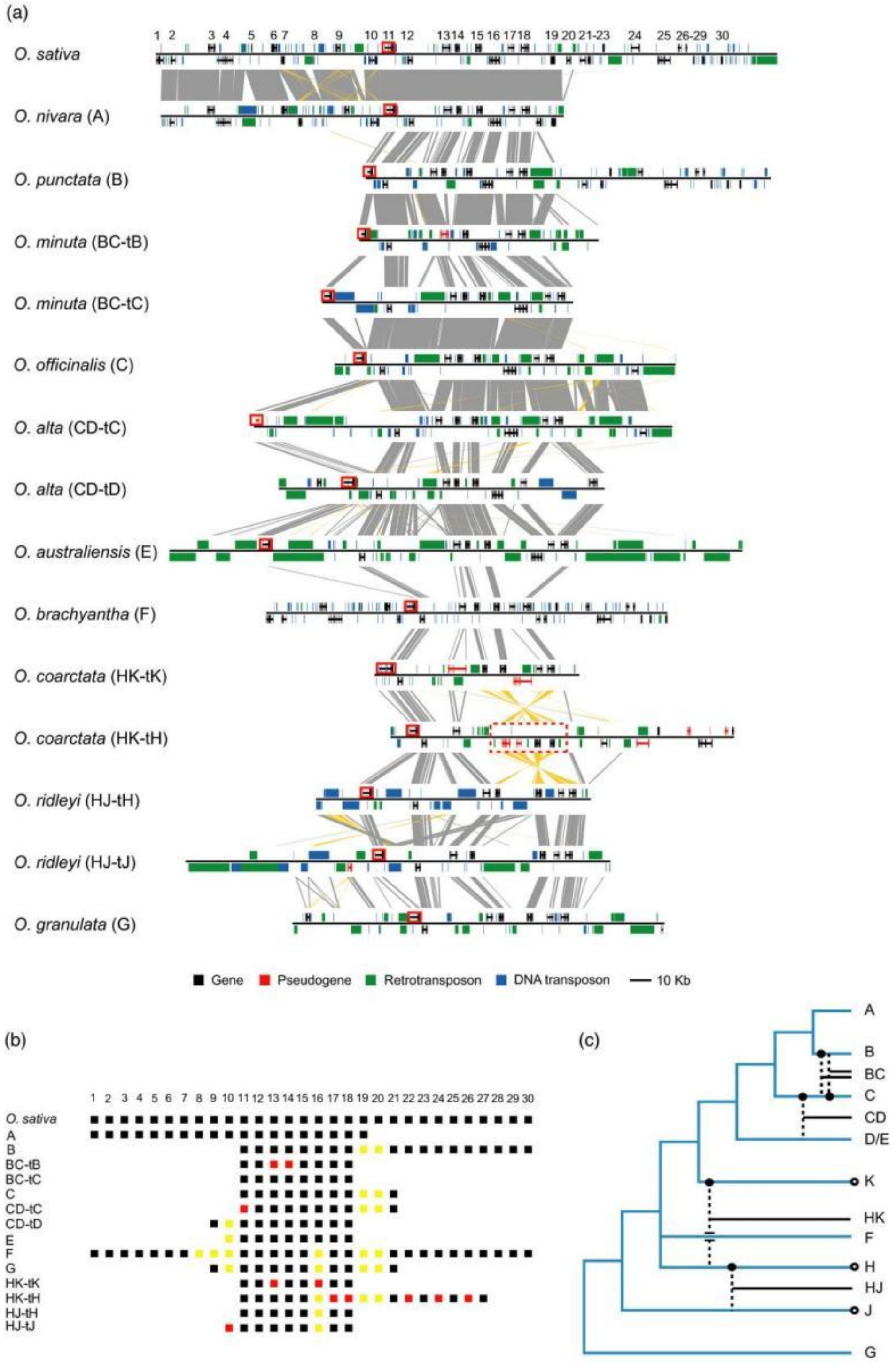

Figure 1 Sequence comparison of the orthologous DEP1 region across the rice genus *Oryza* and evolutionary relationships among 10 genome types (Adopted from Zou et al., 2020)

Image caption: a: Syntenic view of the DEP1 region across *Oryza*. Similar sequences are connected by gray lines if the matching segments are in direct orientation, or by yellow lines if the matching segments are in reverse orientation. Genes are colored in black, with every exon shown in black rectangles and connected (with DEP1 highlighted in a red box), while pseudogenes are indicated by red. Retrotransposon and DNA transposon are colored in green and blue, respectively. An~40-kb inversion in HK-tH genome is highlighted in a red dotted box. Gene models are coded using 1~30 and shown above the rice genome (*Oryza sativa*); b: Gene evolution in the DEP1 region. Black squares indicate orthologous genes. Red squares indicate pseudogenes. Yellow squares stand for syntenic gene loss; c: Schematic diagram showing the evolutionary relationships among 10 *Oryza* genome types. Dashed lines represent origins of allotetraploids, with the maternal donors indicated by dark circles. Open circles indicate unidentified diploid genomes (Adapted from Zou et al., 2020)

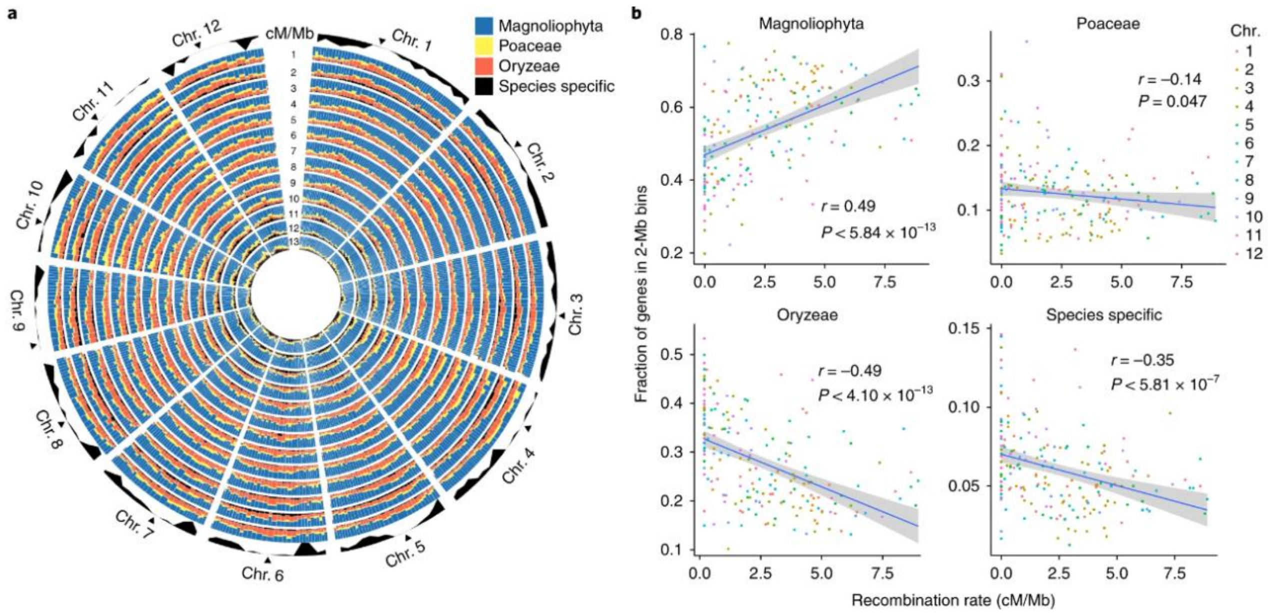

Figure 2 Positional bias of loci derived from ancient and recent families in the *Oryzeae* (Adopted from Stein et al., 2018)

Image caption: a: Each segment represents a stacked histogram of tiled windows of 100 loci. Species: 1: *O. sativa vg. japonica*; 2: *O. sativa vg. aus* (N 22); 3: *O. sativa vg. indica* (IR 8); 4: *O. sativa vg. indica* (93-11); 5: *O. rufipogon*; 6: *O. nivara*; 7: *O. glaberrima*; 8: *O. barthii*; 9: *O. glumaepatula*; 10: *O. meridionalis*; 11: *O. punctata*; 12: *O. brachyantha*; 13: *L. perrieri*. Recombination rate is shown in the outer ring, ranging from 0 to 9 cM/Mb, based on the integrated genetic/physical map of rice (constructed from data from Harushima et al. and McCouch et al.) for *O. sativa vg. japonica* downloaded from http://archive.gramene.org/. Triangles show the position of rice centromeres. b: Differential correlations in *O. sativa vg. japonica* of gene age group prevalence (calculated over 191 2-Mb non-overlapping windows) with chromosome recombination rate. Pearson's correlation coefficient (*r*) and *P* value are shown for each plot (Adopted from Stein et al., 2018)

Several case studies highlight the functional roles of specific novel genetic elements in *Oryza* genomes. For instance, the miR1861 family, organized into distinct clusters in various *Oryza* species, plays a role in regulating responses to salt stress, demonstrating the functional importance of miRNAs in environmental adaptation (Ganie et al., 2017). Another example is the WD40 subfamily, which includes genes involved in anthocyanin biosynthesis and stress resistance. The *OsiWD40-24* gene, in particular, has been found to respond to both phytohormones and abiotic stresses, indicating its role in plant stress resistance (Ke et al., 2023). Additionally, the study of the *Dof* transcription factor family has identified superior haplotypes associated with early flowering, which can be utilized for developing early maturing and climate-resilient rice cultivars.

5 Evolutionary Implications of Novel Genetic Elements in *Oryza*

5.1 Role in speciation and diversification of *Oryza* species

Novel genetic elements play a crucial role in the speciation and diversification of *Oryza* species. The rapid diversification observed in the *Oryza* genus is often mirrored by the emergence and turnover of novel elements such as transposons and new coding and noncoding genes (Stein et al., 2018). These genetic changes are particularly significant in genes related to defense mechanisms and reproductive diversification, which are essential for adaptation to different ecological niches. The presence of lineage-specific expansions of gene families has been linked to morphological and reproductive diversification, highlighting the role of novel genetic elements in driving speciation (Zhang et al., 2014).

5.2 Genetic mechanisms driving the evolution of novel elements

The evolution of novel genetic elements in *Oryza* is driven by several genetic mechanisms, including the activity of transposable elements (TEs). Long Terminal Repeat (LTR) retrotransposons, for instance, have been identified as major contributors to genome size variation and structural changes across the *Oryza* genus (Dai et al., 2022). The proliferation of these elements varies significantly among species, indicating their role in shaping genome architecture and contributing to genetic diversity (Zuccolo et al., 2007). Additionally, the *de novo* origination of protein-coding genes from non-coding DNA sequences has been identified as a significant source of new genetic material, contributing to protein diversity and rapid evolution under positive selection (Zhang et al., 2019).

5.3 Comparative genomics to understand evolutionary trajectories

Comparative genomics provides valuable insights into the evolutionary trajectories of *Oryza* species. By analyzing the genomes of multiple *Oryza* species, researchers have identified extensive genomic structural variations, including segmental duplications and gene family turnover. These studies reveal how specific genetic changes correlate with adaptations to different environments, offering a comprehensive understanding of the evolutionary processes at play (Zhang et al., 2014). The comparative analysis of wild and domesticated rice genomes has also highlighted the role of dispensable genes in reproductive processes, further elucidating the genetic basis of speciation and adaptation (Li et al., 2020).

5.4 Phylogenetic insights into the spread and fixation of novel elements

Phylogenetic studies have provided insights into the spread and fixation of novel genetic elements within the *Oryza* genus. The complex history of introgression among different chromosomes in the young ‘AA’ subclade, which includes domesticated species, underscores the dynamic nature of genetic exchange and the role of novel elements in evolutionary processes. The rapid and distinct diversification of LTR retrotransposon families since the species split over the last 4.8 million years illustrates how these elements have shaped the evolutionary landscape of rice genomes (Zhang and Gao, 2017). Furthermore, the identification of positively selected genes involved in key biological processes such as flower development and stress response highlights the adaptive significance of these novel elements (Feliner et al., 2020).

6 Tools and Techniques for Identifying Novel Genetic Elements

6.1 High-throughput sequencing and bioinformatics approaches

High-throughput sequencing technologies have revolutionized the field of genomics by enabling the rapid and cost-effective sequencing of entire genomes, even for non-model organisms. These technologies, such as single-molecule real-time (SMRT) sequencing, Illumina sequencing, and Hi-C technologies, have been instrumental in generating high-quality *de novo* assemblies of genomes, such as that of *Oryza rufipogon*, a wild progenitor of cultivated rice. The integration of these sequencing technologies allows for comprehensive comparative genomic analyses, which can identify millions of genomic variants, including structural variations (SVs), copy number variations (CNVs), and presence-absence variations (PAVs) that may affect agronomically significant traits (Li et al., 2020). Additionally, bioinformatics tools are essential for processing and analyzing the vast amounts of data generated by high-throughput sequencing. These tools help in identifying molecular markers, genomic regions of interest, and potential contamination from non-target species, which is crucial for accurate evolutionary and functional studies (Leese et al., 2012).

6.2 Genome-wide association studies (GWAS) and functional genomics

Genome-wide association studies (GWAS) are powerful tools for identifying genetic variants associated with specific traits by analyzing the genomes of large populations. In rice research, GWAS has been used to uncover the genetic basis of critical phenotypes and to understand the landscape of genomic divergence during speciation (Ellegren, 2014). Functional genomics approaches, such as transcriptome analysis via RNA sequencing (RNA-Seq), provide insights into gene expression patterns and the functional complexity of the genome. For instance, RNA-Seq has been used to study the transcriptome of *Aspergillus oryzae*, revealing novel transcripts, alternative splicing events, and pathways involved in protein production. These techniques are invaluable for linking genetic variants to phenotypic traits and for understanding the functional roles of genes in various biological processes.

6.3 CRISPR and other gene-editing techniques for functional validation

CRISPR-Cas9 and other gene-editing technologies have revolutionized functional genomics by enabling precise modifications of specific genomic regions. These tools are used to validate the functions of candidate genes identified through high-throughput sequencing and GWAS. By creating targeted mutations or insertions, researchers can study the effects of specific genetic changes on phenotypes, thereby confirming the roles of novel genetic elements. For example, CRISPR has been employed to edit genes in rice to study their roles in traits such as disease resistance, yield, and stress tolerance (Stein et al., 2018). The ability to perform functional validation through gene editing accelerates the process of linking genotype to phenotype and facilitates the development of improved crop varieties.

7 Case Studies

7.1 Detailed analysis of specific novel genetic elements in different *Oryza* species

The genus *Oryza*, encompassing both domesticated and wild rice species, provides a rich tapestry for studying genomic evolution and the emergence of novel genetic elements. Recent studies have highlighted the dynamic nature of the *Oryza* genome, revealing significant insights into the role of novel genetic elements in species diversification and adaptation.

One notable study examined the genomes of 13 domesticated and wild rice relatives, uncovering the rapid species diversification and turnover of transposons and potential new coding and noncoding genes. This research also identified many new haplotypes of disease resistance genes, which are crucial for future crop protection (Stein et al., 2018). The study's comprehensive genomic analysis, including the complete long-read assembly of IR 8 'Miracle Rice', marks a significant milestone in rice research. Further, the *de novo* genome sequencing of five diploid AA-genome species closely related to *Oryza sativa* revealed massive levels of genomic structural variation. This includes segmental duplication and rapid gene family turnover, particularly in defense-related genes. The study documented a large number of positively selected genes involved in flower development, reproduction, and resistance-related processes, which are key to the species' adaptation to diverse ecological niches (Zhang et al., 2014).

In another study, the draft genomes of *Oryza rufipogon* and *O. longistaminata* were analyzed, revealing lineage-specific gene families associated with self-incompatibility and reproductive separation. The expansion of genes encoding NBS-LRR proteins in these outcrossing wild species, compared to selfing rice species, highlights the role of these genes in reproductive diversification and stress responses (Li et al., 2020).

Moreover, the high-quality *de novo* assembly of the *Oryza rufipogon* genome provided insights into the genomic basis of rice adaptation. Comparative genomic analyses identified numerous genomic variants, including large-effect mutations that affect agronomically significant traits. The study demonstrated how lineage-specific expansion of gene families contributed to reproductive isolation and the evolution of mating systems. The exploration of the genomic atlas of the *Dof* transcription factor family across the genus *Oryza* identified 238 *Dof* genes categorized into seven distinct subgroups. This study highlighted the structural and functional diversity of *Dof* genes, which have undergone strong purifying selections and segmental duplications. The findings suggest that these genes play a significant role in regulating gene expression under different climatic conditions, potentially aiding in the development of early maturing and climate-resilient rice cultivars (Tabassum et al., 2020).

7.2 Implications for breeding and crop improvement

The study of transposable elements (TEs) in the genus *Oryza* has profound implications for breeding and crop improvement. TEs are known to influence gene expression and genome structure, which can be harnessed to develop new rice varieties with desirable traits. For instance, TEs can cause changes in gene expression patterns by inserting themselves into various genomic regions, such as promoters, introns, and exons, thereby upregulating or downregulating nearby genes (Figure 3) (Gill et al., 2021). This regulatory capability can be exploited to enhance traits such as disease resistance, stress tolerance, and yield.

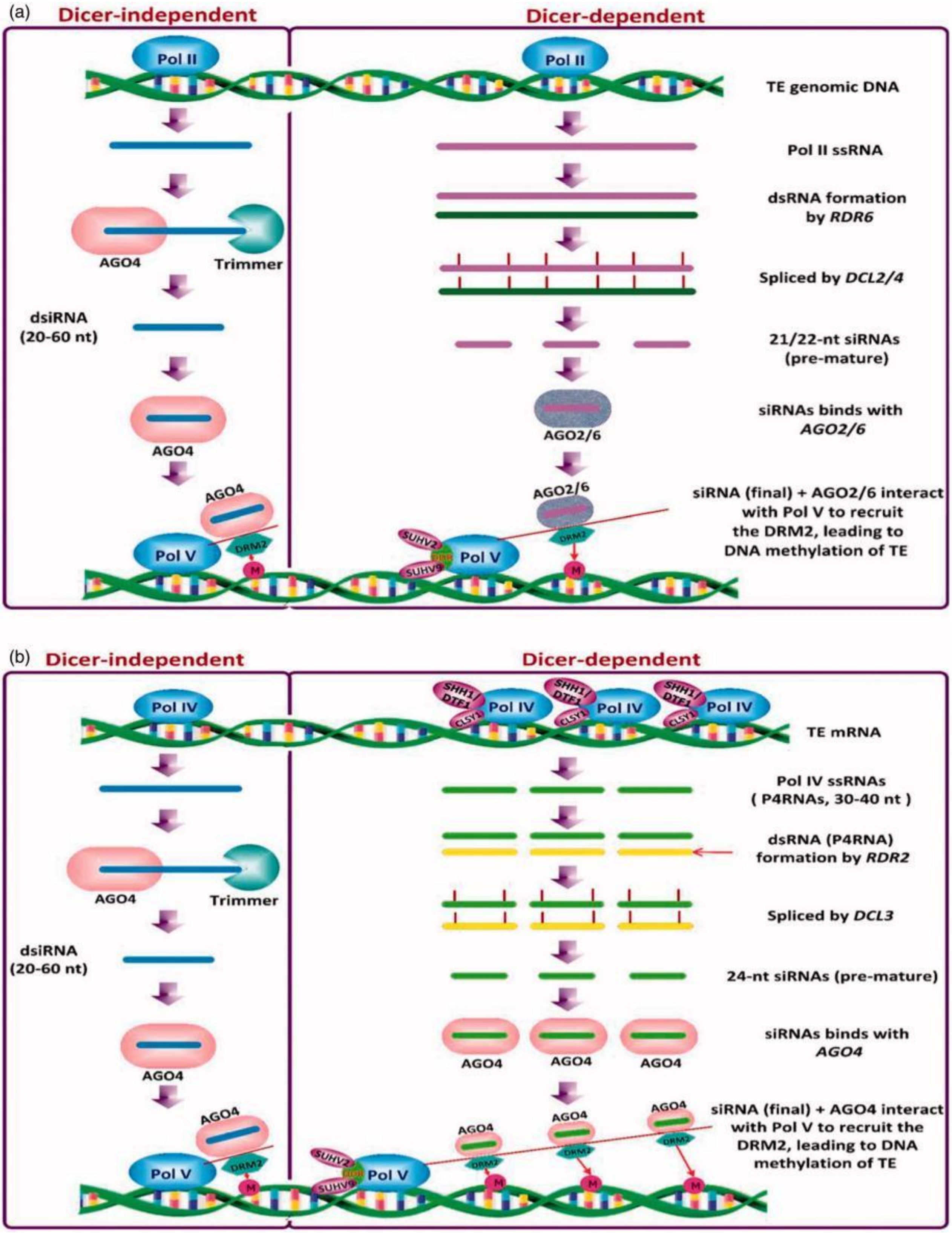

Figure 3 A schematic of two different dicer-independent and -dependent models of RNA directed DNA methylation (RdDM) (Adopted from Gill et al., 2021)

Image caption: a: A representative of the TE initiation and silencing through dsiRNAs (dicer-independent) and siRNAs (dicer-dependent) routes generated from Pol II enzyme; b: maintain TE silencing by targeting of mRNA of TEs through dsiRNAs (dicer-independent) and P4siRNAs (dicer-dependent) pathways produced by Pol IV enzymes (Adopted from Gill et al., 2021)

Moreover, the identification of novel haplotypes and the understanding of genetic conservation and turnover in *Oryza* species provide valuable genetic resources for breeding programs. The complete long-read assembly of IR 8 'Miracle Rice' is a significant milestone, offering a comprehensive genetic blueprint that can be used to introduce beneficial traits into other rice varieties. Additionally, the presence of functionally coupled disease resistance genes in the *Oryza* genome highlights the potential for developing rice varieties with improved resistance to various pathogens (Stein et al., 2018).

The diversity and abundance of TEs, such as MITEs, in the rice genome also contribute to genetic variability, which is crucial for breeding programs. MITEs are associated with a significant number of genes and generate a substantial portion of small RNAs, which play roles in gene regulation and stress responses (Lu et al., 2011). This genetic variability can be leveraged to create rice varieties with enhanced adaptability to different environmental conditions.

7.3 Comparative case studies highlighting evolutionary trends and functional significance

Comparative studies across different *Oryza* species reveal significant evolutionary trends and the functional significance of TEs in genome evolution. For example, the genus *Oryza* exhibits a wide range of genome sizes, primarily due to the proliferation of Long Terminal Repeat (LTR) retrotransposons. These elements have been shown to proliferate to varying extents in different species, contributing to genome size variation and structural diversity. The ancient origin and conservation of these elements across the genus suggest their crucial role in shaping the *Oryza* genome (Zuccolo et al., 2007).

In the *Oryza officinalis complex*, the proliferation of Gypsy-type LTR retrotransposons has led to a larger genome size compared to cultivated *Oryza sativa*, while maintaining overall syntenic relationships with other *Oryza* genomes (Shenton et al., 2020). This indicates that TEs not only contribute to genome expansion but also preserve essential genomic functions.

The role of TEs in creating localized segments with increased rates of chromosomal rearrangements, gene duplications, and gene evolution is evident in the rice blast fungus *Magnaporthe oryzae*. TEs in this pathogen are largely confined to distinct clusters within the genome, which are associated with higher recombination rates and greater sequence diversity (Thon et al., 2006). This localized genomic plasticity facilitated by TEs underscores their role in adaptive evolution and pathogenicity.

Furthermore, the dynamic gain and loss of genes linked to TEs in *Magnaporthe oryzae* highlight the relationship between genome position and gene evolution. This mechanism drives host specialization and adaptation, as seen in the different host-specific subgroups of the pathogen. The frequent gene loss and gain in *Oryza* and *Setaria* infecting lineages, facilitated by TEs, demonstrate their role in enhancing genetic variation and adaptability (Yoshida et al., 2016).

8 Conclusion

In this study, we explored the genomic evolution within the genus *Oryza*, focusing on the role of novel genetic elements. Our key findings reveal that the *Oryza* genus exhibits significant genetic conservation, turnover, and innovation, particularly through the emergence and turnover of novel elements such as transposons and new coding and noncoding genes. The study of allopolyploid species within *Oryza* has provided insights into the process of diploidization and the temporal dynamics of genome evolution post-polyploidy. Additionally, the comparative analysis of gene families across different *Oryza* species has highlighted extensive gene family expansions and the role of tandem duplications and gene losses in driving these expansions.

The importance of novel genetic elements in genomic evolution cannot be overstated. These elements, including transposable elements and *de novo* genes, have been shown to contribute significantly to genome size variation and protein diversity, respectively. The rapid diversification of *Oryza* genomes, driven by these genetic innovations, underscores their critical role in the adaptation and speciation processes within the genus. Moreover, the identification of functionally coupled disease resistance genes and new haplotypes offers promising avenues for future crop protection and improvement.

Looking ahead, the field of genomic evolution in *Oryza* faces several challenges and opportunities. One major challenge is the need for high-quality reference genomes and comprehensive comparative analyses to further elucidate the mechanisms underlying genome evolution. The ongoing development of genomic resources, such as the International *Oryza* Map Alignment Project, aims to address these challenges by providing a genus-wide comparative genomics platform. Additionally, the conservation of wild *Oryza* populations is crucial for maintaining the genetic diversity necessary for future research and breeding efforts. The integration of advanced genomic technologies and interdisciplinary approaches will be essential in overcoming these challenges and unlocking the full potential of novel genetic elements in shaping the genomic landscape of *Oryza*.

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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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