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Genome Polyploidization and Adaptive Evolution in Yellow Pitaya: The Impact of Gene Amplification on Stress Resistance

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Abstract Due to its excellent environmental adaptability and high economic value, yellow pitaya has gradually become an important tropical cash crop. However, the current research on the polyploidization of yellow pitaya genome and its adaptive evolution mechanism is relatively limited. This study mainly aims to reveal the relationship between gene amplification events and stress resistance during the polyploidization of yellow pitaya genome, and explore its adaptation mechanism under environmental pressures such as drought, high temperature, and salt stress. The content of the article includes the type of polyploidization of yellow pitaya genome, the molecular pathway of gene amplification, and the role in regulating the expression of anti-reverse genes. The study has shown that yellow pitaya has experienced multiple genomic replication events, resulting in a large number of amplifications of stress-resistant related genes, among which gene families such as zinc finger protein and NAC transcription factors are particularly outstanding, and the improvement of these gene amplification events to plant stress-resistant ability is confirmed through multi-level bioinformatic analysis. Combined with the research results of previous generations, we will further use multiplier cultivation of new inverse-resistant varieties of yellow pitaya to provide theoretical basis and technical support.

Keywords Yellow pitaya; Genome polyploidization; Gene amplification; Stress tolerance; Adaptive evolution

1 Introduction

Yellow pitaya (*Hylocereus megalanthus*) has received widespread attention in recent years due to its excellent biological adaptability and significant economic value. As a tropical fruit tree with strong adaptability, yellow pitaya can thrive in extreme environments, such as drought, high temperatures, and barren soils, giving it significant global planting potential. This high environmental adaptability mainly comes from its complex gene regulation mechanism (Hu et al., 2022; Xu et al., 2023). In addition to its excellent environmental adaptability, yellow pitaya is also highly praised for its rich nutritional ingredients. The fruit is rich in antioxidants, vitamins and a variety of biologically active compounds. It not only has extremely high edible value, but is also widely used in the food processing and functional health products market. At present, research on yellow pitaya is advancing in depth to improve yield and optimize quality.

Genome-wide replication (genome polyploidization) is one of the important driving forces for biological evolution and environmental adaptation. Polyplification gives organisms stronger adaptability and survival advantages by increasing the complexity and genetic diversity of the genome (Anatskaya and Vinogradov, 2022). In the plant world, polyploidization is widely present and is closely related to growth and development, environmental adaptation and stress resistance. Its mechanism of action mainly includes gene amplification, regulatory network recombination, and epigenetic plasticity. These processes work together to enable plants to adapt to the changing ecological environment. In *Hylocereus megalanthus*, polyploidization may increase tolerance to environmental stress (drought, high temperature, salt stress, etc.) by activating ancient evolutionary mechanisms and reshaping gene regulatory networks.

In yellow pitaya, the amplification of genes such as zinc finger protein and NAC transcription factor and their expression regulation play a key role in the regulation of stress resistance. This study wants to systematically analyze the genome polyploidization and gene amplification phenomena of yellow pitaya, and reveal its specific mechanism in the process of environmental adaptation. Through these studies, we hope to provide new theoretical support and technical means for the genetic improvement of yellow pitaya, and improve its growth performance and economic value under different environmental conditions.

2 Genomic Polyploidization and Evolutionary Mechanism of Yellow Pitaya

2.1 Multiplier type and characteristics of yellow pitaya genome

Polyplification is an important driver of species formation and evolution, and all angiosperm genomes have experienced at least one whole genome duplication during their evolution (Whole genome duplications (WGD). The prevalence of polyploids demonstrates the importance of genome-wide replication in plant evolution and differentiation. The study found that genome-wide replication occurred before the diversification of existing angiosperms, expanding the diversity of key genes and pathways regulating flower and seed development, ultimately making angiosperms dominate the number and distribution of earth (Wang et al., 2023). Pei Yun from the School of Horticulture of Nanjing Agricultural University and several research experts specially systematically analyzed and discussed the relationship between whole genome replication and the formation of new plant phenotypes (Morphological gigantism, flowering time variation, increased secondary metabolite production, optimized agronomic traits, and enhanced stress tolerance, etc.), and its contribution and significance in evolution, providing reference value for innovative polyploid plants. Polyploid yellow pitaya has significant changes in anatomical and physiological properties, and the enlarged cell volume, remodeling of gene expression patterns, and adjustment of biochemical metabolic pathways have jointly enhanced the reversibility of plants (Tossi et al., 2022; Li et al., 2024).

2.2 Role of polyploidization in plant evolution and adaptive advantages

With the continuous innovation of sequencing technology, people have gained a new understanding of the genome of crops and the evolutionary history of genomes. The study identified the significance of whole-genome duplication in species evolution, including altering genomic structure, enriching genetic diversity, changing expression patterns of duplicated genes, and enhancing species adaptability. In Yellow pitaya, polyploidization is associated with increased stress resistance, allowing plants to thrive under harsh environmental conditions (Van De Peer et al., 2020; Anatskaya and Vinogradov, 2022). Faced with global climate change, plants are increasingly exposed to extreme temperatures, droughts and salinity. Polyploid plants often exhibit strong physiological and biochemical characteristics, such as improved antioxidant defenses and altered hormone signaling pathways, which can improve tolerance of biological and abiotic stresses (Khokhar et al., 2024; Alam et al., 2024). The evolutionary success of polyploids is also attributed to their ability to undergo rapid genetic and epigenetic changes, which can lead to activation of stress-responsive genes and recombination of gene regulatory networks (Anatskaya and Vinogradov, 2022).

2.3 Current research status and technical approaches in yellow pitaya genome polyploidization

Through the transcriptome analysis of yellow pitaya, Wu and other experts mentioned the key regulatory networks and gene expression changes in polyploid yellow pitaya in the article "Genetic Contribution of Paleopolyploidy to Adaptive Evolution in Angiosperms", and revealed several significantly enriched stress response pathways, such as antioxidant defense systems and hormone signaling pathways. The activation of these pathways is beneficial to enhancing the tolerance of plants to environmental factors such as drought, high temperature and salt stress. The occurrence of genome polyploidization increases the gene redundancy of plants, and also allows some genes to obtain new adaptive functions through new functionalization and subfunctionalization. In the article, the study found that these transcription factors may enhance plant survival in extreme environments by co-regulating antioxidant enzyme genes and ABA signaling pathway-related genes (Wu et al., 2020).

In terms of technical means, Sun Wenguang, Sun Hang and Li Zhimin analyzed in the Journal of Plant Science that polyploidy can be artificially induced by colchicine or oryzalin, and genomic ploidy can be accurately measured in combination with flow cytometry. The development of high-throughput sequencing technology can also promote in-depth analysis of the polyploidized genome of yellow pitaya. Based on chromosome collinear analysis and gene family evolution tracking methods, it can be used to identify the polyploidized genes retained in Yellow pitaya and their functions in environmental adaptation.

3 Molecular Mechanisms of Gene Amplification

3.1 Formation pathways of gene amplification (gene duplication, tandem amplification, etc.)

Gene amplification is formed through a variety of pathways, with the most common mechanisms that enable gene replication and tandem amplification. Gene replication involves duplication of the entire genome or part of the genome, which is particularly significant during polyploidization (Tossi et al., 2022; Li et al., 2024). Tandem amplification refers to the continuous repetition of genes on chromosomes. In yellow pitaya, gene amplification may enhance its adaptability to environmental stress through some pathways including whole genome replication (WGD), tandem replication and fragment replication. In studying the "Effect of GRF Gene Stress in Dragon Fruit", Cai Xiaowei identified 11 genes encoding GRF transcription factors on the Dragon Fruit genome, named HpGRF1~HpGRF11. Collinear analysis of the genome found that fragment repetition events on the genome were the key drivers of GRF gene expansion of Dragon Fruit.

3.2 Effects of gene amplification on gene expression regulation

Gene amplification usually involves multiple levels of genetic and epigenetic regulation, including chromatin remodeling, adjustments of gene regulatory networks, and changes in cis regulatory elements. In yellow pitaya, the key transcription factor family, the DNA binding proteins Dof and NAC (NAM, ATAF1/2, CUC2), were found to achieve a significant increase in expression levels through gene amplification. NAC proteins are the largest family of plant-specific transcription factors, expressed in various developmental stages and in different tissues of plants, involved in various growth and development processes, and regulate plant responses to environmental stress. NAC transcription factors play a regulatory role in the response to abiotic stress. Research has found that NAC transcription factors often do not simply enhance plants' tolerance to a certain abiotic stress, but coordinate the regulation of multiple abiotic stress networks. Zhang Dan and Ma Yu-hua have studied the NAC transcription factors in rice, bananas, watermelons and other plants in response to various abiotic stresses and growth and development. The network of NAC transcription factors responding to abiotic stress is very complex. It not only has cascade interactions with different family transcription factors, but also has signaling, protective enzymes, various stress-induced genes, and plant hormone interactions to regulate the comprehensive tolerance of plants to abiotic stress. This enhanced expression promotes activation of genes related to stress resistance, allowing plants to show stronger tolerance in adversity conditions such as drought, high salt and temperature stress (Xu et al., 2023 ; Khokhar et al., 2024).

3.3 Bioinformatics analysis of gene amplification in yellow pitaya

Bioinformatics analysis of yellow pitaya genome reveals the complexity of intrinsic gene amplification. Through high-throughput sequencing technologies-PacBio-SMRT and Illumina HiSeq, researchers were able to construct chromosomal genome assembly of yellow pitaya to identify gene amplification events. These analyses show that yellow pitaya undergoes genome-wide triploxation and recent genome-wide replication events that drive gene amplification (Chen et al., 2021). Genome replication events often lead to recombination of genomic structures and diversification of gene functions, thereby enhancing plants' adaptability to environmental stress. Bioinformatics analysis also revealed the presence of a large number of transposons and repeats in the genome of yellow pitaya, which may play an important role in gene amplification and genome evolution.

4 Correlation Between Gene Amplification and Stress Resistance

4.1 Role of gene amplification in drought resistance

Gene amplification can enhance drought resistance in plants, especially polyploid species. In the case of fluorobenzoate, chromosomal multiplication can mediate rising drought tolerance through abscisic acid (ABA) signaling pathway. In autodiploid, gene expression with ABA biosynthesis and signal transduction increased compared with diploid. (Rao et al., 2020) revealed that plants are continually subjected to adverse external stimuli, which can affect their productivity and growth. Differences in gene composition and expression patterns lead to homopolyploid plants showing different physiological phenomena, where enhanced environmental adaptability is a powerful phenotype conferred by polyploidy (Figure 1). The underlying mechanisms of the difference in stress tolerance between diploid and autodiploid at the molecular level are not yet known. In their study, the full-length transcription curve obtained by combining single-molecule real-time (SMRT) sequencing of high-quality single-RNA molecules used as backgrounds with next-generation transcriptome and proteome techniques to detect changes in the molecular mechanisms of autoconstitutive dinuclear image. Compared with diploids, tetraploids showed 78.4% ABA content of 78.4% under natural conditions, with excellent stress phenotype and substantial differences under severe drought stress.

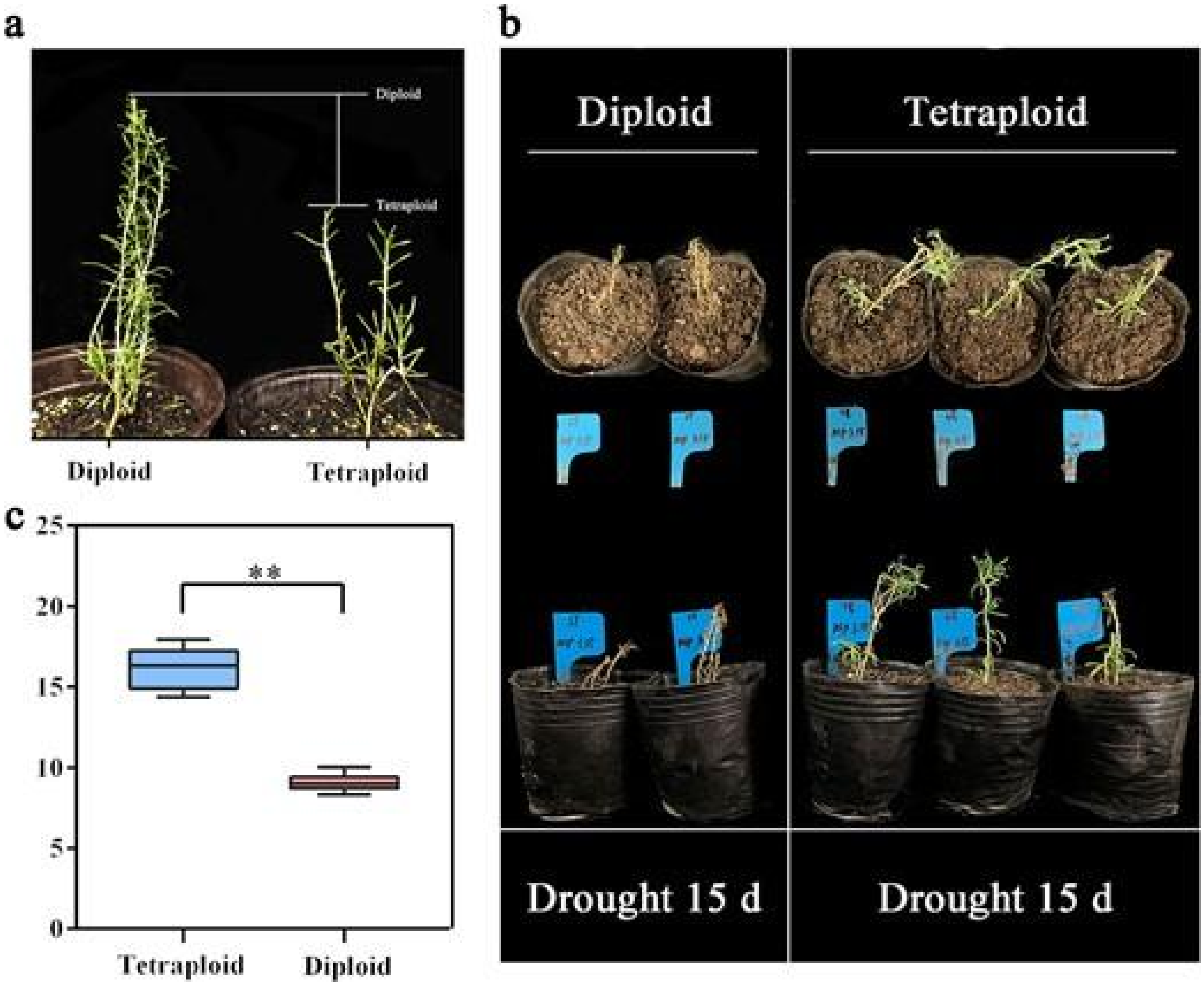


Figure 1 a: Phenotypes in *L. ruthenicum* of different ploidies grown in the greenhouse for 1 month. b: Phenotypic status of *L. ruthenicum* seedlings under salt and drought stress. c: Box plot of ABA contents (Adopted from Rao et al., 2020)

4.2 Mechanisms of gene amplification in salt stress response

Gene amplification also significantly contributes to the salt stress response in plants. In tetraploid rice, polyploid induces DNA hypomethylation, thereby enhancing the expression of stress-responsive genes, including genes involved in tussolate biosynthesis and signaling pathways. This epigenetic modification allows for a rapid and robust response to salt stress, which is achieved through increased salt response gene expression and increased Jasmyleneoleic acid isoleucine (JA-ILE) content. Feedback regulation between polyploid-induced DNA hypomethylation and stress-induced hypermethylation contributes to inhibition of transposable elements (TES) and TE-related genes (Wang et al., 2021). Yellow pitaya is grown in a wide ecological range due to drought-tolerant, heat-tolerant and barren soil. Zinc finger proteins play a role in plant growth and stress responses by interacting with DNA, RNA and proteins. In total, 81 CCCH-type zinc finger protein genes were identified from the dragon fruit genome. Transcriptomic analysis showed that nine of them, including HuTZF3, responded to both salt stress and heat stress. RT-qPCR results show that HuTZF3 is expressed in all test organs of dragon fruit, and the expression is high in the roots and stems, which confirms that HuTZF3 expression is induced by salt stress and heat stress. Subcellular localization showed HuTZF3-targeted processed body (PB) and stress granules (SG).

Heterologous expression of HuTZF3 can improve the salt and heat resistance of Arabidopsis, reduce oxidative stress, and improve the activity of catalase and peroxidase. Therefore, HuTZF3 may participate in posttranscriptional regulation by localizing PB and SG, thereby promoting salt and heat tolerance in Yellow pitaya (Xu et al., 2023).

4.3 Functional analysis of amplified genes related to antioxidant defense and disease resistance

Transcriptome analysis of pitaya under stress conditions revealed increased activities of antioxidants such as H_2O_2 , POD, CAT, APX, and SOD, as well as elevated proline content, indicating a strong antioxidant defense capacity.. The study identified 141 common differentially expressed genes (DEGs) related to stress tolerance, many of which involve signal transduction and hormonal pathways, including abscis and auxin (Khokhar et al., 2024). The role of the zinc finger protein HUTZF3 amplified in yellow pitaya is particularly noteworthy in reducing oxidative stress and improving catalase and peroxidase activity, thereby improving salt and heat resistance (Zaman et al., 2024). Studies have revealed the key HT tolerance mechanisms of pitaya by conducting comprehensive transcriptome and proteome analysis of two comparative varieties C-130 (heat-tolerant) and H17-10 (thermal-sensitive). They identified a total of 5783 degrees (differentially expressed genes) and 2101 DEPs, of which 376 degrees Celsius and DEP were significantly correlated. Enrichment analysis of secondary metabolites, phytohormone signaling, MAPK signaling pathways-protein processing in plants, endoplasmic reticulum, pyruvate metabolism, cysteine and methylation metabolism as key molecular reactive machinery biosynthesis. In particular, heat shock transcription factor (HSF), glutathione metabolism and brass sterol (BR) are important for pitaya's thermal tolerance and are the main inducing genes in these pathways.

5 Genetic And Epigenetic Regulation of Adaptive Evolution

5.1 Adaptive role of genetic variation and genomic rearrangement

Genetic variation and genomic rearrangement play a role in the adaptive evolution of yellow pitaya, especially through processes such as polyploidy and hybridization. Polyploid or genome-wide repeat is an evolutionary mechanism that provides genetic redundancy, thereby increasing adaptability and species formation (Alix et al., 2017). The main mechanisms that affect plant genome evolution and how polyploid events affect these effects and vice versa are outlined in the review of Carlos M. Vicient and Josep M. Casacuberta. These include direct effects on genes, effects on the epigenetic state of chromatin approaching genes by providing them with new coding or regulatory sequences, and more subtle effects by imposing multiple evolutionary constraints on different chromosomal regions. Polyploidization often causes a burst of transposition that may be due to a relaxation of its epigenetic control, and in the short term, this may increase the rate of gene mutations and changes in gene regulation due to TE insertion near genes or the insertion of genes. Over the longer period, TE outbreaks may cause global changes in genome structure due to inter-element recombination, including losses in large genomic regions and losses in chromosome rearrangements, thus reducing genome size and chromosome number, as part of a process called diploidization (Vicient and Casacuberta, 2017).

In yellow pitaya, polyploids have been shown to generate immediate genetic redundancy, which can enhance stress and adaptability to various environmental conditions. Genome rearrangements, such as chromosomal rearrangements and transposable element activation, further promote genetic diversity and adaptive potential by promoting rapid genomic recombination and novel expression patterns (Paun et al., 2007). The presence of repeated genes in polyploids can diversify protein function or regulation, thereby facilitating the ability of plants to adapt to different ecological walls (Wendel, 2004).

5.2 Effect of epigenetic modification (DNA methylation, histone modification) on gene amplification

Polyploid or genome-wide repetition occurs in certain animals and many flowering plants, including many important crops, and the prevalence of polyploid in the plant kingdom shows that it is an important evolutionary feature of plant formation and crop domestication. Natural and synthetic polyploid studies reveal rapid and dynamic changes in genomic structure and gene expression after polyploid formation. There is growing evidence that epigenetic modifications can alter homologous gene expression and reprogram gene expression networks, allowing polyploids to establish new cell types, grow vigorously and promote adaptation in local environments. (Song and Chen, 2015) This review focuses on developmental regulation and epigenetic changes, including DNA methylation and histone modification in polyploidy. In yellow pitaya, epigenetic changes lead to activation or silencing of specific genes, which helps phenotypic variation and improves adaptability. Histone modifications also play an important role in regulating gene expression by altering chromatin structure and accessibility, which may affect the expression of genes involved in stress responses and other adaptive traits. These epigenetic mechanisms have enabled yellow pitaya to adapt to the local environment and resist various stresses.

5.3 Regulation of stress adaptation in yellow pitaya by miRNAs and transcription factors

Adversity stress can negatively affect the growth and development of plants, and over the long evolution. Plants have a complex regulatory network to deal with adverse environments, and miRNA plays an important role in this regulatory network. An article summarizes the research on the regulatory effects of miRNAs and their target genes in recent years, including miRNAs (miR160/miR167, miR159, miR156 and miR164) using target genes (miR398 and miR395) using target genes, which can provide more effective improved ways to enhance plant stress resistance using genetic engineering methods. MiRNAs cleavage and degrade or inhibit translation of target mRNA by pairing with target mRNA specific bases, thereby exerting negative regulatory functions after transcription. Most of the target genes of miRNA are transcription factors, which are mainly involved in basic biological processes such as plant growth and development, signal transduction and response to adversity stress. Plants are affected by a variety of environmental stresses during their growth and development. Most biological and abiotic stresses will cause oxidative stress, damaging the cellular structure and ultimately leading to plant death. The molecular mechanisms of miRNA mediate plant defense are complex and diverse, which can not only regulate the expression of host target genes, but also manipulate the expression of pathogenic genes across the border (Scarrow et al., 2020). microRNA (miRNA) and transcription factors are key regulators of stress adaptation in bird's nest fruits. In yellow pitaya, miRNAs are involved in the regulation of genes related to stress resistance, allowing plants to adapt to adverse environmental conditions. Regulatory networks are conducive to the adaptive evolution of yellow pitaya, which enables plants to respond effectively and withstand various stresses, thereby enhancing their survival and reproductive success.

6 Genome Polyploidization and Agricultural Applications

6.1 Breeding strategies and improvement of stress-resistant varieties in yellow pitaya

Polyploid plants have multiple groups of chromosomes, which enable them to show stronger survivability when facing extreme environmental stress. Polyplification triggers a series of physiological and biochemical changes, including cell size enlargement, gene expression pattern remodeling and optimization of metabolic pathways, thereby improving the tolerance of plants to stress conditions (Tossi et al., 2022). In yellow pitaya breeding research, polyploidization can be used to cultivate varieties that are more tolerant to high temperature, drought and salt stress. As climate change intensifies, improving crop environmental adaptability has become the key to sustainable agricultural development. Polyploid plants show superior performance in stress resistance. Artificial induction of polyploidization usually relies on specific chemical reagents, and some studies have shown that the increase in tolerance is not directly attributed to polyploidization in all cases, but is regulated by a comprehensive regulation of multiple genetic and epigenetic factors (Li et al., 2024).

6.2 Potential role of genome polyploidization in fruit quality enhancement

The process of polyploidization results in an increase in cell size and changes in the physiological and biochemical properties of the plant, which can directly affect the quality of the fruit. Polyploid plants often show improved characteristics, increased size or enhanced nutritional content or better taste, which is very desirable in the agricultural market. The genetic diversity introduced by polyploids may also lead to the development of new fruit characteristics, capable of improving color and texture, which can enhance the sales of yellow pitaya. Compared with diploids, genomic doubling may have multi-layered effects on the morphology, vitality and physiology of polyploids. Some experts studied the related changes in autopolyploids of two somatic new induced polyploids belonging to the genus, namely, diploid-autotetraploid and triplocell-autohexaploid Hylocereus (Cactaceae family), and studied stomata, fruit, seed, embryos and pollen, and concluded that genome doubling does not necessarily bring fitness advantages, and the degree of changes induced by autopolyploidy depends on the genetic background of the donor genotype.

6.3 Applications of molecular breeding and gene-editing technologies in yellow pitaya improvement

Gene editing tools can be used to target and regulate specific genes related to stress resistance, thereby cultivating yellow pitaya varieties that can better adapt to environmental challenges (Khokhar et al., 2024; Alam et al., 2024). Combining molecular breeding technology with genome polyploidization can further enrich the genetic diversity of Yellow pitaya, enhance its adaptability, and promote the cultivation of high-yield and stress-resistant varieties. Integrating transcriptome and genome analysis can systematically analyze regulatory networks and metabolic pathways related to stress responses, thereby accurately identifying key genes and molecular markers, and providing scientific basis for targeted breeding (Xu et al., 2023). As the impact of global climate change on agricultural production intensifies, utilizing molecular breeding and gene-editing technologies can fully exploit the genetic potential of pitaya, enhancing its stress resistance and productivity under extreme environmental conditions.

7 Comparative Genomics Analysis of Genome Polyploidization in Yellow Pitaya

7.1 Comparative analysis of genome structure between yellow pitaya and related species

When comparing the genome structures of yellow pitaya and its relative species, the researchers found that the species experienced whole-genome triploxation (WGT) and the most recent whole-genome duplication (WGD). This phenomenon is similar to the genomic evolution pattern of other species in the Cactaceae family, suggesting that polyploidization events play a key role in the adaptive evolution of plants in this family. Genome polyploidization is a widely present phenomenon in the evolution of angiosperms and often gives plants stronger environmental adaptability.

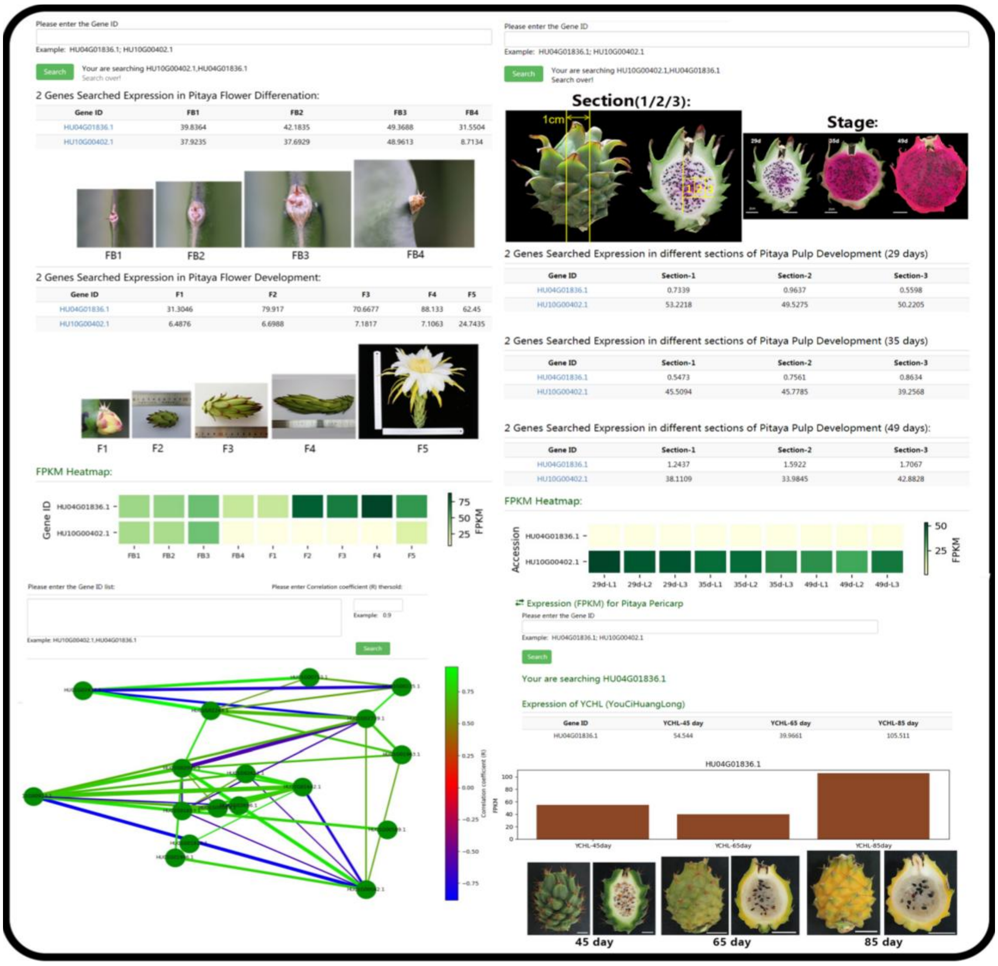
Chen et al. (2022) studied the genomic variants and structural characteristics of yellow pitaya and found that this species not only experienced earlier WGT events, but also experienced WGD during recent evolution. These polyploidization events not only increase the complexity of the genome, but also provide a rich source of genetic variation, thereby enhancing the plant's environmental adaptability. Polyploidization events are often accompanied by gene amplification, especially gene families associated with stress resistance, secondary metabolism, and development (Figure 2). In yellow pitaya, transcription factor families such as NAC, WRKY and Dof all showed significant amplification trends. Repeats of these genes may enhance plants' antioxidant capacity, osmoregulation ability, and tolerance to drought and salt stress.

7.3 Evolutionary trajectory of yellow pitaya revealed by gene collinearity analysis

Gene collinearity analysis is an important method to reveal the evolutionary trajectory of species, and can have an in-depth understanding of genome structural mutation, gene family evolution and adaptive evolution. In the genome study of yellow pitaya, researchers found there were a large number of collinear gene pairs in its genome, indicating that the species experienced multiple recombination and amplification events during its evolution. ‘Dragon Fruit Transcriptome Sequencing, Gene Expression and Functional Analysis’ this paper uses high-throughput sequencing technology to study the gene expression of flower buds, fruits and branches of dragon fruit at different stages of development.

The results showed that a total of 468.68 Gb of original data were obtained by transcriptome sequencing, and 239 152 transcripts and 162 519 unigenes were obtained by de novo assembly, and about 53.74% of unigenes were annotated. Through GO and KEGG enrichment analysis, some tissue-specific GO entries and metabolic pathways were found, such as the terpenoid skeleton bioanalytic metabolic pathway enriched in Fl510. The study also identified and expressed analysed the candidate genes involved in flower development, including *COL* genes, *FT-like* genes, meristem-determinal genes and organ-determinal genes.

Specifically, the chromosomal structure of Yellow pitaya is highly similar to its relative species, but there are also cases of chromosomal fragment rearrangement and ploidy changes. This shows that the genome of Yellow pitaya undergoes a complex evolutionary path in the process of adapting to the environment. Some collinear genes are highly conserved in the angiosperm ancestral genome, which may play a key role in early plant physiological functions (such as photosynthesis, hormone signal regulation).



Please enter the Gene ID

Example: HU04G01836.1; HU10G00402.1

Your are searching HU10G00402.1,HU04G01836.1
Search over!

2 Genes Searched Expression in Pitaya Flower Differenation:

Gene ID	FB1	FB2	FB3	FB4
HU04G01836.1	39.8364	42.1835	49.3688	31.5504
HU10G00402.1	37.9235	37.6929	48.9613	8.7134

2 Genes Searched Expression in Pitaya Flower Development:

Gene ID	F1	F2	F3	F4	F5
HU04G01836.1	31.3046	79.917	70.6677	88.133	62.45
HU10G00402.1	6.4876	6.6988	7.1817	7.1063	24.7435

Please enter the Gene ID list:

Example: HU10G00402.1,HU04G01836.1

Please enter Correlation coefficient (R) thersold:

Example: 0.9

Please enter the Gene ID

Example: HU04G01836.1; HU10G00402.1

Your are searching HU10G00402.1,HU04G01836.1
Search over!

2 Genes Searched Expression in different sections of Pitaya Pulp Development (29 days)

Gene ID	Section-1	Section-2	Section-3
HU04G01836.1	0.7339	0.9637	0.5598
HU10G00402.1	53.2218	49.5275	50.2205

2 Genes Searched Expression in different sections of Pitaya Pulp Development (35 days)

Gene ID	Section-1	Section-2	Section-3
HU04G01836.1	0.5473	0.7561	0.8634
HU10G00402.1	45.5094	45.7785	39.2568

2 Genes Searched Expression in different sections of Pitaya Pulp Development (49 days):

Gene ID	Section-1	Section-2	Section-3
HU04G01836.1	1.2437	1.5922	1.7067
HU10G00402.1	38.1109	33.9845	42.8828

Expression (FPKM) for Pitaya Pericarp

Please enter the Gene ID

Example: HU04G01836.1; HU10G00402.1

Your are searching HU04G01836.1

Expression of YCHL (YouCiHuangLong)

Gene ID	YCHL-45 day	YCHL-65 day	YCHL-85 day
HU04G01836.1	54.544	39.9661	105.511

Figure 2 'Expression' module displayed the gene expression data of each tissue in various development stages through the expression calorimetry, histogram and corresponding table forms (Adopted from Chen et al., 2022)

7.2 Similarities and differences in gene amplification patterns between pitaya and other polyploid plants

In the comparison of gene amplification patterns between yellow pitaya and other polyploid plants, the study found the gene amplification of yellow pitaya mainly focuses on stress resistance-related genes, which has a similar evolutionary trend with other polyploid plants (such as Arabidopsis, rice, and wheat). However, the gene amplification pattern of yellow pitaya still shows unique characteristics, especially the amplification of the relevant genes in environmental adaptation, which may be closely related to its unique growth environment. In terms of amplification of stress-resistant genes, the genome of yellow pitaya shows adaptive strategies for extreme environments. The NAC transcription factor family has undergone a large-scale expansion in yellow pitaya, and the family plays a key role in regulating abiotic stresses such as drought, high salt and low temperature. Amplification of the LEA gene family helps to enhance the water stress response in plants, while amplification of the HSP (heat shock protein) gene family may enhance the tolerance of plants in high temperature environments. From an evolutionary perspective, the gene amplification pattern of yellow pitaya has both similar characteristics to other polyploid plants and also shows uniqueness.

8 Future Perspectives

8.1 Predicted long-term evolutionary impact of polyploidization in yellow pitaya

Polyplitis is a process of genomic repetition that may lead to increased genetic diversity and adaptability. Polyploids are often associated with enhanced stress resistance, allowing plants to thrive under harsh conditions such as extreme temperatures, drought and salinity. In the long run, polyploidization of yellow pitaya genes can promote the retention of repeated genes, which may undergo diversification or specialization, thereby helping plants adapt to new ecological walls. This genetic flexibility can lead to evolutionary innovation and increase biological complexity and may transform the dragon fruit gene into a more resilient species capable of withstanding environmental stress (Peer et al., 2017). However, the evolutionary success of polyploids is not guaranteed, as they must overcome initial challenges such as stable chromosomal separation and ecological interactions with diploid progenitors. The potential of polyploid as a “sponge” of adaptive allelic diversity suggests that Yellow pitaya can gain enhanced evolution from increased genetic variability (Baduel et al., 2018).

8.2 Integration of multi-omics approaches to explore stress-resistant genes

The integration of multiomics methods such as genomics, transcriptomics, proteomics and metabolomics provides a systematic research strategy for analyzing the stress resistance of Yellow pitaya. These methods can reveal complex molecular networks and signaling pathways that confer to plants tolerate environmental stress and help identify key genes and regulatory elements closely related to stress response (Zhou et al., 2019). Transcriptomic studies can be used to identify differentially expressed genes under stress conditions, while proteomic analysis can screen for proteins that play a core role in stress adaptation. Combining multi-level data, a fine gene regulation network can be constructed and targeted genes that may be used for genetic improvement. For the study of stress resistance of Yellow pitaya, integrating multiomics data can provide scientific basis for breeding and genetic engineering, thereby improving its adaptability under different environmental conditions. By systematically analyzing the key molecular mechanisms in the biological process, genetic improvement strategies can be optimized, the cultivation of high-resistance varieties can be promoted, and the sustainable cultivation and industrial development of Yellow pitayas can be promoted.

8.3 Application prospects of yellow pitaya genome polyploidization research in ecological agriculture

The study of genome polyploidization in Yellow pitaya has significant application prospects in ecological agriculture. Polyploid plants often exhibit enhanced stress tolerance and can be used to develop varieties that are more resilient to environmental stresses such as drought, salinity, and extreme temperatures. This resilience is particularly valuable in ecological agriculture, where chemical input is minimized, and crops must reliably rely on their inherent stress resistance. By understanding the genetic and molecular basis of polyploid-induced stress tolerance, breeders can develop Yellow pitaya varieties that are more suitable for sustainable agricultural practices. Polyplification can lead to increased yield and improved fruit quality, thereby further enhancing the economic viability of Yellow pitaya cultivation. Insights gained from polyploidization research can also inform the development of other crops, thereby promoting biodiversity and ecosystem stability in agricultural systems (Kreiner et al., 2018). The application of polyploidization research in Yellow pitaya can promote the conservation and preservation of genetic resources and be consistent with the principles of ecological agriculture.

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Conflict of Interest Disclosure

The author confirms that the study was conducted without any commercial or financial relationships and could be interpreted as a potential conflict of interest.

References

Alam O., Khan L., Khan A., Salmen S., Ansari M., Mehwish F., Ahmad M., Zaman Q., and Wang, H., 2024, Functional characterisation of Dof gene family and expression analysis under abiotic stresses and melatonin-mediated tolerance in pitaya (*Selenicereus undatus*), Functional Plant Biology: FPB, 51: FP23269.
https://doi.org/10.1071/FP23269

Alix K., Gérard P., Schwarzacher T., and Heslop-Harrison P., 2017, Polyploidy and interspecific hybridization: partners for adaptation, speciation and evolution in plants, Annals of Botany, 120: 183-194.
https://doi.org/10.1093/aob/mcx079

Anatskaya O., and Vinogradov A., 2022, Polyploidy and myc proto-oncogenes promote stress adaptation via epigenetic plasticity and gene regulatory network rewiring, International Journal of Molecular Sciences, 23(17): 9691.
https://doi.org/10.3390/ijms23179691

Chen J., Xie F., Cui Y., Chen C., Lu W., Hu X., Hua Q., Zhao J., Wu Z., Gao D., Zhang Z., Jiang W., Sun Q., Hu G., and Qin Y., 2021, A chromosome-scale genome sequence of pitaya (*Hylocereus undatus*) provides novel insights into the genome evolution and regulation of betalain biosynthesis, Horticulture Research, 8: 164.
https://doi.org/10.1038/s41438-021-00612-0

Chen C, Li F, Xie F., Chen J., Hua Q., Chen J., Wu Z., Zhang Z., Zhang R., Zhao J., Hu G., and Qin Y., 2022, Pitaya genome and multiomics database (PGMD): a comprehensive and integrative resource of *Selenicereus undatus*, Genes, 13(5): 745.

Hu X., Xie F., Liang W., Liang Y., Zhang Z., Zhao J., Hu G., and Qin Y., 2022, HuNAC20 and HuNAC25, two novel NAC genes from yellow pitaya, confer cold tolerance in transgenic arabidopsis, International Journal of Molecular Sciences, 23(4): 2189.
https://doi.org/10.3390/ijms23042189

Khokhar A., Hui L., Khan D., You Z., Zaman Q., Usman B., and Wang H., 2024, Transcriptome profiles reveal key regulatory networks during single and multifactorial stresses coupled with melatonin treatment in pitaya (*Selenicereus undatus* L.), International Journal of Molecular Sciences, 25(16): 8901.
https://doi.org/10.3390/ijms25168901

Kreiner J., Stinchcombe J., and Wright S., 2018, Population genomics of herbicide resistance: adaptation via evolutionary rescue, Annual Review of Plant Biology, 69: 611-635.
https://doi.org/10.1146/annurev-arplant-042817-040038

Li X., Zhang L., Wei X., Datta T., Wei F., and Xie Z., 2024, Polyploidization: a biological force that enhances stress resistance, International Journal of Molecular Sciences, 25(4): 1957.
https://doi.org/10.3390/ijms25041957

Paun O., Fay M., Soltis D., and Chase M., 2007, Genetic and epigenetic alterations after hybridization and genome doubling, Taxon, 56(3): 649-656.
https://doi.org/10.2307/25065850

Peer Y., Mizrachi E., and Marchal K., 2017, The evolutionary significance of polyploidy, Nature Reviews Genetics, 18: 411-424.
https://doi.org/10.1038/nrg.2017.26

Rao S., Tian Y., Xia X., Li Y., and Chen J., 2020, Chromosome doubling mediates superior drought tolerance in Lycium ruthenicum via abscisic acid signaling, Horticulture Research, 7: 40.
https://doi.org/10.1038/s41438-020-0260-1

Scarrow M., Wang Y., and Sun G., 2020, Molecular regulatory mechanisms underlying the adaptability of polyploid plants, Biological Reviews, 96(2): 394-407.
https://doi.org/10.1111/brv.12661

Song Q., and Chen Z., 2015, Epigenetic and developmental regulation in plant polyploids, Current Opinion in Plant Biology, 24: 101-109.
https://doi.org/10.1016/j.pbi.2015.02.007

Tossi V., Tosar L., Laino L., Iannicelli J., Regalado J., Escandón A., Baroli I., Causin H., and Pitta-Álvarez S., 2022, Impact of polyploidy on plant tolerance to abiotic and biotic stresses, Frontiers in Plant Science, 13: 869423.
https://doi.org/10.3389/fpls.2022.869423

Van De Peer Y., Ashman T., Soltis P., and Soltis D., 2020, Polyploidy: an evolutionary and ecological force in stressful times, The Plant Cell, 33: 11-26.
https://doi.org/10.1093/plcell/koaa015

Wang L., Cao S., Wang P., Lu K., Song Q., Zhao F., and Chen Z., 2021, DNA hypomethylation in tetraploid rice potentiates stress-responsive gene expression for salt tolerance, Proceedings of the National Academy of Sciences, 118(13): e2023981118.
https://doi.org/10.1073/pnas.2023981118

Wang J.Y., Yang Z.Y., Lei T.Y., Zhang Y., Xiao Q.M., Yu Z.J., Zhang J.Q., Sun S.R., Xu Q., Shen S.Q., Yan Z.M., Fang M.N., Ding Y., Liu Z.H., Zhu Q.W., Ren K., Pan Y.X., Liu H.B., and Wang J.P., 2023. A likely autotetraploidization event shaped the Chinese mahogany(*Toona sinensis*) genome, Horticultural Plant Journal, 9(2): 306-320.

Wendel J., 2004, Genome evolution in polyploids, Plant Molecular Biology, 42: 225-249.
https://doi.org/10.1023/A:1006392424384

Xu W., Jian S., Li J., Wang Y., Zhang M., and Xia K., 2023, Genomic identification of CCCH-type zinc finger protein genes reveals the role of HuTZF3 in tolerance of heat and salt stress of yellow pitaya (*Hylocereus megalanthus*), International Journal of Molecular Sciences, 24(7): 6359.
https://doi.org/10.3390/ijms24076359

Zaman Q., Garg V., Raza A., Nazir M., Hui L., Khan D., Khokhar A., Hussain M., Wang H., and Varshney R., 2024, Unique regulatory network of dragon fruit simultaneously mitigates the effect of vanadium pollutant and environmental factors, Physiologia Plantarum, 176(4): e14416.
https://doi.org/10.1111/ppl.14416

Zhou J., Wang Z., Mao Y., Wang L., Xiao T., Hu Y., Zhang Y., and Ma Y., 2020, Proteogenomic analysis of pitaya reveals cold stress-related molecular signatur, PeerJ, 8.
https://doi.org/10.7717/peerj.8540

Vicient C.M., and Casacuberta J.M., 2017, Impact of transposable elements on polyploid plant genomes, Annals of Botany, 120(2): 195-207
https://doi.org/10.1093/aob/mcx078