Genetic Diversity and Molecular Marker Discovery of Adaptive Traits in Triticeae Crops

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Abstract Triticeae crops, including wheat, barley and rye, are of concern because of their important role in the global food supply, and their adaptive traits, such as drought, salt and alkali tolerance and disease resistance, are key determinants of their productivity and stability. The formation of adaptive traits is affected by many environmental and genetic factors, and its genetic diversity is of great significance to the adaptive ability and genetic improvement of Triticeae crops. This study summarized the genetic diversity of adaptive traits in Triticeae crops and its evaluation methods. In particular, the use of molecular marker technologies such as single nucleotide polymorphism (SNP) and simple sequence repeat (SSR) in the assessment and utilization of these traits, Molecular markers not only reveal the complexity of genetic diversity, but also accelerate the study of genes associated with adaptive traits, providing a powerful tool for molecular assisted breeding. Bioinformatics methods combined with molecular markers will further promote the study of adaptive traits of Triticeae crops, and provide a scientific basis for coping with climate change and improving food security.

Keywords Triticeae crops; Adaptive traits; Genetic diversity; Molecular marker; Bioinformatics

In the context of global food security challenges, Triticeae crops, as one of the staple foods of mankind, play an irreplaceable role in ensuring the stability of food supply and responding to the needs of the growing population. Triticeae, including wheat, barley, rye, etc., not only accounts for an important share of global food production, it is also a key source of animal feed and biomass energy (Angus et al., 2015). With the increasing impact of climate change on agricultural production conditions, the study of adaptive traits of Triticeae crops has become an important scientific frontier to ensure food security..

Adaptive traits, including but not limited to drought resistance, saline-alkali tolerance, disease resistance and the ability to adapt to extreme climatic conditions, are the key factors for Triticeae crops to survive and reproduce in changeable environments. These traits not only directly affect the growth and development of crops, but also directly affect the yield of crops. It is also of great significance for improving crop stress resistance, reducing the impact of agriculture on the environment and promoting sustainable agricultural development (Blum, 2014).

The purpose of this study was to investigate the genetic diversity of adaptive traits in Triticeae crops and the application and discovery of molecular markers in this process. Through an in-depth analysis of the adaptive responses of Triticeae crops to different environmental stresses, this study aims to reveal those key genetic factors, how they regulate the adaptive responses of crops, and how this knowledge can be used to guide future breeding efforts. In the context of molecular marker technology as a powerful tool to help scientists identify genes associated with important agronomic traits (Ha et al., 2022) and thus accelerate crop improvement procedures, this study will detail the application of molecular marker technology in the assessment of genetic diversity.

Barley Research on adaptive traits of Triticeae crops and their genetic diversity is of far-reaching significance for optimizing agricultural production, improving crop yield and quality, and coping with global climate change. By exploring the genetic potential of Triticeae crops, researchers can not only enhance crop stress resistance, but also provide scientific basis and technical support for sustainable agricultural development. With the continuous

progress of molecular biology technology, the application of molecular markers provides an unprecedented opportunity for researchers to analyze the genetic mechanism of Triticeae crops adaptive traits from a new perspective and method, and then guide future crop improvement and breeding strategies.

1 An Overview of Adaptive Traits of Triticeae Crops

1.1 The species and importance of Triticeae crops

Triticeae crops are an important part of the global agriculture and food system, including wheat, barley, rye, oats and many other types. These crops play a crucial role in maintaining global food security, not only because they grow steadily in different climates and soil conditions, but also because they form the basis of the daily diet of people in many countries (Gao et al., 2023).

Wheat is one of the world's most important food crops, widely used in the production of bread, pasta and other foods, and plays a central role in the global food supply. Barley is not only an important food raw material, especially in the manufacture of beer, but also an important animal feed. Rye, despite its small area of cultivation, is an important crop for making bread and other foods in certain regions such as Eastern Europe and Russia (Feldman and Levy, 2015). Valued for its rich nutritional value, not only consumed as a healthy breakfast food, but also widely used in feed, oats are rich in dietary fiber, which is particularly beneficial for improving heart health.

Triticeae crops are important far beyond their immediate value as food. They also play an important role in agro-ecosystems, promoting biodiversity, maintaining soil health, and holding a special place in different cultures. It is an integral part of many festivals and traditional customs (Feldman and Levy, 2015). As the global population continues to grow and climate change poses increasingly severe challenges to agricultural production, it is particularly important to study and improve the adaptive traits of Triticeae crops. By improving the yield, adaptability and nutritional value of Triticeae crops, we can not only ensure the stability of global food supply, but also prepare for possible food security challenges in the future.

1.2 Definition and classification of adaptive traits

Adaptive traits refer to the traits or characteristics developed by organisms during long-term evolution that can help them better adapt to specific environmental conditions and improve survival and reproductive success (Ovsyannikov and Shpitonkov, 2020). These adaptive traits are particularly critical in the breeding and scientific research of Triticeae crops, as they are directly related to growth performance, yield, and resistance to environmental stresses such as abiotic (e.g. drought, salinity, temperature extremes) and biological (e.g. disease, pest infestation) factors.

The classification of adaptive traits can be divided into four categories: abiotic adaptive traits, biological adaptive traits, morphological and physiological adaptive traits, and reproductive adaptive traits. Abiotic adaptive traits enable crops to withstand abiotic environmental stresses such as drought, salinity, low temperature or high temperature, which is particularly important for food production in arid and saline soil areas (Ovsyannikov and Shpitonkov, 2020). Bioadaptive traits refer to the resistance of crops to diseases and pests, which can help reduce crop loss and protect yield and quality. Morphological and physiological adaptive traits, such as root depth, leaf size, photosynthetic efficiency, etc., affect the resource acquisition and utilization of crops, and then affect the overall growth performance and adaptability. Reproductive adaptive traits are related to the regulation of flowering period, seed setting rate and seed production, which determine the reproductive ability of crops and the ability to adapt to different growing seasons.

1.3 The formation and influencing factors of adaptive traits

The formation of adaptive traits is a core aspect of biological evolution, involving the response of Triticeae crops to environmental pressures over a long period of evolution and artificial selection. The formation and development of these traits are the result of the interaction between genetic factors and environmental factors, which provide the material basis for adaptive traits. New traits are generated through gene variation and

recombination, and the variation conducive to survival will be retained and accumulated by natural selection to form specific adaptive traits (Guzzon et al., 2017). For example, drought resistance, salt tolerance, disease resistance and other traits are expressed through the action of specific genes or genomes, and the expression and regulation of these genes determine the ability of crops to adapt to environmental stress.

Environmental factors also play a decisive role in the formation of adaptive traits. Environmental factors such as different climatic conditions, soil types and pressure of pests and diseases promote the corresponding adaptive changes of Triticeae crops. Crops exposed to a specific environmental pressure for a long time will gradually develop traits that adapt to the environment, such as crops in arid areas often have better drought tolerance (Wadgymar et al., 2022). Human selection has also significantly influenced the formation of adaptive traits, with farmers and breeders accelerating the process of crop adaptation to specific environments by breeding individuals with desired traits, such as the selection of hardy varieties to adapt to cold and warm regions.

The formation of adaptive traits is a direct reflection of the interaction between genes and environment. Whether a genetic variation becomes a dominant adaptive trait depends not only on the variation itself, but also on its adaptability and performance in a specific environment. Environmental changes can also promote the adjustment of gene expression patterns and affect the development of adaptive traits. The formation of adaptive traits is a complex multi-factor interaction process, including genetic diversity, natural and human selection and environmental conditions.

2 The Importance of Genetic Diversity in Triticeae Crops

2.1 The concept of genetic diversity
Genetic diversity refers to the diversity of genetic composition within a species, which reflects the differences between individuals at the genetic level. This diversity is the basis of biological evolution and is crucial for the survival of species and the adaptation to environmental changes. Genetic diversity includes not only genetic differences between individuals, but also genetic variation between different populations and populations, which can be expressed in various forms (Swarup et al., 2020), including polymorphisms at single gene loci, combinations of different genes in the genome, and structural variations on chromosomes.

In agriculture, genetic diversity of crops is an important component of agricultural biodiversity and is of great value for crop improvement, disease management, and adaptation to environmental change (Figure 1). High genetic diversity means that crops have a wider range of adaptability and can grow in more diverse environmental conditions, as well as greater resistance to pests and diseases and abiotic stresses (such as drought, salinity, etc.) (Swarup et al., 2020). Genetic diversity is also an important resource for crop breeding, which breeders rely on to develop new varieties that improve crop yield, quality, nutritional value, and resilience to specific environmental conditions.

2.2 Relationship between genetic diversity and adaptive traits in Triticeae crops
Genetic diversity plays a key role in the formation and development of adaptive traits in Triticeae crops, which provides crops with the ability to adapt and survive in the face of environmental stresses, both abiotic and biological. This diversity means that there is a wide range of genetic variation in the gene pool of crops that underlies their resistance to drought, salinity, extreme temperature conditions, and disease and pest attacks (Wang et al., 2017). For example, specific genetic variants may enable certain wheat varieties to maintain growth in low water conditions or survive in cold environments, and genetic diversity contains resistance genes that allow Triticeae crops to resist attacks by various pathogens and pests, thus protecting crop yield and quality from being affected.

Genetic diversity not only enhances the adaptability of Triticeae crops to environmental changes, but also has a direct impact on their productivity and stability. Crops with rich adaptive traits can maintain relatively stable yields under changeable environmental conditions and reduce production risks caused by environmental fluctuations (Pour-Aboughadareh et al., 2017). Genetic diversity also provides a rich resource for breeding, and by

screening and utilizing the favorable genes in these genetic variants, breeders are able to breed new varieties with excellent characteristics that are not only better adapted to environmental pressures, but also meet market demands for crop quality and nutritional value.
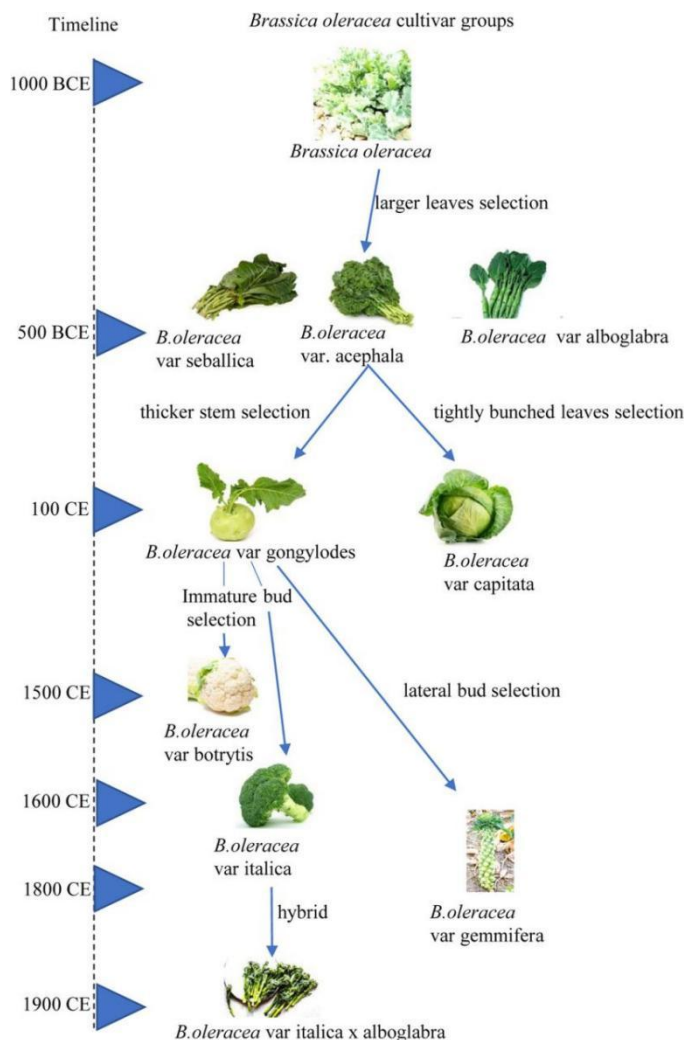

Figure 1 An example of remarkable genetic diversity existing in a plant family (Take the cultivar groups of *Brassica oleracea* as an example) (Swarup et al., 2020)

2.3 The role of genetic diversity in genetic improvement of Triticeae crops

Genetic diversity plays a crucial role in the genetic improvement of Triticeae crops and provides a valuable resource for breeding. It enables breeders to select genes from a wide gene pool for specific adaptive traits, such as drought tolerance, salt tolerance and cold resistance. Thus, the adaptive ability of crops to abiotic environmental stress can be significantly improved (Marzeih et al., 2018). Genetic diversity contains resistance genes that are key to crop resistance to various pests and diseases, and by integrating these genes into new crop varieties, it can effectively reduce the dependence on chemical pesticides, reduce production costs, and promote environmental sustainability. Genetic diversity also offers the possibility to improve the quality and nutritional value of crops, such as increasing protein content, improving vitamin and mineral content, and meeting market and consumer demand for high-quality food.

Genetic diversity also facilitates the optimization of the genetic background of Triticeae crops and the development of new varieties. Through cross-species mating and genetic recombination, breeders can create varieties with new genetic combinations that may exhibit superior performance, adaptability or quality characteristics. In the face of the challenges posed by global climate change, genetic diversity provides a key

resource to address this global issue, enabling Triticeae crops to adapt to new climatic conditions and ensuring the stability and sustainability of global food production (Girma, 2017). The protection and rational use of the genetic diversity of Triticeae crops is of great significance for promoting the progress of agricultural science and technology, achieving food security and sustainable development. Through modern biotechnology, such as molecular markers and gene editing technologies, genetic diversity can be used more accurately and efficiently, bringing new opportunities for genetic improvement and breeding of Triticeae crops.

3 Genetic Diversity Assessment Methods and Tools

3.1 Overview of traditional evaluation methods
The traditional assessment methods of genetic diversity are mainly based on morphological analysis, physiological and ecological characteristics measurement, and biochemical marker analysis, which provide basic means for understanding and describing the diversity of plant genetic resources. Although these methods are relatively basic in the face of modern molecular marker technology, they still play an important role in resource-limited environments (Govindaraj et al., 2015).

Morphological analysis is a preliminary assessment of genetic differences between plants by observing and measuring plant appearance characteristics, such as plant height, leaf shape, flower color and seed shape. This method is simple and intuitive, but may be affected by environmental factors, and the resolution is limited. The measurement of physiological and ecological characteristics involves more complex experimental conditions, and reflects the adaptability of plants to the environment by assessing their photosynthetic efficiency and salt-alkali tolerance, and reveals the physiological basis of genetic diversity (Govindaraj et al., 2015). Biochemical markers, such as isozyme analyses of proteins and enzymes, have been widely used for genetic analysis of germplasm resources because they can directly reflect genotype differences, although they can only detect the genetic variations encoding these molecules.

3.2 Application of molecular marker technology in genetic diversity assessment
The application of molecular marker technology to the assessment of genetic diversity has revolutionized the face of modern genetics and breeding research, providing a way to accurately analyze and compare the genetic makeup of different individuals or populations at the DNA level. These techniques allow the assessment of genetic diversity to be independent of environmental factors, greatly improving the accuracy and efficiency of the analysis (Ramesh et al., 2020).

Restricted fragment length polymorphism (RFLP) technique reveals genetic variation by analyzing length differences of DNA fragments. Although the operation is cumbersome, it provides the basis for early genetic diversity research. Amplified fragment length polymorphism (AFLP) technology combines the advantages of PCR and restriction enzyme digestion to generate a large number of markers without the need for specific sequence information and is suitable for a wide range of genetic analyses. Simple sequence repeat (SSR) or microsatellite markers are important tools for genetic diversity assessment, phylogenetic analysis, and breed identification due to their high polymorphism and ubiquity in the genome (Soriano, 2020). Single nucleotide polymorphism (SNP) markers, with their high density and high degree of automation, have become the first choice for fine genetic analysis and genome selection breeding.

These molecular marker techniques not only promote a deeper understanding of genetic diversity, but also enable scientists to quantify and characterize the genetic structure of species, the genetic differences between populations, and effectively conserve and use genetic resources. For breeding, the application of molecular marker technology accelerates the identification of favorable genetic characteristics and the process of variety improvement, making it possible to breed new varieties that adapt to environmental changes and meet human needs.

3.3 Application of bioinformatics methods to genetic diversity assessment
With the rapid development of high-throughput sequencing technology, the application of bioinformatics methods in genetic diversity assessment has become an integral part, especially when processing and analyzing big data.

Through bioinformatics tools, scientists are able to perform sequence alignment and mutation detection, and identify genetic variants such as single nucleotide polymorphisms (SNPS) and insertions/deletions (Indels), which provide a basis for understanding genetic differences between individuals and populations (Hoban et al., 2022). Bioinformatics can also calculate population genetic parameters such as allele frequency, heterozygosity, and genetic distance to quantify genetic diversity and analyze genetic differentiation between populations.

Using bioinformatics methods, scientists can build phylogenetic trees to reveal evolutionary relationships between species or populations, which has important implications for understanding species differentiation, population history, and the origin and spread of genetic resources. The use of genome-wide association studies (GWAS) and selective signal analysis further allows researchers to identify genes or genetic regions that control important agronomic traits, as well as genetic regions that have historically been subject to natural or artificial selection. This provides insights into the evolution of adaptive populations.

4 Application of Molecular Markers in Adaptive Traits of Triticeae Crops

4.1 Molecular marker discovery and development

In the field of wheat crop research and breeding, the discovery and development of molecular markers have become the core technology to improve breeding efficiency and accelerate genetic improvement (take wheat as an example (Figure 2)). With the wide application of high-throughput sequencing technology, scientists can obtain a large amount of genomic data, providing rich resources for the rapid discovery of molecular markers (Song et al., 2023). Common types of molecular markers include simple sequence repeats (SSRS), single nucleotide polymorphisms (SNPS), and insertions/deletions (InDels), among which SSRs are widely used in genetic diversity studies due to their high polymorphism and genetic stability. SNP markers are suitable for fine genetic analysis and molecular assisted selection because of their high density and high throughput in the genome.

By comparing the genome sequences of different varieties or germplasm resources, scientists can identify potential molecular marker sites, which are then experimentally verified for polymorphism and genetic stability, ensuring their validity in subsequent studies. These validated molecular markers are widely used in the fields of genetic structure analysis, variety identification, genetic diversity assessment and molecular assisted breeding of Triticeae crops, which greatly improves the accuracy and efficiency of breeding, and also critically promotes the mining of functional genes. Through association analysis and gene mapping, scientists were able to identify genes controlling important agronomic traits, providing important information for in-depth understanding of the genetic mechanism of traits and guiding molecular design and breeding.
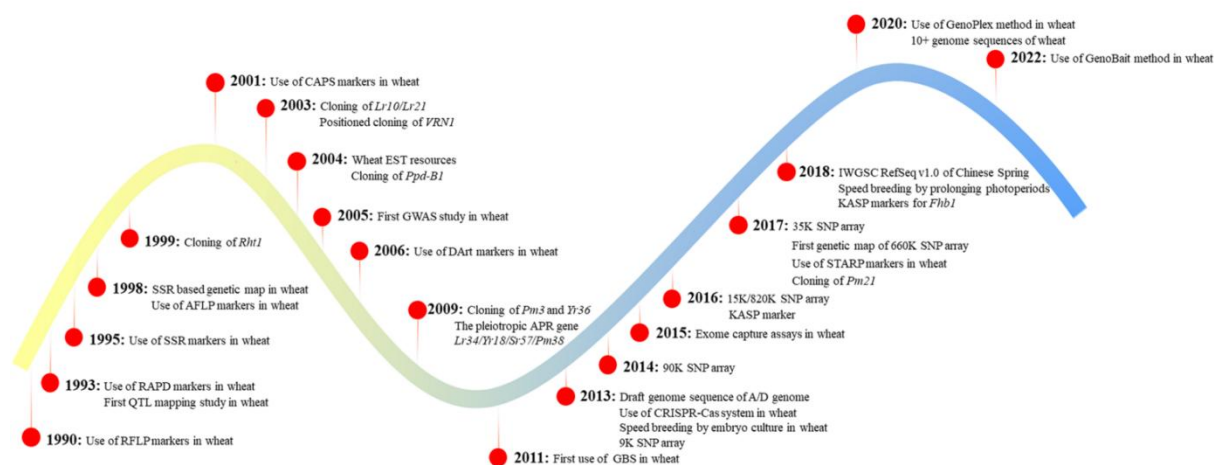

Figure 2 Timeline of application of molecular markers in wheat breeding and research (Song et al., 2023)

4.2 Case study of association between molecular markers and adaptive traits

In the study of Triticeae crops, the association between molecular markers and adaptive traits provides an effective means to accelerate crop improvement and improve resistance. A foreign research team aims to improve the

drought tolerance of wheat through marker assisted selection (MAS) technology. In the face of drought challenges brought about by global change, the development of wheat varieties with high drought tolerance has become a priority goal (Sunilkumar et al., 2023). In this study, quantitative trait locus (QTL) was used to identify several QTLS related to drought tolerance by comparing the performance of wheat varieties under different water conditions. These QTLS control key traits such as water use efficiency, root depth and leaf transpiration and are critical for wheat growth under drought conditions.

By integrating this important QTL information into the breeding program, the research team was able to significantly accelerate the breeding process of drought-tolerant varieties, improving the accuracy and efficiency of selection. This work eventually led to the development of several wheat varieties that demonstrated significant drought tolerance, which demonstrated good yield performance and stability in field trials in arid areas. This case not only demonstrates the great potential of molecular marker technology in revealing the genetic basis of crop adaptation traits and promoting resistance breeding, but also provides a strong scientific support for ensuring food security under global climate change. This breeding strategy based on molecular markers has become an indispensable part of modern crop improvement, opening up a new chapter of crop adaptive improvement.

4.3 Application prospect of molecular marker-assisted selection

Molecular marker-assisted selection (MAS) technology has shown broad application prospects in wheat crop breeding, marking that crop improvement has entered a new era of high efficiency and accuracy. By utilizing molecular markers associated with key agronomic traits, MAS can significantly accelerate the process of variety improvement in Triticeae crops, especially for traits such as stress resistance and disease resistance that are time-consuming, costly, or heavily influenced by the environment. This method not only improves the efficiency of breeding and reduces the uncertainty in the selection process, but also enables breeders to make precise selection at the seedling stage and significantly shorten the breeding cycle (Hasan et al., 2021).

The application of MAS technology also helps to improve the adaptability and stability of crops. By precisely improving crop tolerance to abiotic stresses such as drought and salinity, and improving resistance to major pests and diseases, crops can better adapt to environmental changes and ensure the sustainability of agricultural production. MAS also provides the possibility for deep mining and utilization of precious traits in genetic resources, including the transfer of good traits from wild species to cultivated varieties to enrich the genetic diversity of crops. With the development of modern biotechnology such as gene editing, the role of MAS in precision breeding has become more important, it can not only be used to identify editing targets, but also verify editing effects after gene editing to ensure the accurate achievement of breeding targets.

5 Outlook

The role of Triticeae crops has become particularly important in meeting the challenges posed by global climate change and population growth. These challenges require not only improved crop yield and quality, but also improved crop resilience to various abiotic and biological stresses. In this context, it is particularly critical to explore the genetic diversity of Triticeae crops and the discovery and application of molecular markers, which provide a window to reveal the genetic potential of crops and guide researchers to move towards the goal of sustainable development.

However, research in this area also faces a number of challenges, including the complex genetic mechanisms of adaptive traits, the limited availability of genetic resources, and the limitations of molecular marker techniques in terms of high-throughput identification, cost-effectiveness, and data analysis. Adaptive traits are often controlled by multiple genes and affected by environmental factors, which makes it difficult to accurately identify and utilize related genes. Although researchers have accumulated a large number of genetic resources, the effective mining and application of these resources still need to be strengthened. Although molecular marker technology has made progress, some technical and economic obstacles still need to be overcome in practical applications.

In the face of these challenges, the future research direction will focus on three main areas: first, strengthen the

basic research on the genetic and molecular mechanism of wheat crop adaptive traits to provide a scientific basis for breeding; Secondly, it is to optimize and develop new molecular marker technologies to improve the application efficiency of these technologies in genetic resource mining and breeding. Finally, by integrating bioinformatics, genomics and modern breeding techniques, comprehensive assessment and efficient use of genetic resources are promoted.

With the development of modern biotechnology such as molecular marker technology and gene editing, the genetic diversity of Triticeae crops and its application in breeding will show unprecedented potential. Systematic assessment and utilization of genetic diversity can not only reveal new genes related to adaptive traits, but also accelerate the process of adaptive improvement of Triticeae crops. The application of molecular markers will further improve the accuracy and efficiency of breeding, shorten the breeding cycle, and achieve more targeted and efficient breeding strategies.

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