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The Role of Traditional Breeding in Modern Tea Cultivar Development

Lian Chen [1], Lianming Zhang [2]
1 Institute of Life Sciences, Jiyang Colloge of Zhejiang A&F University, Zhuji, 311800, Zhejiang, China
2 Traditional Chinese Medicine Research Center, Cuixi Academy of Biotechnology, Zhuji, 311800, Zhejiang, China
Corresponding author: lianming.zhang@cuixi.org
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Abstract Tea (*Camellia sinensis*) is a valuable crop of global economic importance, and cultivar breeding is essential to ensure the quality-based development of the tea industry. Classical breeding methods have given numerous reasons for the selection of tea cultivars and enabled the establishment of high-yielding, high-quality, and stress-enduring cultivars through seed selection, elite tree selection, hybrid breeding, and clonal propagation. However, its inherent disadvantages of long cycle and low efficiency have limited its ability to keep up with the requirements of precise trait improvement. With the rapid advance in molecular breeding technologies, the integration of traditional breeding with marker-assisted selection (MAS), genomic selection (GS), and gene editing (CRISPR) has emerged as a principal approach in modern tea breeding. This study systematically overviews the past achievements and developments of conventional tea breeding, describes its advantages and disadvantages in the current breeding system, and discusses integration methodologies and common cases of traditional and molecular breeding. It is suggested that future directions are to enhance breeding efficiency, develop germplasm application, and address such issues as climate change. Re-evaluation of the value of traditional breeding and its firm anchor with modern molecular technology will provide theoretical basis and practical directions for establishing a successful, precise, and sustainable tea breeding system.
Keywords Tea breeding; Traditional breeding; Cultivar improvement; Molecular breeding; Precision breeding

1 Introduction

Tea (*Camellia sinensis*) is among the most economically valuable and culturally diverse beverage crops on the globe. As global consumption continues to rise, the tea crop comes under intensifying pressure for cultivars to exhibit high yield, improved quality traits (taste, aroma, biochemical constitution), and biotic and abiotic stress tolerance. Moreover, demands from consumers for health-promoting constituents and specialty tea types (i.e., green, black, oolong) further increase the need for precise trait improvement in breeding programs. However, issues with long generation periods, limited genetic bases for commercial cultivars, and environmental unpredictability hinder the ability to address such shifting breeding requirements (Wang et al., 2020).

Traditional breeding methods have been at the heart of the past evolution of tea production. Methods such as bulk selection, vegetative propagation of superior plants, and crossing have made possible the development and dissemination of numerous high-quality, high-yielding cultivars. Such methods have played a key role in the development of characters including leaf form, biochemical composition (e.g., catechins, theanine, caffeine content), disease resistance, and adaptation to specific agro-ecological zones. Well-known cultivars such as 'Longjing 43' and 'Fuding Dabaicha' are results of traditional breeding efforts, which continue to maintain the backbone of modern tea production systems(Chen et al., 2023a; Li, 2024).

Molecular breeding techniques-marker-assisted selection (MAS), genomic selection (GS), and CRISPR/Cas-based genome editing-have revolutionized plant breeding in most crops over the last few years. Their utilization in tea is constrained by the fact that tea is a perennial crop, having a very big and complex genome, lacking functional genomics infrastructure, and long breeding cycles. Thus, there is a need to rejuvenate the invaluable contribution of traditional breeding techniques, which have associated with them the utmost phenotypic selection accuracy,

application of germplasm variability, and field proof of trait validation. The integration of traditional breeding with molecular techniques is showing great potential to overcome existing bottlenecks and accelerate the development of superior tea varieties (Xia et al., 2020; Li et al., 2023b).

This study provides a comprehensive picture of the role played by conventional breeding in tea cultivar development. It advocates the use of conventional breeding techniques and existing technological developments in molecular technology to maximize efficiency and accuracy in breeding. By highlighting effective integration strategies and addressing the challenges raised, the review offers advice in support of the development of a robust, contemporary tea breeding system based upon set principles and underpinned by molecular advancements to meet the shifting requirements of the tea industry.

2 Traditional Tea Breeding Methods and Their Development

2.1 Seed selection and elite tree selection

Traditional tea breeding started with the selection of elite individuals from diversified seedling populations. The method relies on the identification of elite trees with desirable traits like yield, quality, and stress resistance through agronomic qualities. Morphological description is increasingly becoming a cost-effective approach for initial selection, but molecular markers are increasingly being used to confirm genetic variability and elite status for safeguarding and using valuable germplasm resources (Bandara et al., 2024; Ni et al., 2024).

2.2 Hybrid breeding and systematic selection

Hybridization is the basis of tea breeding that provides scope for the integration of favorable traits from heterogenous parents. Successive selection with subsequent controlled hybridization has produced cultivars that possess increased yield, quality, and tolerance to abiotic and biotic stresses. Hybrid breeding is complemented by physical and chemical mutagenesis to create new variation, and early selection among promising hybrids is increasingly being helped by molecular and phenotypic screening (Ranatunga, 2019).

2.3 Clonal propagation and cultivar dissemination

Clonal propagation, primarily through cuttings, allows one to quickly propagate and disseminate elite cultivars and offer homogeneity at the plantation scale. The method does speed up the spread of superior genotypes but has a tendency to lead to genetic bottlenecks, thus the need to preserve genetic diversity using constant selection and conservation (Bandara et al., 2024).

2.4 Achievements and representative cultivar cases of traditional breeding at different stages

Traditional breeding methods have initiated the development and use of a plethora of high-yielding and high-quality new tea cultivars. As an example, selection of nitrogen-efficient cultivar such as BY1 and Longjing 43 (LJ43) has significantly enhanced sustainable tea cultivation on low-input conditions (Zheng et al., 2025). In recent decades, there have been better cultivars like LC6, LC7, and LC17, which were bred with a systemic strategy, exhibiting superior performances in both agronomic quality and biochemical quality, as precious examples of higher yields and better qualities at the same time (Li et al., 2023a; Shen et al., 2023).

Until now, more than 130 national-level tea cultivars have been developed and registered in China, with each of them demonstrating superior adaptability to different processing technologies and regional ecological conditions, thereby giving strong guarantee for the continued development of China's tea industry. With the application of multi-disciplinary technologies such as molecular markers, genomic selection, phenomics, and multi-omics integration, efficiency and accuracy in tea breeding have been enhanced step by step. The role and contribution of these technologies to cultivar development are illustrated in Figure 1.

3 Application of Traditional Breeding in Tea Trait Improvement

3.1 Breeding and application of high-yield, high-quality cultivars

Traditional breeding through phenotypic selection and hybridization has been an important factor in the development of quality and yield high tea cultivars. Recent genomic studies have identified major genetic loci and candidate genes responsible for yield, leaf shape, and flavor factors and have provided a scientific basis for elite

line selection and accelerating the improvement of such traits in breeding programs (Kong et al., 2025). Genome prediction models are increasingly complementing traditional methods to enable more efficient selection for quality traits such as metabolites catechins and caffeine (Yamashita et al., 2020; Lubanga et al., 2021).

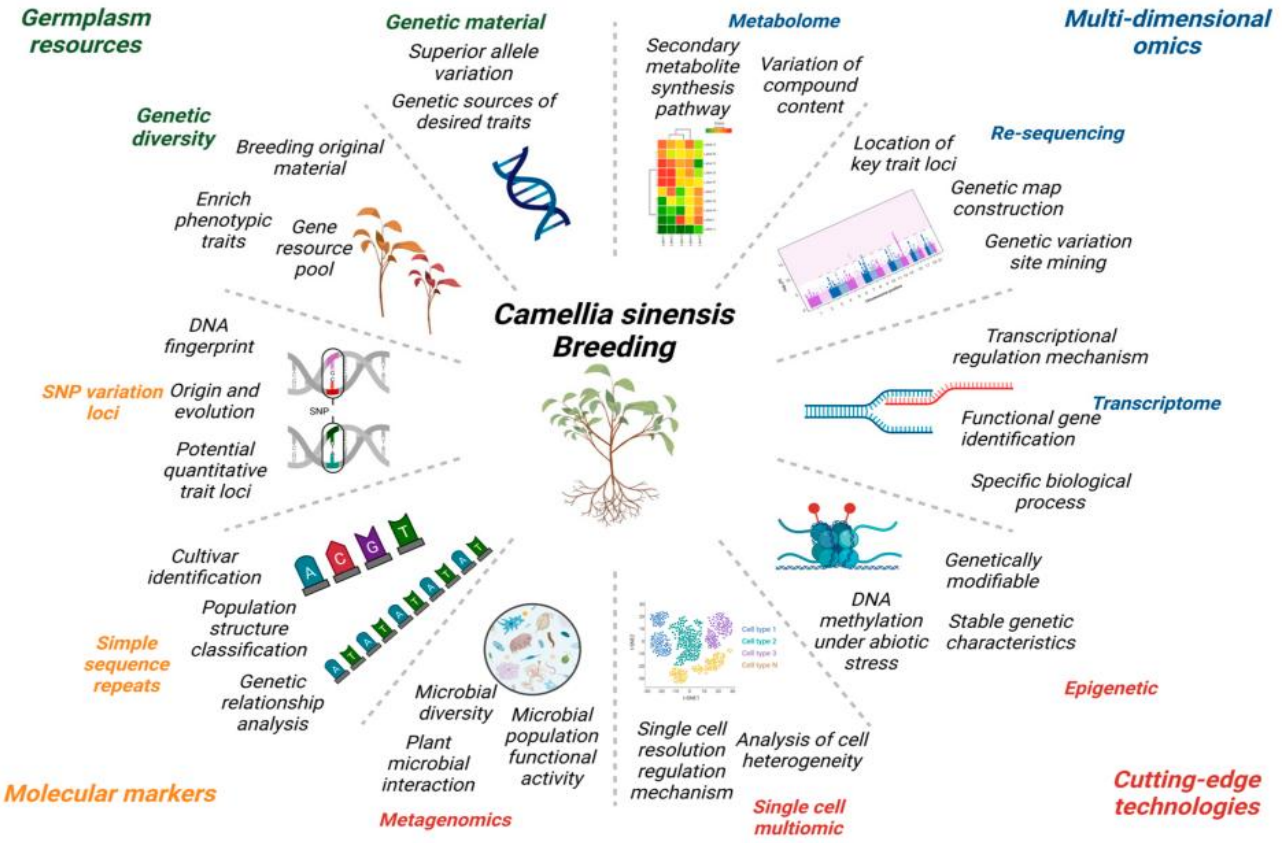

Figure 1 Diagram of the role or contribution of multiple perspective-based techniques to tea plants breeding. lmage was created with the tools of BioRender (https://app.biorender.com/(accessed on 28 June 2023)) (Adopted from Li et al., 2023a)

3.2 Practices in breeding disease and pest-resistant, stress-tolerant varieties

Conventional breeding has depended on selecting naturally disease-resistant, pest-resistant, and environmentally stress-tolerant individuals. Exploitation of diverse germplasm, including wild relatives, has assisted in the formation of stress-resistant cultivars, although constraints such as low cross-compatibility exist (Mukhopadhyay et al., 2015; Ranatunga, 2019). Marker-assisted selection and QTL mapping are increasingly being used to screen for and introgress the resistance trait into breeding programs (Xu et al., 2018; Malebe et al., 2021).

3.3 Development of specialty cultivars for green tea, black tea, oolong tea, etc.

Traditional breeding has allowed for the identification and propagation of cultivars specific to green, black, and oolong teas, among other tea types. Biochemical profiling coupled with sensory evaluation and genetic analysis has enabled the development of cultivars with unique flavor profiles and processing amenability (Kong et al., 2025). GWAS and metabolite profiling have revealed genetic variations linked to specialty traits, enabling targeted breeding of tea products (Kong et al., 2025).

3.4 Utilization of regional adaptability and eco-type germplasm resources

Regional eco-types and germplasm resources have been at the core of breeding programs to guarantee local condition adaptability and retention of genetic diversity. Population genetic research reveals widespread genetic divergence and adaptation among tea accessions from different regions and provide a rich resource for breeding regionally adapted cultivars (Kong et al., 2025). Use of wild and local germplasm continues to add to the resilience and sustainability of tea production systems (Li et al., 2023b).

4 Advantages and Limitations of Traditional Breeding

4.1 Advantages: Stable genetic base and strong adaptability

Traditional breeding tools such as phenotypic selection and clonal multiplication have established a solid genetic base in tea cultivars. These tools take advantage of local adaptation and natural genetic variability and yield cultivars with superior adaptability to diverse environments and capacity for withstanding local stresses. The use of elite local germplasm ensures that new varieties well fit specific regional conditions, which is a factor in sustainable tea production (Vavilova and Korzun, 2023).

4.2 Limitations: Long breeding cycles and low efficiency

One of the major limitations of traditional tea breeding is its lengthy breeding period, usually over 16 years from choice to release of a cultivar. The process is tiresome and time-intensive, involving poor selection efficiency due to tea being a perennial crop and needing intensive field testing. It decelerates the rate of genetic advancement and delays the release of new varieties with desirable traits (Mukhopadhyay et al., 2015; Tuwei and Corley, 2019; Lubanga et al., 2022).

4.3 Insufficient understanding of complex trait genetic mechanisms

Traditional breeding relies heavily on phenotypically expressed characters, which are often influenced by complex genetic and environmental interactions. The lack of in-depth understanding of the genetic mechanisms governing key agronomic and quality traits limits the precision of selection. The recent advances in genomics and multi-omics are now bridging these gaps, but traditional methods alone cannot yet stringently analyze complex trait inheritance (Xia et al., 2020; Yamashita et al., 2020).

4.4 Challenges in the conservation of genetic diversity in cultivars

Whereas natural variation has been exploited by traditional breeding, recurrent selection and vegetative propagation have the potential to narrow the genetic base, which results in enhanced disease, pest, and environmental stress susceptibility. Conservation of genetic diversity is also constrained by limitations in utilization of wild relatives due to cross-incompatibility and genetic drag. Conservation of genetic diversity is being necessitated increasingly by including broader germplasm resources and newer molecular tools to conserve and enhance genetic diversity in tea breeding programs (Mukhopadhyay et al., 2015).

5 Integration Strategies of Traditional Breeding with Modern Molecular Breeding Technologies

5.1 Combining precise phenotyping with marker-assisted selection (MAS)

Integration of phenotypic evaluation in detail with marker-assisted selection (MAS) enhances the precision and efficiency of selection in desirable characteristics in tea breeding. Molecular markers such as SNPs and SSRs are more and more used for the detection and tracing of genes related to yield, quality, and resistance against stresses, allowing breeders to make more precise decisions earlier in the breeding process and reduce the application of time-consuming field trials (Ranatunga, 2019). Bioinformatics software and massive databases also facilitate better genotypic and phenotypic data integration for MAS (Xia et al., 2019).

5.2 Complementary application of traditional hybrid breeding and genomic selection (GS)

Traditional hybridization remains crucial for generating genetic diversity, whereas genomic selection (GS) employs genome-wide marker data to predict breeding values and propel genetic gain. Simulation experiments show that GS can greatly improve genetic gain as well as reduce breeding cycles relative to phenotypic selection alone, and is hence an effective complement to traditional hybrid breeding, especially in limited environments (Kumar et al., 2016; Yamashita et al., 2020). GS is most beneficial when applied early at seedling stages, thus making the selection more precise and affordable (Lubanga et al., 2022).

5.3 Collaborative innovation in utilizing traditional germplasm and functional gene mining

The integration of traditional germplasm resources and emerging gene mining technologies, such as pangenomics and multi-omics, enables us to uncover new alleles and functional genes for key agronomic traits. The

high-quality pangenomes and GWAS enable the identification of candidate genes for bud flush time and flavor and other characteristics, which are the foundation for the purposeful use of diverse germplasms in breeding programs (Zhang et al., 2020a; Kong et al., 2025) (Figure 2). This synergistic approach ensures the maintenance and utilization of genetic diversity while enabling precise trait improvement (Chen et al., 2023b).

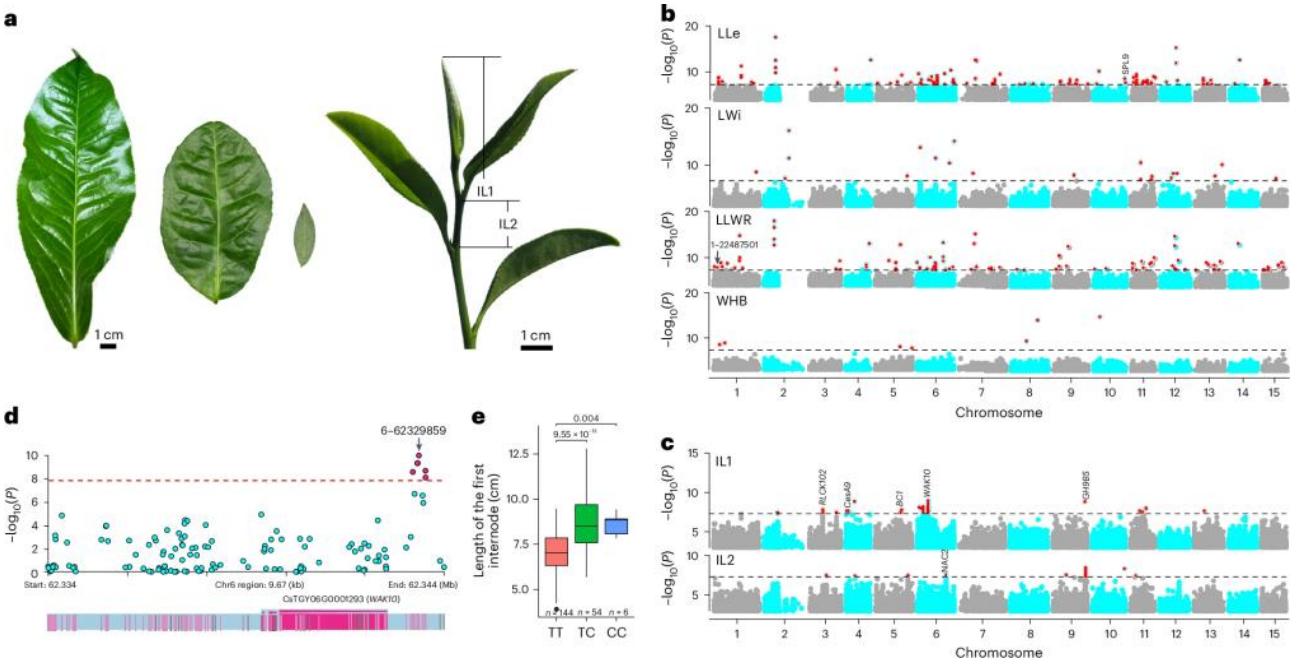

Figure 2 GWAS for agronomic traits in young bud (Adopted from Kong et al., 2025)

5.4 A new model of precise traditional breeding empowered by gene editing (CRISPR)

Gene editing technologies, particularly CRISPR, offer unprecedented precision for in vivo editing of single genes for important traits. While still in its early days in tea, the integration of CRISPR with traditional breeding has the ability to rapidly add or enhance traits such as disease resistance, quality, and stress tolerance. The integration of CRISPR with traditional breeding, together with genomics and MAS, is a new model for precise and effective tea breeding (Xia et al., 2020; Li et al., 2023a).

6 Case Studies

6.1 Successful cases of tea quality trait improvement

The integration of genome-wide association studies (GWAS) and genomic prediction (GP) with traditional breeding has enabled the mapping of candidate genes and SNP markers that are associated with key quality-related metabolites, such as catechins and caffeine (Zhang et al., 2020b; Luo et al., 2024). For example, through RAD-seq and GWAS, precise predictions for catechin and caffeine at moderate levels have been achieved, allowing for more effective selection for good quality tea accessions and accelerating the breeding of high quality cultivars (Yamashita et al., 2020). Good quality pangenome resources have also facilitated the identification of allelic variants for flavor and bud flush timing, further augmenting genomics-assisted quality improvement (Chen et al., 2023a).

6.2 Technological integration pathways in developing resistant cultivars

Multi-omics approaches, i.e., genomics and transcriptomics, have been utilized to identify disease and stress resistance molecular markers and candidate genes. Currently, these markers are used in marker-assisted selection (MAS) to complement traditional breeding to enable the production of cultivars with enhanced resistance to abiotic and biotic stresses. The use of SNP markers and QTL mapping has increased the effectiveness of resistance line selection, and coordination with single-cellomics and pangenomics in the future will be expected to improve resistance breeding (Meegahakumbura et al., 2018; Shen et al., 2024).

6.3 Directed breeding examples of region-specific tea cultivars

Population genomics and molecular marker analysis have been used to characterize genetic diversity and structure in regional tea germplasms. Genome resequencing of tea accessions, for instance, revealed strict selection on disease resistance and flavor traits in target populations, guiding the development of regionally adapted cultivars through marker-assisted and genomic selection strategies (Niu et al., 2019). Moreover, SNP marker sets have been developed to allow for rapid identification and discrimination of region-specific varieties, empowering targeted breeding and conservation efforts (Li et al., 2023b; Shen et al., 2024).

7 Prospects and Strategies for Traditional Breeding in Modern Tea Cultivar Innovation

7.1 Trends in integrating technologies to enhance breeding efficiency and precision

The integration of genomic selection (GS), genome-wide association studies (GWAS), and multi-omics with traditional breeding is now increasingly promoting breeding efficiency and accuracy. GS, indeed, has the ability to significantly accelerate genetic gain and shorten breeding cycles, even in low-input schemes, by enabling early and accurate selection of high-quality genotypes (Lubanga et al., 2022). New trends include the application of single-cellomics, pangenomics, and advanced bioinformatics for further optimizing trait selection and accelerating cultivar development (Li et al., 2023c).

7.2 Conservation and innovative utilization of traditional breeding germplasm banks

Germplasm banks remain the foundation of tea breeding and provide the genetic diversity for both classical and molecular breeding. Advances in genomics and pangenome assembly have made characterization and utilization of the resources possible to identify new alleles and functional genes for utilization in targeted breeding (Chen et al., 2023a). Conservation strategies now target both the preservation and innovative use of many landraces and wild relatives toward sustainable breeding in the long term (Chen et al., 2023b; Li et al., 2023a).

7.3 Breeding strategies to address climate change and diversified market demands

New breeding strategies are increasingly geared towards the development of climate-resilient, stress-tolerant cultivars to address the issues caused by climate change. Genomics-enabled breeding, transgenics technologies, and molecular markers are being used for enhancing resistance to biotic and abiotic stresses and for catering to changing market demands for quality, specialty, and health-promoting tea products (Ranatunga, 2019; Li et al., 2023a; Ramakrishnan et al., 2023). Both traditional and molecular methods need to be combined for rapid adaptation to environmental changes as well as to consumer needs (Li et al., 2023b; Ramakrishnan et al., 2023).

7.4 Institutional and policy support for the integrated development of traditional and modern breeding

Institutional collaboration and policy facilitating are key to effective integration of traditional and modern breeding. Interdisciplinary collaboration between breeders, geneticists, and biotechnologists, as well as research infrastructure investment and training, is needed to make technology adoption possible and innovation (Nivetha et al., 2024). Policy contexts need to enhance the preservation of genetic resources, allow for germplasm transfer, and support the use of sophisticated breeding technologies (Ranatunga, 2019).

8 Concluding Remarks

Traditional breeding technology has laid the foundation for tea plant genetic improvement and contributed to the release of high-yielding, high-quality, and stress-resistant cultivars. The selective breeding method, hybridization, and clonal multiplication have been pivotal in the accumulation of elite genetic stock and enhancement of tea cultivars to meet different ecological niches and market requirements.

Given the rapid progress of molecular breeding technologies, an urgent compounding of these technologies with traditional breeding methods is needed. Molecular tools like marker-assisted selection (MAS), genomic selection (GS), and gene editing can enhance the efficiency, accuracy, and scope of traditional breeding by enabling specific trait selection and functional gene discovery. A synergy combining phenotype-based selection and molecular data will overcome the limitations of each method individually.

Future breeding of tea would emphasize developing a modern, scientific breeding platform where traditional breeding is the basic strategy to be supplemented by molecular technology for precision improvement. This supplementary framework will not only preserve the merits of genetic stability and flexibility inherent in traditional breeding but will also address problems of dissecting complex traits, reducing breeding cycles, and climate resilience. Enhancing the synergy between conventional breeding skills and cutting-edge molecular tools is critical to sparking sustainable innovation and competitiveness in global tea industry.

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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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