

Advances and challenges in kiwifruit (*Actinidia* spp.) genetic improvement: A comprehensive review

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Abstract

Actinidia spp. (kiwifruit) has transitioned from a regional Chinese fruit to a crop of global economic and nutritional significance. This spread reflects the genus *Actinidia*'s rich genetic diversity and systematic dissemination efforts. Kiwifruit Commercial production now centers on key regions including China, New Zealand, Italy, and Greece. The fruit's distinctive nutritional chemistry, marked by exceptionally high concentrations of vitamins C, E, and K, underpins its dietary value. We review the utilization of *Actinidia* genetic resources as reservoirs for enhancing yield, quality, and resilience. Conventional techniques (selective breeding, interspecific hybridization) and modern biotechnologies are analyzed comparatively, encompassing marker-assisted selection (MAS), genomic selection, and mutagenesis. Emphasis addresses CRISPR-Cas9 transformative capacity for precise editing of disease resistance loci, nutritional biosynthetic pathways, and abiotic stress tolerance genes. These integrative approaches enable development of improved cultivars with optimized yield, organoleptic profiles, enhanced postharvest stability, and climate resilience. Despite these advances, we identify persistent challenges in trait introgression and manipulation of regulatory pathways, proposing doable strategies toward sustainable global production.

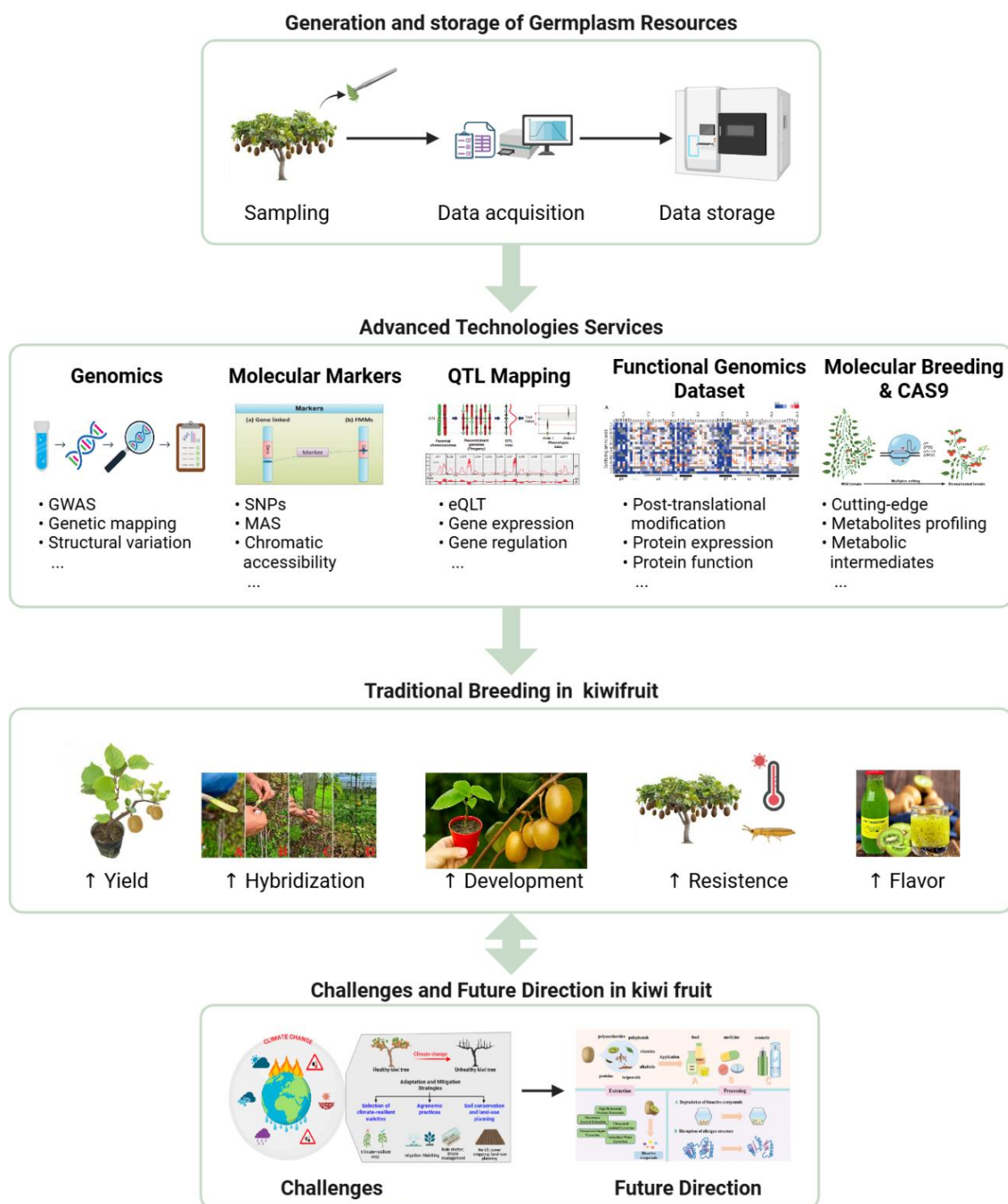
Keywords: Kiwifruit, Breeding, Genetic diversity, CRISPR/Cas9, Fruit quality, Trait improvement, KASP, MAS

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Graphical abstract



Introduction

Kiwifruits (*Actinidia* spp.), tracing their origins to China's Yangtze River valley mountains, belong to the family *Actinidiaceae* (Hazarika et al., 2022). Global commercial production relies mainly on just three species: *A. deliciosa* (green-fleshed) and *A. chinensis* (yellow-fleshed) and kiwiberry, *A. arguta* (Hazarika et al., 2022). A key characteristic of *Actinidia* is its remarkable chromosomal variation, exhibiting a ploidy level from diploid ($2n=2x=58$) to octoploid ($2n=8x=232$) genotypes. These varying ploidy levels reflect its extensive genetic diversity and adaptability (Qi et al., 2023). Given shifting customer preferences and changing environmental conditions, kiwifruit breeding projects are becoming increasingly important. Breeders choose the best offspring from the hybrid population they produce and give them to farmers to satisfy these requirements. To maintain the sustainability and robustness of kiwifruit production in warmer climates, where chilling hours are no longer consistently reached, breeding efforts going forward must give priority to these traits (Asadi et al., 2024). Current breeding initiatives harness this inherent variation using complementary methods. Such as colchicine treatment is used to manipulate ploidy to enhance fruit quality and stress tolerance. Interspecific hybridization crosses species boundaries to improve desirable characteristics. Molecular marker-assisted selection (MAS) has efficiently tapped into the existing genomic resources (Hanley, 2018; De Mori and Cipriani, 2023). Due to the growing need for novel cultivars, breeding efforts have expanded in recent years. However, the rate of breeding success is greatly influenced by the dioecious character of *Actinidia* and the variance in ploidy level. Reducing the amount of time spent breeding is also crucial (Atak et al., 2012). These integrated strategies drive cultivar improvement while preserving the valuable genetic diversity found in wild *Actinidia*, whose wide ploidy range and species diversity remain a vital genetic reservoir for tackling emerging cultivation challenges.

Kiwifruits are dioecious, perennial climbing vines, exhibit distinct sexual dimorphism with separate male and female individuals (Ferguson et al., 2023). Plants can extend up to 10 meters, with ovate leaves characterized by acute apices and cordate bases. They produce small, fragrant flowers in shades from cream to pale yellow. Every species of *Actinidia* is dioecious, meaning that the male and female flowers develop on different kiwifruit trees. Obtaining female females is

often preferred in breeding research. However, pollination also greatly depends on male plants. Examining the floral traits of the genotypes derived from breeding research is therefore essential (Atak et al., 2018). These flowers develop into distinctive berries with several unique attributes: an oval to cylindrical form, thin and pubescent skin, fleshy arils packed with numerous small black seeds, and vibrant flesh coloration-green, yellow, or red-producing a characteristic balance of sweetness and acidity.

In Chinese history, documented kiwifruit cultivation dates back early as the Tang Dynasty (618-907 AD), marking a significant phase in *Actinidia* domestication (Ferguson et al., 2023). The domestication of wild relatives over centuries in Chinese agriculture has greatly shaped the genetic diversity in modern cultivated varieties, with different species selected for their unique fruit qualities and adaptations. The modern kiwifruit global industry started in the century, following the introduction of *A. deliciosa* seeds to New Zealand from China. The disruptive development came with horticulturist Hayward Wright's breeding of the 'Hayward' cultivar, which became the cornerstone of commercial production starting in the 1970s (Ferguson et al., 2023). Cultivation subsequently expanded worldwide during the late 20th century, establishing major production bases in Italy, Greece, Iran and Chile (Testolin and McNeilage, 2023). Current global output exceeds 3 million metric tons annually, harvested from over 90,000 hectares, with China, Italy, New Zealand, and Greece as leading countries in production (Tait et al., 2018a).

China's position as the world's foremost kiwifruit producer is undisputed, supplying over 52% of the global volume. Annual production reaches approximately 2.3 million tons, underpinned by extensive farming operations in key provinces like Shaanxi and Sichuan, coupled with favorable climatic conditions. This dominance results from the strategic expansion of the orchard area and the integration of advanced farming practices. Output exceeding 2 million tons annually not only satisfies substantial domestic demand but also powers a robust export sector, cementing China's central role. Other significant contributors include Italy and New Zealand, yielding roughly 523,120 and 603,523 tons per year, respectively. New Zealand is renowned for premium quality fruit, exemplified by the Zespri brand, while Italy benefits from optimal growing environments in regions such as Lazio and Piedmont. Together with notable production from Greece, Iran,

and other nations, these countries maintain a consistent, year-round supply to international markets (Global Data, 2025; Figure 1).

Nutritionally, kiwifruit is exceptionally dense, offering high concentrations of vitamin C (surpassing citrus fruits), vitamin E, vitamin K, folate, potassium, and dietary fiber, establishing them as a valuable component of health-conscious diets (Vaidya et al., 2022). This study examined key quality factors of red-fleshed kiwifruit that were cultivated in three distinct areas in northern Iran. Greater ascorbic acid content (AAC), total phenolic content, and antioxidant activity were found in fruits grown in the area with cooler summer temperatures and greater elevation than in the other two areas, both during harvest and during storage (Asadi et al., 2024). The global kiwifruit market continues its steady growth trajectory, fueled by rising production and the introduction of novel cultivars. Modern omics technologies have significantly accelerated research, enabling far more precise breeding methodologies (Wang et al., 2023). The availability of high quality reference genomes for major commercial species and cultivars has dramatically enriched genomics resources, offering critical insights into the genetic architecture controlling vital horticultural characteristics (Testolin and McNeilage, 2023). Genomics tools are used for

marker assisted selection and the identification of genes controlling fruit quality, yield potential, stress tolerance and sex determination. Genome editing with CRISPR/Cas is a powerful tool for targeted editing of key fruit attributes such as flavor, shelf life, and nutritional profile. Similarly, progress in cryopreservation and tissue culture techniques is enabling long-term conservation, international exchange, and utilization of precious *Actinidia* genetic resources. Integrative use of these techniques is vital for kiwifruit breeding and genetic improvements.

In this review, genomics technologies for improving kiwifruit genetics and cultivation are discussed. Applications of genomic selection, dissecting complex genotype and phenotype relationships, targeted gene editing, functional molecular markers, and germplasm evaluation have been discussed. Successful applications of these cutting-edge approaches, addressing current challenges in cultivation and quality improvement, are included. In essence, this review discusses the transformative impact of integrated genomics and systems biology. Designing state of the art molecular tools with computational analyses, interdisciplinary frameworks to create new opportunities for targeted germplasm improvement is emphasized.

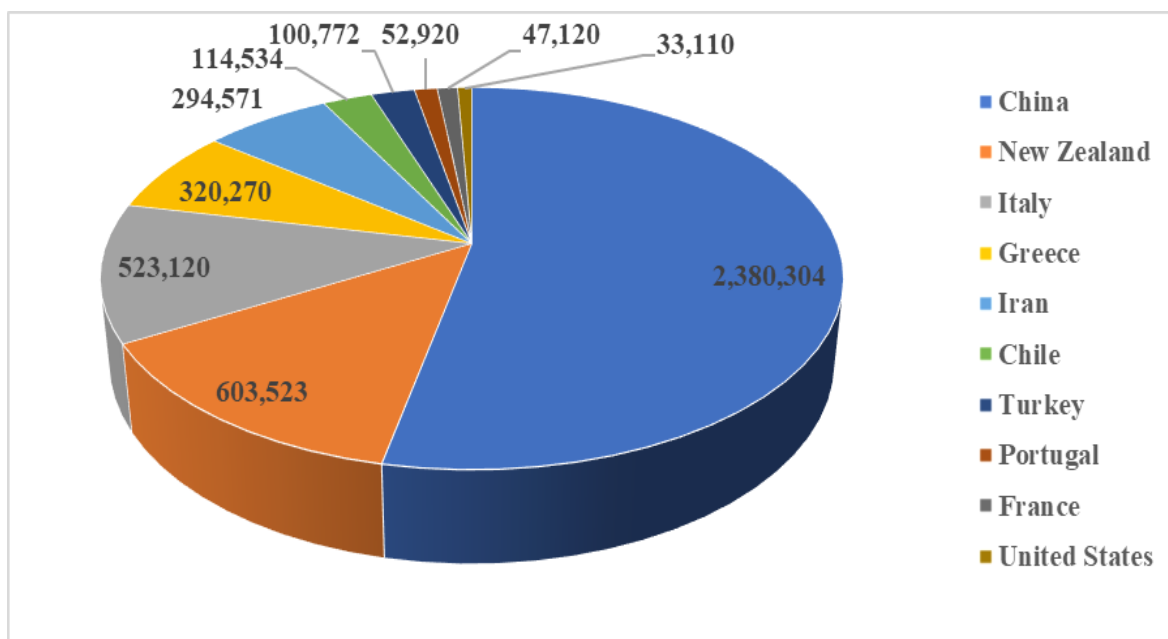


Figure-1. Top kiwifruit-producing (Tons) countries in 2025 (<https://worldstats.com>).

Genetic and genomic resources

China is the centre of origin of the *Actinidia* genus. Taxonomic studies currently identify around 76 distinct species, predominantly in the central, southern, and western regions of the country (Satpal et al., 2021; Table 1). The *Actinidia* spp. They are distributed from China to surrounding regions, namely, Northern Myanmar, Vietnam, and the Eastern Himalayas (Pathak et al., 2023). This wider distribution of *Actinidia* spp. reflects its genetic and phenotypic diversity. Major phenotypic and phenological differences include growth habits, flowering time, fruit shape, size, and peel texture flavour nuances, and resilience to diverse environmental stresses (Xie et al., 2019; Wang et al., 2012).

Several species form the commercial backbone of the industry. *A. chinensis*, also known as Chinese gooseberry, has yellow-coloured cultivars. The fruit size of these cultivars is small, spherical, with smooth skin and intense sweetness (Hazarika et al., 2022). *A. deliciosa* produces green fruits of large size, oval shape with fuzzy skin (Satpal et al., 2021). According to Pinto and Vilela (2018), *A. arguta* can be grown commercially in subtropical climates. The hybrids of *A. kolomikta* exhibit red flesh pigmentation (Hale et al., 2018). Wild relatives of the domesticated kiwifruit species, *A. indochinensis*, *A. polygama*, and *A. eriantha*, can be used to introduce disease resistance and new horticultural traits (Wang et al., 2002; Ferguson and Huang, 2007).

Future sustainable genetic improvements in kiwifruit depend on maintaining genetic diversity. Thus, gene banks for both wild and domesticated kiwifruit germplasms are kept up to date by the major kiwifruit-producing nations. For instance, Wuhan is home to China's primary kiwifruit gene bank. The significant genetic diversity is confirmed by molecular profiling. Molecular profiling is used to validate the substantial genetic diversity in such germplasm collections (Wang et al., 2021; Chłosta et al., 2021). Phenotypic characterization is also performed to assess the breeding and genetic values of these germplasm collections (Cheng et al., 2022; Figiel-Kroczyńska et al., 2021). These genotypic and phenotypic datasets are used as a reference for genetic improvement.

The core collections in these gene banks are utilized for genetic gain in breeding programs. The *ex-situ* and *in-situ* approaches are used synergistically to wild *Actinidia* populations (Debenham and Pathirana, 2021). This integrated approach ensures the continuity of the genus entire genetic repertoire. As an irreplaceable resource for improvement programs, *Actinidia* diversity is systematically catalogued in global germplasm repositories. Current initiatives prioritize large collections, characterization, and evaluation of both wild germplasm and cultivated varieties, establishing a vital genetic baseline for future cultivar innovation. A particularly fruitful strategy involves the strategic introgression of useful traits from wild relatives into elite breeding lines, successfully generating novel kiwifruit cultivars with enhanced agronomic performance and greater market success.

Table-1. Kiwifruit germplasm and its features.

Species (Genotype)	Distribution	Ploidy	Sex	Cultivation Status	Flesh Color	Features
<i>A. callosa</i>	Many provinces in China, as well as Bhutan, India, and Nepal	2n = 58, 116	Dioecious	Cultivated	Grayish green	Forests, thickets, slopes, streambanks; 400–2600 m..
<i>A. deliciosa</i>	Mountainous regions of central and southwestern China, New Zealand, Italy, Chile, France, Greece, and USA	2n=174	Dioecious	Widely cultivated	Green flesh	In its native range, it grows in mountain forests at elevations of 800–1400 m.

<i>A. chinensis</i>	Anhui, Fujian, Guangdong, Guangxi, Henan, Hubei, Hunan, Jiangsu, Jiangxi, S Shaanxi, Yunnan, Zhejiang.	—	Dioecious	Widely cultivated	Various colors	Sparse secondary forests, tall grassy thickets on low mountains; 200–600 m.
<i>A. arguta</i>	Widespread across central, eastern, and northeastern China, Japan, and Korea	2n = 58, 116, 174, 232	Dioecious	Widely cultivated	Greenish yellow or purple-red	Mountain forests, thickets, streamsides; 700–3600 m
<i>A. polygama</i>	Widespread in central, northeastern, and southwestern China, Japan, Korea, and Russia	2n = 58, 116	Dioecious	Widely cultivated	—	Mountain forests; 500–1900 m.
<i>A. macrosperma</i>	China: Anhui, Guangdong, Hubei, Jiangsu, Jiangxi, Zhejiang.	2n = 116	Dioecious	—	Orange	Forest margins on low mountains, thickets, low mountain slopes.
<i>A. latifolia</i>	China: Anhui, Fujian, Guangdong, Guangxi, Guizhou, Hainan, Hunan, Jiangxi, Sichuan, Taiwan, Yunnan, Zhejiang, and Southeast Asia	2n = 58	Dioecious	—	—	Forests, thickets, mountain slopes, valleys; 400–800 m.
<i>A. carnosifolia</i>	China: Guangdong, Guangxi, Guizhou, Hunan, Yunnan.	—	Dioecious	Wild	—	Mountain forests, thickets; 1400–2500 m.
<i>A. hemsleyana</i>	N Fujian, E Jiangxi, S Zhejiang	2n = 58	Dioecious	Wild	—	Low mountain forests; 500–900 m
<i>A. tetramera</i>	China: Chongqing, Gansu, Henan, Hubei, Shaanxi, Sichuan, Yunnan.	2n = 58	Dioecious	Wild	—	Mountain forests, thickets, moist places; 1100–2700 m.

<i>A. eriantha</i>	China: Fujian, Guangdong, Guangxi, Guizhou, Hunan, Jiangxi, Zhejiang.	2n = 58	Dioecious	Cultivated	–	Forests, tall grassy thickets on low mountains; 200–1000 m.
<i>A. valvata</i>	China: Anhui, Fujian, Guangdong, Hubei, Hunan, Jiangsu, Jiangxi, Zhejiang.	2n = 116	Dioecious	Wild	–	Sparse forests, thickets, low mountain valleys; ca. 1000 m.
<i>A. cylindrica</i>	China: Guangxi	2n = 58	Dioecious	–	Yellowish green	Low mountain forests, thickets; 400–800 m
<i>A. polygama</i>	China: Anhui, Chongqing, Gansu, Guizhou, Hebei, Heilongjiang, Henan, Hubei, Hunan, Jilin, Liaoning, Shaanxi, Shandong, Sichuan, Yunnan. Other Countries: Japan, Korea, Russia	2n = 58, 116	Dioecious	Cultivated	Orange	Mountain forests; 500–1900 m.
<i>A. indochinensis</i>	China: Fujian, Guangdong, Guangxi, Yunnan. Other Countries: Northern Vietnam.	2n = 58	Dioecious	Cultivated	–	Dense mountain forests; 600–1300 m.
<i>A. melliana</i>	Guangdong, Guangxi, Hainan, Hunan, Jiangxi	2n = 58	Dioecious	Wild	–	Mountain forests, thickets; 200–1300 m.

Genomics

Documenting genetic diversity across *Actinidia* germplasm mainly relies on microsatellite (SSR) and single-nucleotide polymorphism (SNP) markers (Guido, 2024). These molecular tools have been used for the construction of high-density linkage maps, leading to advanced genetic research. For example, the map developed from crossing *A. chinensis* var. *chinensis* 'Hongyang' with *A. chinensis* var. *deliciosa*

'Qingyuanzhenzhu' it integrates more than 3,000 SNP markers across 29 linkage groups (Popowski et al., 2021).

Such maps prove indispensable for quantitative trait locus (QTL) mapping. Researchers leverage them to pinpoint genomic regions governing commercially vital traits (Table 2). Successes to date include mapping QTLs for fruit morphology, soluble solid content, flesh color development, ripening behavior,

ascorbic acid levels, and resistance to *Fusarium* pathogens (Li et al., 2022). These discoveries illuminate the genetic architecture underlying key characteristics while directly enabling marker-assisted selection in breeding pipelines.

A major leap forward came with the Kiwifruit Genome Database (KGD, <https://ngdc.cncb.ac.cn/databasecommons/>), established by Yue et al. (2024). This open-access hub integrates critical resources: complete genome assemblies, annotated gene sequences, metabolic pathway data, transcriptome datasets, and comparative genomics tools (Wang et al., 2025).

Crucially, Zhang et al. (2018) revolutionized gender identification in breeding. Their work dramatically refined the sex-determination region (SDR), narrowing it to a precise 1 Mb subtelomeric segment on chromosome 25. Through comprehensive whole-genome comparisons Yue et al. (2024) unravelled the Y chromosomes origin and evolutionary trajectory. They pinpointed *SyGl* and *FrBy* as the core sex-determining genes and illustrated their role in shaping the Y chromosome's evolution.

Table-2. Overview of kiwifruit genomics studies.

Authors	Year	Key Findings
Crowhurst et al.	2008	Identified genes associated with flavor and fragrance-related genes, pigmentation, and ripening physiology through a cross-species EST database. This provided insights into the genetic regulation of these traits, enabling targeted breeding approaches.
Huang and Liu	2014	Elucidated the role of natural hybridization and introgression in improving agronomic traits, including pathogen resistance, fruit quality parameters, and yield potential in kiwifruit cultivars.
Zhang et al.	2018	Quercetin's toxic actions against fungal infections and suppression of defensive mechanisms may be linked to its inhibitory effects on <i>P. expansum</i> blue mold.
Wu et al.	2019	Assembled a high-quality reference genome for <i>Actinidia chinensis</i> , significantly improving the resolution of genomic analyses and facilitating precision breeding strategies.
Tahir et al.	2020	Mapped quantitative trait loci (QTLs) associated with resistance to <i>Pseudomonas syringae</i> pv. <i>Actinidiae</i> (Psa), supporting the development of kiwifruit cultivars with enhanced canker resistance.
Popowski et al.	2021	Constructed a high-density genetic map, enabling the identification of QTLs governing fruit morphology and disease resistance, thereby advancing marker-assisted selection.
Lu et al.	2022	The population structure and level of genetic diversity of the <i>A. arguta</i> germplasm were uncovered by this investigation. The trait-marker pairs derived from association mapping may be useful in gene mapping genomics research and molecular marker-assisted breeding.
Yao et al.	2022	Performed whole-genome sequencing and comparative genomic analysis of <i>A. eriantha</i> , expanding the genetic diversity available for breeding programs.

Li et al.	2025	Developed a high-density genetic map and identified QTLs linked to growth-related traits, enabling the selection of kiwifruit genotypes with optimized developmental characteristics.
Wang et al.	2023	Designed a comprehensive SNP genotyping array for high-throughput genetic mapping and QTL analysis of fruit quality and yield-related traits.
Akagi et al.	2023	Uncovered recurrent neo-sex chromosome evolution, providing mechanistic insights into sex chromosome dynamics in <i>Actinidia</i> species.
Xia et al.	2023	Achieved a chromosome-scale genome assembly, offering a high-resolution genomic framework for functional studies and breeding.
Yue et al.	2024	Investigated the evolutionary origin and structural dynamics of the Y chromosome in kiwifruit, advancing understanding of sex determination systems in the genus.
Wu et al.	2025	Identified pronounced SV variability within intronic regions of the <i>MED25</i> and <i>TTG1</i> genes among different accessions. These findings suggest potential functional roles for these genes in regulating trichome development and fruit size determination.
Wang et al.	2025	Identified 26 DEGs associated with sugar metabolism pathways. The genes <i>SUS</i> , <i>INV</i> , <i>SPS</i> , <i>HK</i> , <i>malZ</i> , and <i>GPI</i> were found to have strong functions in sugar metabolism in <i>A. valvata</i> .

Molecular markers and QTL mapping

DNA markers are widely used in plant species for marker assisted selection (MAS) in breeding programs (Rehman et al., 2025). MAS helps breeders to introgress one or few major genes in kiwifruit elite cultivar in shorter period and with high accuracy. MAS is effective in kiwifruit for one or few major genes, however for minor genes this is not effective due to complex *Actinidia* species genome landscapes (Qi et al., 2023). A high-density 135K SNP array developed for *A. arguta* (Wang et al., 2023) can be effectively used to mine new QTNs/genes associated with traits of economic importance through GWAS or linkage analysis. The discovery of novel QTNs/genes and their associated SNPs markers add to MAS tool kit for kiwifruit. The conversion of highly associated SNPs to KASPs markers can make the MAS platform more efficient and higher throughput (Rehman et al., 2021).

The advantage of using MAS is that it can reduce breeding cycle >30% with high selection accuracy (Boopathi and Boopathi, 2020). The precise selection by functionally validated trait-linked markers, substantial gains in breeding efficiency through

reduced breeding cycles. With the advent of high throughput gel free KASP markers the potential for simultaneous improvement across multiple trait is now possible (Kumawat et al., 2020). Microsatellite (SSR) and SNP markers are still used for genetic diversity assessments in *Actinidia* germplasm collections (Guido, 2024), for conservation and active breeding purposes. Collectively, these molecular markers form a useful toolkit for advancing kiwifruit improvement while maintaining the genus's genetic diversity.

A practical application of MAS in kiwifruit breeding is combating *Pseudomonas syringae* pv. *actinidiae* (*Psa*). The *Psa* has inflicted severe economic losses across global kiwifruit industries (Tahir et al., 2020). To deal with this bacterial pathogen, SSR markers for found to be tightly linked with the resistance genes and used for MAS applications in hybrid progenies (Tahir et al., 2020; Konishi-Sugita et al., 2022). These markers have also been used for mapping of genomic regions conferring resistance to the highly virulent *Psa* strains. Early-stage selection of resistant seedlings using the validated MAS kit facilitates the strategic pyramiding of multiple resistance genes into a single elite cultivar. Due to its precision, time, cost and

labour effectiveness, MAS remains an important technology for designing kiwifruit varieties with durable, broad-spectrum resistance against Psa and other pathogens.

A landmark in kiwifruit genomics is the development of a high-density SNP array of 135K genome wide unique markers (Wang et al., 2023). This SNP array scales up genome-wide polymorphism analysis. This SNP array can be used for large scale genetic diversity analysis in large germplasm collections, genome wide analysis to find new genes of economic importance and detect quantitative trait loci (QTL) underpinning major agronomic traits.

The integrated use of MAS with complementary genomic technologies holds great promise for kiwifruit improvement.

Functional genomic databases

Global significance of Kiwifruit (*Actinidia* spp.) is mainly due to its unique nutritional contents. It has high C levels with balanced phytonutrient composition. The first reference genome of the kiwifruit was released in 2013. After the release of reference genome extensive genomic and transcriptomic datasets have emerged for *Actinidia* spp. To centralize, analyze, and share genomics data, Chinese scientists have established the Kiwifruit Genome Database (KGD) at

<http://kiwifruitgenome.org/> (Yue et al., 2020). KGD functions as the primary database for kiwifruit genomics. It integrates all publicly accessible genome assemblies and gene sequences. The platform enriches these resources with gene functional annotations, curated metabolic pathways, and extensive transcriptome profiles generated from diverse RNA-Seq experiments. (Figure 2). Designed to bridge basic discovery and applied science, KGD equips users with intuitive bioinformatics tools and visualization interfaces. Key features include:

- i. The NCBI BLAST sequence search engine for homology searches.
- ii. The JBrowse genome browser for detailed genomic region exploration.
- iii. A dedicated genome synteny viewer for evolutionary comparisons.
- iv. Analytical modules for differential gene expression.
- v. Gene Ontology (GO) term enrichment analysis.
- vi. Integrated pathway mapping tools.

These interconnected resources within KGD streamline genomic investigation and directly enable translational applications, accelerating kiwifruit breeding and genetic enhancement efforts (Yue et al., 2020).

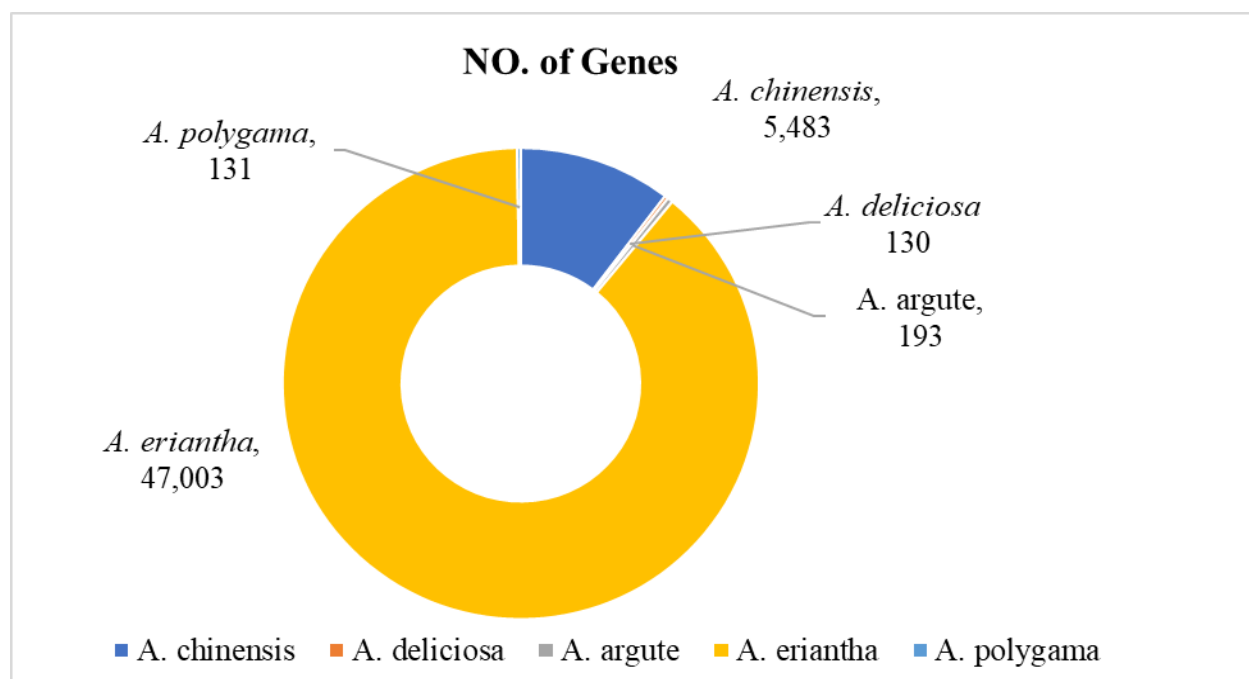


Figure-2. Number of genes annotated in *Actinidia* spp genomes.

Breeding achievements

Conventional breeding

Modern kiwifruit breeding increasingly harnesses integrated multi-omics approaches to decode and engineer complex traits for superior varieties. Combining genomic, transcriptomic, proteomic, and metabolomics data creates a powerful platform for uncovering the genetic and biochemical foundations of key agricultural characteristics, enabling precision breeding strategies. Significant advances in polyploidy genetics and genomic selection have accelerated improvement in *Actinidia arguta* (kiwiberry), with measurable gains in fruit quality, yield potential, and stress tolerance. Complex chromosome inheritance patterns in polyploidy kiwifruit, demand precise breeding models that utilize both probabilistic and empirical relationship matrices

for accurate breeding value estimation (Mertten et al., 2023). The commercial impact of cultivars such as yellow-coloured 'Hort16A' and *Psa*-tolerant 'Zesy002' demonstrates how these techniques have reshaped the kiwifruit industry (Wu et al., 2020). Future breeding efforts must address challenges such as pathogen resistance, climate adaptation, and enhanced fruit quality.

Exploring the underutilized species of kiwifruit such as *A. callosa* and *A. strigosa* can lead to the development of germplasm for cold tolerance. Breeding cold and frost resistance kiwifruit cultivars can extend commercial cultivation to Northern and hilly regions of Pakistan (Khan et al., 2023; Padhan et al., 2024). Based on agroclimatic conditions of kiwifruit growing regions in China, we identified four regions in Pakistan that can be suitable for commercial cultivation of kiwifruit (Table 3).

Table-3. Suitable regions for commercial cultivation of kiwifruit in Pakistan.

Region	Provinces/Areas	Key Advantages	Major Constraints	Suitability Level
Northern Highlands	Gilgit-Baltistan, Chitral, Swat, Abbottabad	High altitude chill, high diurnal temp variation, water from glaciers	Rugged terrain, infrastructure & market access	High
Pothohar Plateau & AJK	Islamabad-Rawalpindi, Mirpur, Pattoki	Existing horticulture sector, market access, cooler climate	Water availability in dry periods, site selection	Medium-High
Balochistan Highlands	Quetta, Ziarat, Kalat	Cold winters, vast land area	Extreme water scarcity, need for tech investment	Medium
Microclimates (Sindh/Punjab)	Northern Sindh, Sulaiman Foothills	Proximity to infrastructure	Extreme heat, requires extensive protective cultivation	Low (Experimental)

The integrated use of omics approaches can accelerate the exploration complex polygenic traits in kiwifruit (Mertten et al., 2023). Transcriptomic analyses uncover gene expression networks underlying stress responses, fruit development, and ripening regulation. Parallel metabolomics and proteomic investigations provide biochemical context by tracing metabolic fluxes and protein interactions that define fruit quality, sensory attributes, and nutritional profiles (Mertten et al., 2023).

This holistic approach revolutionizes kiwifruit improvement by offering precision in genetic

manipulation. Synthesizing multi-omic datasets equip breeders to predict hybrid performance more reliably, refine selection protocols, and significantly reduce variety development timelines (Nazir et al., 2024). The approach creates a toolkit for targeted improvement of fruit quality, nutritional value, and climate resilience. By exploring biological systems at molecular level, data-driven breeding decisions now achieve what was once impossible-marking a paradigm shift from phenotypic selection to predictive, knowledge-driven cultivar design.

Hybridization

Artificial hybridization with wild relatives confers a promising approach to improve cultivated kiwifruit, introducing disease resistance, cold tolerance, novel fruit pigmentation, prolonged postharvest life, and superior flavor and sugar profiles. China explored and utilized wild germplasm resources and innovative breeding techniques and developed 156 new cultivars of kiwifruit in 42 years. Eight cultivars ('Hongyang', 'Xuxiang', 'Cuixiang', 'Donghong', 'Guichang', 'Jinyan', 'Miliang 1' and 'Jintao') covered planting area of more than 6667 ha (Zhong et al., 2021). Such research expands the genetic toolkit for breeders and advances basic knowledge of *Actinidia* reproductive biology.

Despite these achievements, a pressing challenge lies in the introgression of desirable wild traits while avoiding negative linkage drag. To mitigate the effect of negative linkage, drag extensive backcrossing to discard unwanted genetic material and recover optimal phenotypes, is required. Fortunately, marker-assisted selection and genomic technologies are now accelerating this refinement, allowing precise tracking and selection of target genomic regions during backcrossing programs.

Accelerating *Actinidia* breeding

Mutation breeding

Mutation breeding has proven its potential to create novel genetic variation leading to development of new varieties in plants (Arain et al., 2021). Both chemical mutagens and radiation mutagens have been used to artificially induce DNA changes in kiwifruit. Screening for desired novel mutations are traditionally performed by phenotypic evaluation of mutation populations. Nowadays sequencing can be used to identify novel mutations at early generations. In kiwifruit physical irradiation has been used to develop a new cultivar with determinate fruiting and early maturation traits in *A. deliciosa* (Varkonyi-Gasic et al., 2019). Similarly, days to ripening and fruiting have been selected from a mutation population created through chemical (EMS) mutation (De Mori et al., 2020). Mutation breeding is still in use for producing viable commercial phenotypes (Mohamed et al., 2022). Use of colchicine to induce polyploidy is also practiced to create new genetic diversity of

commercial significance. Through chromosome doubling new tetraploid *A. chinensis* varieties have exhibited number of favorable agronomic traits, such as larger size, improved fruit quality, and decreased seediness (Lv et al., 2024).

CRISPR-Cas genome editing

Clustered regularly interspaced short palindromic repeats (CRISPR/Cas9) has revolutionized genome editing of the targeted genomic region and has been widely used in plants to improve traits of economic values (Taj et al., 2022; Mubarik et al., 2021). Like in other plant species CRISPR/Cas9 genome editing is also being applied to edit kiwifruit genes (Table 4). However, CRISPR/Cas edited kiwifruit is not yet available in market for consumers. Herath et al. (2022) edited a growth habit related gene (BFT) and created a perennial phenotype without disturbing flowering cycles. Likewise, De Mori et al. (2020) produced stable hermaphroditism in a male *A. chinensis* var. *chinensis* genotype using CRISPR/Cas9 genome editing. In grapevine MLO gene CRISPR-Cas9 knockout created durable resistance to powdery mildew disease (Wan et al., 2021). Base editing using the CRISPR/Cas system is another advantage that can be used in kiwifruit improvement. For example, in rice *OSALS* gene has been modified using the CRISPR/Cas base editor to confer herbicide resistance (Ma et al., 2023). For metabolic engineering CRISPR sgRNA libraries can be utilized to induce NHEJ-mediated indels in major metabolic genes such as sucrose synthase, modulating sugar metabolism (Li et al., 2020). Unlike other DNA mutation methods, CRISPR/Cas9 edit genome precisely at targeted sites. *Cis*-genesis can be used to incorporate genes from compatible species like conventional breeding at molecular levels. The precision of CRISPR/Cas9 was shown by Salonia et al. (2020), who knocked out a citrus anthocyanin gene to produce non-pigmented fruit. Similarly, CRISPR/Cas9 can be successfully used to produce desired fruit flavours and textures in kiwifruit. However, practical applications of CRISPR/Cas9 edited fruit traits are still facing many hurdles. Regulatory confusions considering CRISPR/Cas9 editing like transgenic crops and the critical need for consumer acceptance should be addressed to ensure market viability.

Table-4. CRISPR/Cas Applications in Kiwifruit (*Actinidia* spp.).

Target Trait Category	Trait	Target Genes	Outcome	Reference
Fruit Quality	Carotenoid Biosynthesis (Albedo Phenotype)	<i>AcPDS</i> (paired-sgRNA/Cas9 system)	Elevated frequency of mutagenesis and production of the albino phenotype in plantlets.	Keul et al., 2022
	Metabolic Regulation (e.g., Red Flesh)	Multi-omics data integration for target ID	To find the important regulatory genes for quality attributes, metabolic maps are constructed.	Shu et al., 2023
Plant Architecture & Phenology	Dormancy Regulation	AcBFT2	Produced a genotype that grew continuously without influencing the time it took to blossom.	Herath et al., 2022
	Juvenile Phase & Flowering Time	CENTRORADIALIS-like genes	Created a compact plant with quick terminal flowering from a climbing perennial with lengthy juvenility.	Varkonyi-Gasic et al., 2019
Disease Resistance	Bacterial Canker Resistance	Base editing in <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> (Pathogen)	The pathogen itself uses the dCas9-BE3 and dCas12a-BE3 systems for base editing.	Liu et al., 2023
	General Disease Resistance	Editing genes associated with plant immunity	Potential to reduce susceptibility to diseases and lower need for chemical inputs.	Wang et al., 2018
Breeding Efficiency	Sex Determination	SyGI gene (in tetraploid kiwifruit)	Manipulated sex determination using targeted mutagenesis in order to breed.	De Mori et al., 2020
	Multiplex Editing	Optimized paired-sgRNA/Cas9 systems	Multiplex genome editing with high efficiency to target many traits at once.	Wang et al., 2018

Agrobacterium-mediated transformation systems

An efficient *Agrobacterium*-mediated transformation system has been established for commercially important *Actinidia* species (*A. arguta*, *A. chinensis*, *A. deliciosa*, and *A. eriantha*) using leaf explants (Yao et al., 2023; Zhang et al., 2024; Quiroz and Stange Klein, 2025). Root tip removing method (Li et al., 2024) and stable plastid transformation is also reported in kiwifruit (Chen et al., 2025). To make transgenic plants with enhanced climate resilience, disease resistance and abiotic stress tolerance, these established protocols and techniques are useful references.

Synthetic directed evolution (SDE) applications

Longer juvenile periods and high heterozygosity are the two inherent challenges for breeding kiwifruit, a dioecious perennial vine (Nazir et al., 2024). Synthetic directed evolution (SDE) is a very useful method to create new genetic diversity to speed up genetic improvement (Yasmeen et al., 2023; Butt et al., 2020). By combining localized sequence diversification (LSD) with cycles of selective pressure, SDE evolves gene functions to develop novel variants with improved traits (Wang et al., 2021). Up till now, various applications of kiwifruit SDE are reported (Rao et al., 2021). Selection pressure of sucrose-rich media on callus during shoot regeneration stage can

lead to the evolution of sucrose synthase enzymes with superior kinetics (Nazir et al., 2024). Elite alleles from SDE are identified by sequencing for their useful integration into elite kiwifruit lines. Repeated SDE cycles increase the number of such variants. The SDE method is more applicable for improving kiwifruit traits such as fruit quality, phytonutrient contents, yield potential, resistance to pathogens, and tolerance to abiotic stresses (Zhu et al., 2020). A key advantage of SDE over other approaches is its ability to improve multiple high-value traits simultaneously while preserving the elite genetic backgrounds of cultivars. The integration of mutagenesis and genomics can begin a new era in kiwifruit breeding, ensuring rapid cultivars development with sustainable production and profitability.

Challenges in kiwifruit improvement

Prioritizing fruit size and external quality traits

The major focus of kiwifruit breeders has been on enlarging fruit size and fruit appearance considering these two traits of better market value. Due to this focus significant progress has been made in improving the fruit's physical characteristics to increase market value (Li et al., 2021). Through traditional selection methods breeders have successfully altered fruit shape, skin fuzz, color intensity, and fruit symmetry to gain better market appeal and economic value (Burdon, 2018). These breeding efforts have resulted in developing a range of kiwifruit skin colours such as shades from greens to red, yellow and orange colour types. This gene pool is a working genetic reservoir for future kiwifruit breeders to design fruit for distinct market preferences (Burdon, 2018). In addition to conventional selection from natural populations, ploidy manipulation like induced polyploidy with colchicine has also been used to enhance fruit size. Moreover, interspecific hybridization coupled with marker assisted selection better utilize genetic diversity for future kiwifruit improvement (Hanley, 2018). Despite the applications of advanced techniques such as CRISPR/Cas9, advances in sterile tissue culture and cryopreservation are boosting the preservation, sharing, and use of valuable kiwifruit genetic resources (Nazir et al., 2024), the irregular fruit shape is still a challenge for Kiwifruit breeders. Irregular shapes and deformities are still posing problems by reducing commercial value of kiwifruit

produce. Although there is no universal standard of an ideal kiwifruit morphology but it keeps varying depending on the target consumer group and the fruit's end use. Thus, breeding programs must continuously adjust their selection criteria to meet these evolving and varied market demands.

Disease and pest resistance in breeding programs

Breeding for diseases and pest resistance is a permanent breeding task to develop new lines with new resistance genes against ever evolving pathogens and pests. Major pathogen threat to kiwifruit production is *Pseudomonas syringae* pv. *actinidiae* (*Psa*) causing devastating bacterial canker and vine die-back (Tahir et al., 2020; Liu et al., 2022). To tackle *Psa* and other such pathogens, breeders must develop marker assisted selection (MAS) platform for robust and high throughput selection for resistance genes (Table 5). Among existing molecular marker competitive allele-specific PCR (KASP) assay are gel free, high-throughput and cost effective (Rehman et al., 2021). Furthermore, the use cisgenics, and genome editing for conferring disease tolerance traits in an elite cultivar are also have great promise. The transfer of vital resistance genes cloned from wild *Actinidia* species and other related species can be achieved efficiently integrating with MAS. Meanwhile, breeding programs target resistance against major pathogen, some secondary diseases and pest are overlooked. For example, in some regions the fungus *Botrytis cinerea* (gray mold) and several damaging viruses cause significant production loss due to the unavailability of resistant cultivars against these pathogens (Li et al., 2023). Each new resistance genes are evaluated for its mode of action and major or minor effect before deploying it into a kiwifruit breeding for disease resistance (Cheng et al., 2022). Among major kiwifruit traits in breeding programs, disease resistance has always been among top objectives (Zhu et al., 2020). These multiple approaches are used to identify, clone, characterize new disease resistance genes from all related genetic resources and incorporate them in different breeding program to combat the existing pathogen threats.

Root autotoxicity

Root autotoxicity is phenomenon wherein root exudates from a given plant have toxic effects on itself. This is common problem faced by Kiwifruit growers.

This occurs when chemicals released by the roots accumulate in the soil, impeding new plant growth and making orchard replanting difficult (Okada and Kato-Noguchi, 2021). Okada and Kato-Noguchi (2021) directly confirmed this effect, showing growth inhibition in experiments using extracts from kiwifruit roots. D'Ippolito et al. (2021) studied kiwifruit vine decline syndrome (KVDS). KVDS is associated with water stagnation and soil anoxic conditions causing root rot disease. Waterlogging and low oxygen in the root zone have a negative, rapid, and significant effect on the growth of kiwifruit. Together, these findings capture the two-pronged thrust of current kiwifruit research: breaking down barriers to successful cultivation while actively improving the fruit's nutritional profile and resilience in adverse environments.

Mitigating abiotic stress for yield and quality

Breeding for abiotic stress tolerance is a continuous breeding objective in kiwifruit. Among abiotic stresses drought stress is a pressing problem. Drought stress was mitigated by exogenous melatonin through the activation of the ascorbic acid–glutathione (AsA–GSH) cycle, carotenoid biosynthesis, and protective enzyme systems (Zhao et al., 2017).

Salinity is a second major abiotic stress in kiwifruit. To tackle these abiotic stresses at genetic level, Yin et al. (2012) mapped parts of this complex response, specifically tracking how *AdERF* gene activity shifts when fruit faces abiotic stress after harvest. Yuan et al. (2018) revealed clear differences in salt tolerance between varieties; 'Watt' seedlings outperformed 'Hayward', largely due to their *WRKY* transcription factors. In recent years, protective cover systems have become increasingly used in kiwifruit orchards against various stress factors that have increased with climate change (Atak and Borracci, 2024).

Optimizing yield through vine architecture and physiology

Kiwifruit harvest is the outcome of complex interplay between vine structure, physiological processes, and environmental responses. A combination of plant architecture attributes such as the number of fruits a vine sets and retains, the uniformity and size distribution of those fruits, the timing and synchronization of bud differentiation and flowering, and the vine's overall capacity for light interception and photosynthetic efficiency throughout the growing

season, determine final kiwifruit production. Optimizing yield is not merely a matter of increasing fruit number but rather balancing sink strength (fruit load) with source capacity (leaf area and carbohydrate production). Studies have shown that overburdening vines with excessive fruit sets can reduce individual fruit size and sugar accumulation due to limitations in source strength. Therefore, canopy management practices that regulate leaf to fruit ratios, light penetration, and shoot vigor are critical for maintaining both yield and fruit quality. To fully exploit genomic selection tools for higher productivity, breeders require detailed insights into how candidate genes regulate architectural traits like shoot elongation, branching patterns, internode length, and bud fertility (Krishnappa et al., 2021). Vine architecture helps vines hold onto high yields consistently, even when facing pests, diseases, or tough environmental stresses. Second, it makes vines compatible with the mechanical harvesters increasingly used in modern orchards. Improper pruning during the spring or summer can trigger excessive vegetative regrowth. This is largely due to competition for carbohydrates between the regrowing shoots and developing fruit, which can significantly hinder the accumulation of high fruit DMC (Minchin et al., 2010). Designing optimal vine architectures suited to specific growing conditions and compatible with mechanical harvesting is essential for ensuring consistent, high yields (Nazir et al., 2024).

Climate adaptation and resilience in kiwifruit breeding

Breeders are trying to develop climate-resilient kiwifruit since weather extremes become more common (Table 5). Utilizing wild *Actinidia* relative and mining their genetic diversity for key survival traits is one of the key strategies for future kiwifruit breeding. For example, delayed bud-break causes vines to remain dormant through dangerous late frosts or controlled growth shutdown, which helps plants to conserve water during droughts. Building resilience against winds, hail, and floods means cracking a complex genetic landscape. To solve this, breeders conduct rigorous field trials across different growing regions, looking for vines that perform reliably regardless of the weather. Only this groundwork can deliver locally adapted varieties capable of keeping yields up the scenario of climate change.

The sustainability of growing *A. chinensis* and *A. deliciosa* cultivars in Te Puke, New Zealand, is

impacted by climate change, namely temperature variations, which could make Te Puke unusable for kiwifruit farming by the end of the century (Tait et al., 2018b). Kiwifruit Early Decline Syndrome (KEDS) has worsened and spread more widely in recent years, affecting kiwifruit orchards worldwide and significantly impacting the viability of rural farmers' economies. This syndrome is thought to be a result of occurrences brought on by climate change and is characterised by the abrupt collapse and death of afflicted plants. In addition to indirectly causing hypoxic soil conditions, high temperatures have a direct impact on the physiology, growth, and photo assimilator allocation of kiwifruit plants (Bardi, 2020; Bardi et al., 2020). Temperatures between 3 and 5 degrees Celsius above room temperature during the critical phases of kiwifruit development direct resources towards vegetative growth, which dramatically lowers the fruit's amounts of vitamin C and carbohydrates. Furthermore, exposure to heat has a detrimental effect on the growth, flowering, and fruit ripening of vines in later seasons (Wang et al., 2024). Degreening can also be a significant problem in some yellow-fleshed varieties. Two aspects of degreening differences exist particularly, the inherent genotype difference in degreening capacity and temperature dependence of degreening process. Due to climate change, kiwifruit productivity is greatly impacted by frost, as seen by earlier last-frost dates and quicker bud burst. As a result, there is a greater chance of spring frost damage. Given these

results, immediate adaptive actions are needed to protect kiwifruit output from the growing risk of climate change-induced frost damage. These tactics could better equip communities to lessen the consequences of climate change and maintain kiwifruit production in the face of changing environmental difficulties by educating stakeholders and policymakers (Jeong et al., 2018). For kiwifruit to flower and fruit, a cooling temperature of less than 7 °C for 700–1000 hours is essential. A study found that high intensity cold has varying effects on kiwifruit plants. Small-sized fruits, late maturity and harvest, and the dropping of old leaves were specifically mentioned. Fruit hardening was also seen. It was suggested that freezing temperatures be avoided and that young kiwifruit plants be shielded from freezing and extremely cold temperatures (Wang et al., 2024). Natural catastrophes have a major effect on different stages of kiwifruit development. Frost damage during tree dormancy and germination, summer dryness during fruit development, high-temperature sunburn during fruit maturity, and continual rain disasters are all significant factors (Qin et al., 2021). Breeders can create kiwifruit cultivars that are more resilient to harsh weather events by emphasizing qualities like heat tolerance, drought resistance, and disease resilience. The overall sustainability and stability of kiwifruit production systems may be enhanced by these climate-resilient kiwifruit cultivars, which may also lessen crops' vulnerability to weather-related harm.

Table-5. Overview of Kiwifruit (*Actinidia* spp.): Pathways, Traits, Genes and Markers.

Key Pathways Identified	Key Traits Under Study	Genes/Markers Identified	Author and Year
L-ascorbic acid metabolism, sugars, starches, and phytohormones	Fruit quality and anthocyanin accumulation	–	Li et al., 2015
Polymorphism of molecules	Diversity analysis and genotype identification	RAPD markers	Kamboj et al., 2020
Ester biosynthesis associated with ripening	Fruit ripening and ester content	AdFAD1, AdALDH2, AdAT17, AdNAC5, AdDof4	Zhang et al., 2020
Pathways of phytohormones	Fruit development	CPPU, IAA	Wu et al., 2020
Pathogen response mechanisms	Plant growth and defense responses	B. cinerea	Zambounis et al., 2020

Pathways for hydrogen sulphide signalling	Ripening delay	PG, EXP	Lin et al., 2020
Phenolic synthesis pathways	Fruit development and ripening	AcLDOX2, Ac5GGT1, and Ac5AT2, TF: bHLH74-2 and AcMYB4-1	Liang et al., 2020
Fruit growth and maturity, ethylene-induced fruit ripening, and floral bud and flower development	Transcriptional control of floral bud, flower, and fruit development, and ethylene response	AP2/ERF, bHLH, MYB	Brian et al., 2021
Nitric oxide regulation during fruit softening	Regulation of the NO softening response.	(CNGC1, CPK1, CIPK2, CML31, CML48, and ZIFL1)	Yang et al., 2021
Cold response, starch breakdown, cellulose degradation, and trehalose synthesis	Involved in the cold response	CBF3, MYC2, and MYB44	Sun et al., 2021
Chlorophyll degradation pathways	Chlorophyll degradation	AcSGR1	Tu et al., 2021
Maturation pathways	Fruit maturation	MYB, MADS-box	Burdon et al., 2021
Transcriptomic pathways	Tissue-specific transcriptomics	AP2/ERF, bHLH	Salazar et al., 2021
Starch degradation and fermentation pathways	Alcoholic off-flavor development	AMY, PDC	Huan et al., 2021
Flavor formation pathways	Flavor formation	AMY/BAM, ADP, AGPase and TFs: ERF, NAC, MYB and bHLH	Wang et al., 2022
Plant growth and development, phytohormone signal transduction, and stress reactions	TIFY gene family functions	TIFY gene family (JAZ, ZML, TIFY, PPD)	Tao et al., 2022
Flavonoid biosynthesis and chalcone synthase gene family	Parthenocarp in seedless kiwifruit	Chalcone synthase (CHS) gene family	Jia et al., 2022
Metabolic regulatory networks in development	Kiwifruit quality improvement	MM vs GM	Shu et al., 2023
Phenolic synthesis and phytohormone pathways	Achieve growth inhibition and enhance stress response	PAL, C4H, 4CL, ABA, CA, and JA	Niu et al., 2023
Comparative gene expression pathways	Gene expression differences	52 TFs (WRKY, NAC)	Guo et al., 2024
Cell wall metabolism pathways	Postharvest softening	PE-related genes.	Wang et al., 2024
Metabolomic and transcriptomic pathways	Determining the rate of ripening and quality	AcBAM3L, AcBAM3.1, Acc31818 (PHS) and 12 TFs	Yang et al., 2024

Future direction

The future of kiwifruit breeding relies on mining the unexplored genes in wild relatives. To understand the adaptability of wild genetic resources, breeders must implement rigorous, multi-environment trials capturing phenotypic plasticity through systematic phenotyping and genotyping approaches. Multi-omics integration is basic to scale up kiwi fruit breeding. By using predictions of genomic estimated breeding values (GEBVs), precise parental selection for complex, polygenic traits can be achieved. Genomics, transcriptomics, metabolomics, proteomics can facilitate improving crossing strategies and fast-track cultivar development. This data-centric approach proves essential for improving key traits such as flavor, phytonutrient levels and shelf-life. In recent years, protective cover systems have become increasingly used in kiwifruit orchards against various stress factors that have increased with climate change (Atak and Borracci, 2024). In certain yellow-fleshed types, degreening can also be a serious issue. There are two main features of degreening differences: the temperature dependence of the degreening process and the intrinsic genotype difference in degreening capacity (Ghasemnezhad et al., 2021). Improving fruit quality remains a principal breeding objective in Kiwi Fruit research. Current breeding efforts focus on improving flavours, textures, visual appeal, enriching health-promoting compounds, and shelf-life after harvest. Breeders are mining novel alleles from wild *Actinidia* relatives to designing future Kiwi fruit cultivars with resistance against major threats like *Psa*, fungal rots and viruses. This comprehensive breeding approach underpins the development of elite cultivars meeting both emerging market and sustainable farming needs. Plant architecture and physiology are also key attributes for increasing productivity. Breeding programs select for ideal growth habits, synchronized flowering, and canopy structures that maximize light capture. These traits directly improve yield stability-ensuring consistent fruit numbers and desirable size distributions. Ideal plant architecture with proper orchard management practices can lead to overall production efficiency.

Conclusion

The integration of traditional breeding approaches with modern biotechnology can scale up global kiwi fruit production. The success of this integrative approach can be measured in term of exceptional fruit

quality, superior and reliable yields, and robust disease resistance. These continuous improvements not only establish kiwifruit's global status as a nutritionally potent and economically vital crop but also equip farmers to address the challenges of sustainable production and emerging market demands. In future, kiwifruit's global significance will expand further through the strategic integration of high-throughput phenotyping, advanced genomic selection, innovative breeding methods, systematic exploration of untapped genetic resources, and sustainable soil management practices. This comprehensive, multi-pronged strategy is key to rapidly developing next-generation cultivars boasting enhanced quality, productivity, and adaptability. Ultimately, it ensures kiwifruit remains a commercially viable and nutritionally relevant fruit in our rapidly evolving agricultural world. Use of KASP based MAS in all kiwifruit breeding are inevitable to improve cultivars with new gene introgression responding to emerging agronomic, quality and market needs.

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Contribution of Authors

Shiming H, Yumei F, Saeed Z, Ahmad T & Jihong D: Conceived idea, designed research methodology collected data and manuscript write up.

Sajjad M: Analyzed and interpreted data and critically revised the draft for intellectual content.

Yuexia W: Reviewed and edited the manuscript and provided resources and funding.

All authors read and approved final draft of the manuscript.

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