


Research Insight

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Harnessing Genetic Diversity for Kiwifruit Breeding: Opportunities and Challenges

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Abstract This study expounds how to utilize genetic diversity in kiwifruit breeding, as well as the opportunities and difficulties encountered in this process. It explains the assistance of new technologies such as genomic selection and CRISPR-Cas9 gene editing in improving breeding efficiency. It also introduces the genetic resources of wild kiwifruit varieties. This study hopes to strengthen the protection of these resources and cultivate new kiwifruit varieties that adapt to climate change and meet market demands in the future, aiming to ensure the long-term and stable development of this industry.

Keywords Genetic diversity; Kiwifruit breeding; Omics technologies; Wild germplasm resources; Genomic selection

1 Introduction

Kiwifruit (belonging to the genus *Actinidia*) is a fruit rich in nutrition and of high economic value. It originated in China and has been widely cultivated in countries such as New Zealand, Italy, and Chile with the breeding of new varieties and the advancement of agricultural technology (Hu et al., 2022; Nazir et al., 2024). Kiwifruit is rich in vitamins C, E and K and is a very valuable fruit in the global fruit market.

However, the characteristics of kiwifruit, such as relatively low genetic diversity, a long juvenile period, dioecious plants and highly heterozygous genes, make breeding slow and complex, and require the use of new genetic techniques to improve efficiency. Genetic diversity is particularly important when dealing with these aspects, as it can provide the basis of variation needed for breeding. Ferguson (2007), Zhang et al. (2015), and Oh et al. (2018) hold that understanding and utilizing the diversity within the *Actinidia* genus is beneficial for cultivating better kiwifruit varieties.

This study analyzed how to better utilize genetic diversity in kiwifruit breeding, summarized the current basic situation of kiwifruit research and proposed several ideas for introducing superior traits into the breeding plan by analyzing the genetic resources of the *Actinidia* genus. This study also explored the application prospects of new technologies such as marker-assisted selection and genomic selection, aiming to accelerate the breeding of new varieties that adapt to climate change and meet market demands.

2 Overview of Kiwifruit Genetic Diversity

2.1 Taxonomy and evolutionary history of kiwifruit

Kiwifruit belongs to the Actinidiaceae family. *Actinidia chinensis* and *Actinidia deliciosa* are the two most common and economically valuable varieties. Kiwifruit originated in China and its cultivation history can be traced back hundreds of years. Hu et al. (2022) and Nazir et al. (2024) demonstrated that it is dioecious, which is both a challenge and an opportunity in breeding. Fraser et al. (2009) found in their early research that how the sex of kiwifruit is determined is still under study. Recent research has identified chromosomes that may be related to sex.

2.2 Global distribution of wild and cultivated kiwifruit germplasm

China, New Zealand, Italy and Chile are several major kiwifruits growing countries. These places have suitable climates and have cultivated many new varieties, becoming important kiwifruit production bases (Zhong et al.,

2021; Nazir et al., 2024). Hu et al. (2022) found that the growth environment of some wild kiwifruit species in China has been damaged and they are facing survival threats. Protecting these wild resources has become very urgent. Oh et al. (2018) indicated that kiwifruit germplasm resources from different countries and regions can provide a lot of useful genetic materials for breeding, which is beneficial for improving existing varieties, enhancing the stress resistance of kiwifruit and ensuring its sustainable development.

2.3 Key traits contributed by genetic diversity

Oh et al. (2016) held that the traits in the genetic diversity of kiwifruit are useful for its resistance to pests and diseases, improvement of fruit quality, and enhancement of its adaptability to the environment. The genetic differences between wild kiwifruit and artificially cultivated kiwifruit can be used to breed new species that are more resistant to diseases. Li et al. (2014) and Nazir et al. (2024) found that breeding efforts pay much attention to these aspects, hoping to make new varieties more popular among consumers and meet market demands. Wang et al. (2022) demonstrated that advanced genetic technologies such as SNP genotyping and marker-assisted selection can identify useful traits more quickly and introduce them into new varieties, making breeding faster and more accurate.

3 Advances in Kiwifruit Breeding Techniques

3.1 Traditional breeding approaches

Traditional breeding methods select well-performing individuals from naturally growing populations or combine ideal traits through hybridization between different species, which play a key role in improving fruit quality and disease resistance (Li et al., 2014; Nazir et al., 2024). The genus *Actinidia* has a rich genetic diversity, providing many options for breeding work. Breeders can select suitable parents based on different traits. Ferguson's (2007) early research found that traditional breeding has a long cycle and high investment, and it takes several generations to see stable improvement effects.

3.2 Modern breeding tools and techniques

The studies of Zhang et al. (2015) and Nazir et al. (2024) demonstrated that MAS can recognize and screen molecular markers related to specific traits, which is beneficial for rapidly identifying individuals with ideal genes in plants and improving breeding efficiency. Pinheiro et al. (2020) also found that it can accurately select gender-related individuals and reduce the uncertainty in the breeding process, solving the problem of dioecious kiwifruit.

Genomic selection (GS) is to use the information of the entire genome to predict the breeding value of plants (Li et al., 2024). It is suitable for selecting relatively complex traits such as fruit quality and yield. The application of GS in kiwifruit has become more feasible because there is now a reference genome of *Actinidia chinensis*. However, kiwifruit breeding materials have the characteristics of polyploidy and high heterozygosity, which bring some technical difficulties to practical operations.

3.3 CRISPR-Cas9 and genome editing applications

The recent study by Nazir et al. (2024) demonstrated that the CRISPR-Cas9 gene editing technology can precisely modify the genome directly, eliminating undesirable traits or enhancing the desired favorable ones. It can assist researchers in cultivating new varieties with stronger disease resistance and better fruit quality more quickly. Li et al. (2022) demonstrated that CRISPR-Cas9 has great potential in kiwifruit breeding and may make up for the deficiencies of traditional breeding and molecular marker-assisted breeding.

4 Utilizing Wild Relatives in Kiwifruit Breeding

4.1 Unique traits from wild kiwifruit species

Wild kiwifruit species such as *Actinidia eriantha* and *Actinidia kolomikta* have abundant genetic resources. Wild species have some characteristics that cultivated varieties do not possess. They have stronger disease resistance or their fruits have a unique flavor. Cheng et al. (2019) found that the flower-shaped kiwifruit can resist the common canker disease in kiwifruit, and its fruit has a special taste, which has received much attention in breeding. Liao et

al. (2019) and Qi et al. (2023) also found that wild species have significant genetic differences in fruit sugar content, carotenoid content, chlorophyll content, etc. These characteristics are of great value for improving fruit quality and stress tolerance.

4.2 Case study: incorporating disease resistance traits from wild relatives

Researchers often choose wild varieties in kiwifruit breeding projects because they value their genes for strong disease resistance. The varietal kiwifruit is regarded as an excellent breeding material due to its particularly strong resistance to canker disease. Its disease resistance comes from some special gene families, which have undergone positive selection to help it better resist diseases (Liu et al., 2017).

The combination of interspecific hybridization and molecular marker selection can introduce useful traits into common commercial varieties. Scaglione et al. (2015) and Oh et al. (2018) demonstrated that techniques such as SNP markers and GBS can quickly identify plants with target traits from hybrid offspring, not only saving time but also enabling more accurate selection of the desired traits. Nazir et al.'s research in 2024 found that some new kiwi varieties with stronger disease resistance and better fruits were developed using this method (Figure 1).

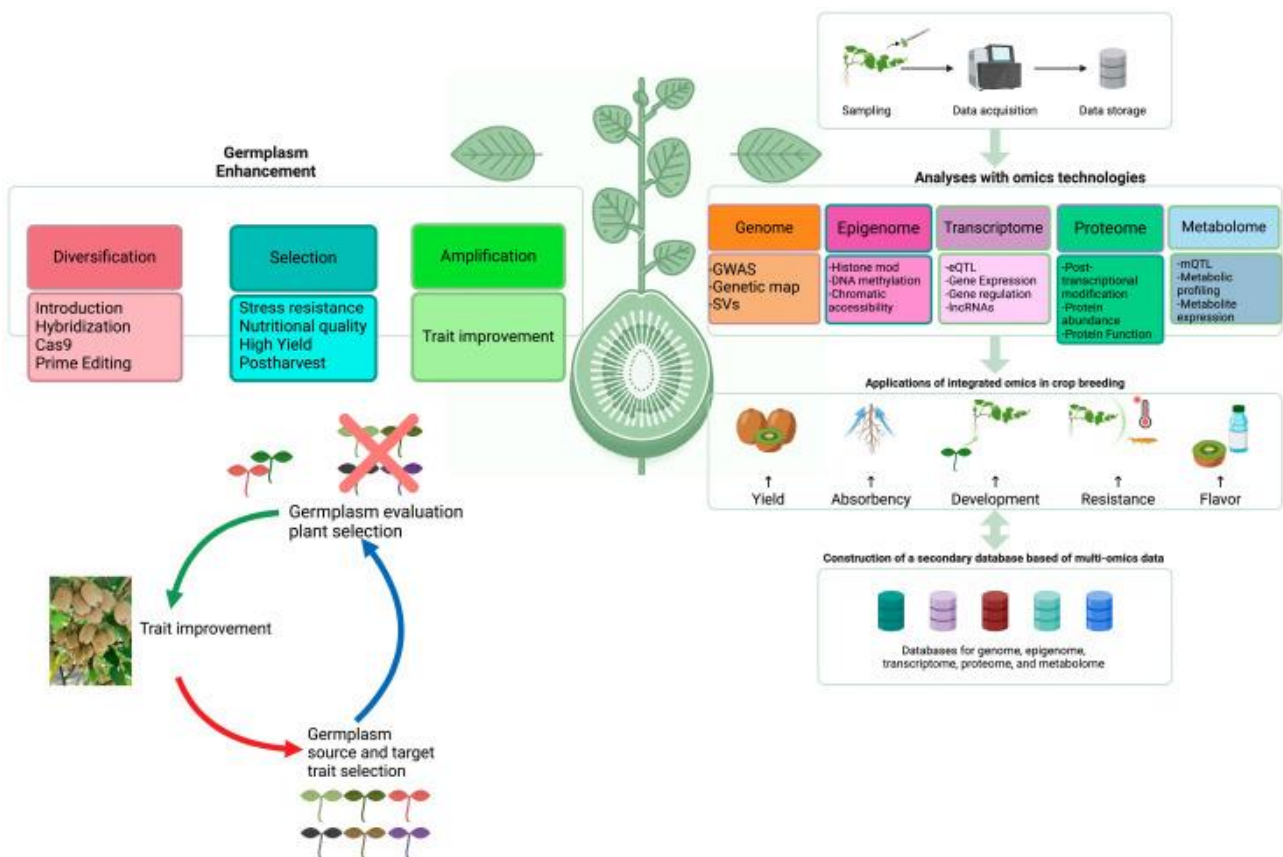


Figure 1 Integrative omics framework in kiwifruit breeding and trait enhancement (Adopted from Nazir et al., 2024)

The research by Liao et al. (2017) and Hu et al. (2022) demonstrated that introducing wild kiwifruit varieties into the breeding system not only cultivated new varieties that are more adaptable to external pressure and have better taste, but also expanded the genetic basis of cultivated varieties, making them more resilient to climate change or new diseases. Shu et al. (2023) hold that this indicates the significance of protecting wild species, as these wild resources are crucial for enhancing the stability and competitiveness of the entire kiwifruit industry.

5 Challenges in Harnessing Genetic Diversity

5.1 Narrow genetic base in cultivated varieties

Kiwifruit began to be commercialized on a global scale relatively late, and the breeding work was not systematic enough. Many varieties originated from very few genetic lineations (Zhang et al., 2015). This makes it difficult for

breeders to introduce more superior traits and limits the ability of kiwifruit to adapt to different environmental changes (Hanley, 2018). Sekhon et al. (2019) indicated that insufficient genetic diversity makes kiwifruit more prone to diseases. Bacterial canker disease caused by *Pseudomonas syringae* pv. *actinidiae* has already had a significant impact on many kiwifruit-growing areas.

5.2 Limitations in germplasm collection and preservation

Ferguson's early research, that is, in 2007, found that institutions such as HortResearch Kiwifruit Germplasm Resource Bank had collected a considerable amount of genetic resources, but it was still quite difficult to actually apply these wild resources to breeding. Hu et al. (2022) hold that environmental changes and the destruction of the growth environment of wild species put many precious genetic resources at risk of loss. The genetic structure of kiwifruit is relatively complex (such as its high heterozygosity and polyploid characteristics), which makes the genetic analysis and breeding process more troublesome and hinders the utilization of diversity (Wang et al., 2022). Sekhon et al.'s research in 2019 demonstrated that the prevalence of Psa, a bacterial disease, has exacerbated this issue, posing a threat to the survival of many important genotypes in the germplasm bank.

5.3 Challenges in integrating diverse traits into elite cultivars

The characteristics of kiwifruit, such as dioecious plants, long juvenile period and climbing growth pattern, all make the breeding process more complicated (Hanley, 2018). Zhang et al. (2015) argued that even with high-density genetic maps and the identification of gender-related genetic markers, it is still very difficult to truly integrate good traits. Li et al. (2014) indicated that the genetic background of kiwifruit is very complex, and many are polyploids, requiring special breeding methods such as hybridization between polyploids. There are many difficulties in the practical operation of technologies such as SNP genotyping chips and genomic selection to stably incorporate complex traits into commercial varieties.

6 Opportunities for Future Kiwifruit Breeding

6.1 Leveraging advanced genomic tools for diversity exploration

Modern omics technologies such as genomics, proteomics and metabolomics have changed the understanding of kiwifruit biology and made breeding more targeted (Zhang et al., 2015; Nazir et al., 2024). Breeders can use these techniques to conduct more in-depth research on the genetic diversity of the *Actinidia* genus and integrate useful traits into new varieties. Methods such as MAS, GS, and CRISPR-Cas9 gene editing are useful for precisely improving traits and are important tools for cultivating excellent kiwifruit varieties. High-density SNP genotyping chips, GBS and other technologies can better locate useful genes, support QTL analysis and promote the rapid breeding of high-quality varieties (Figure 2) (Oh et al., 2018; Shu et al., 2023).

6.2 Building international collaborations for germplasm exchange

Sharing the genetic resources of kiwifruit in various regions is crucial for developing new varieties that adapt to different environments (Ferguson, 2007; Nazir et al., 2024). Cooperation enables researchers to collect, evaluate and utilize germplasm resources more comprehensively and ensure access to genetic materials from more diverse sources. Li et al. (2014) and Hu et al. (2022) also found that international cooperation is beneficial for introducing good traits such as enhanced disease resistance and stress tolerance of wild species into breeding programs and improving the overall performance of new varieties.

6.3 Expanding breeding targets to address climate change and market demands

Future breeding projects must take into account issues such as extreme weather and disease pressure. Bacterial canker disease (Psa) is a very serious threat that requires specialized disease-resistant varieties to deal with (Sekhon et al., 2019). Consumers' demands for taste, nutrition and appearance are also getting higher and higher. New varieties should also improve in these aspects. Early research by Gea (2011) indicates that the combination of traditional breeding methods and modern genomic technology enables breeders to produce kiwifruit varieties that can withstand environmental pressure and meet market preferences more quickly, making the entire industry more sustainable and competitive.

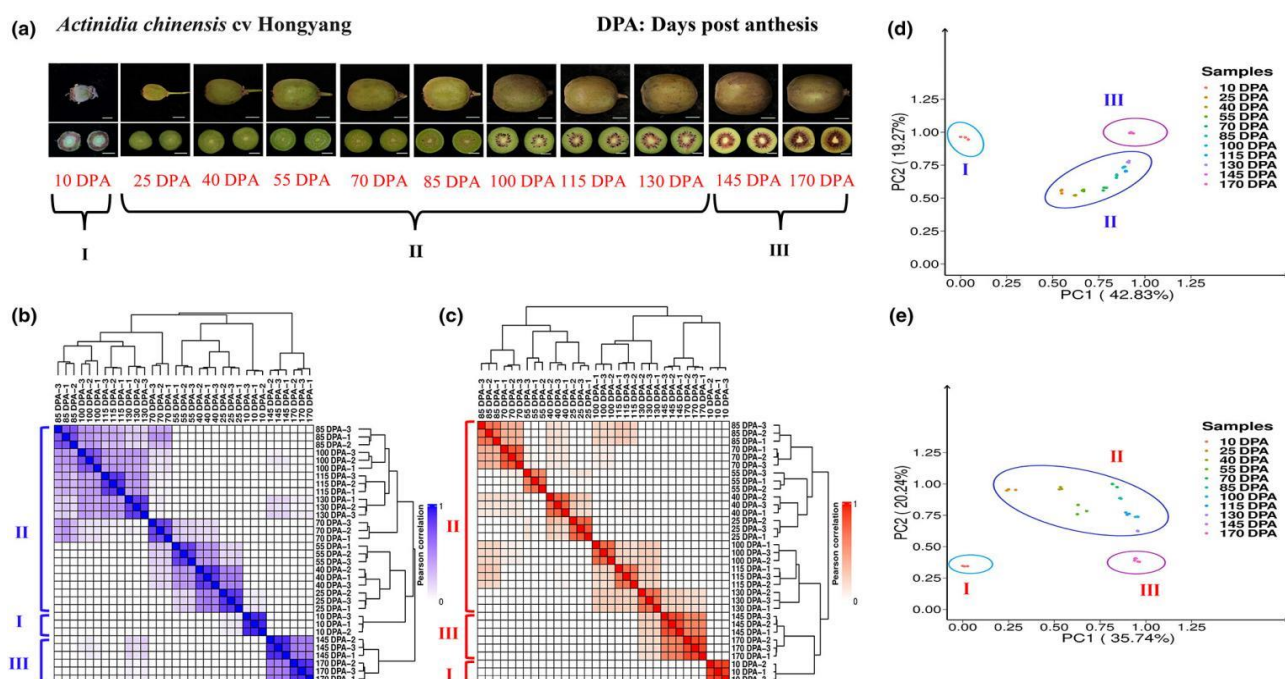


Figure 2 Summary of metabolome and transcriptome data sets (Adopted from Shu et al., 2023)

Image caption: (a) Phenotypic changes in kiwifruits (*Actinidia chinensis* cv Hongyang) at 11 different fruit developmental and ripening stages (FDRs). Intact and sectioned kiwifruits were photographed at 10, 25, 40, 55, 70, 85, 100, 115, 130, 145, and 170 d postanthesis (DPA). Bar, 1 cm. (b, c) Cluster analysis for metabolomes (b) and transcriptomes (c). The color scales 0 – 1 represent Pearson correlation coefficient. (d, e) Principal component analysis for metabolomes (d) and transcriptomes (e). Kiwifruits at the 11 FDRs can be categorized into three major Groups I, II, and III based on purple, green, or yellow phenotypes in pericarps (a), metabolomes (b, d), and transcriptomes (c, e) (Adopted from Shu et al., 2023)

7 Conclusion and Future Directions

The genetic diversity of the genus *Actinidia* is rich, providing a strong foundation for variety improvement. Advanced technologies such as genomics and transcriptomics enable researchers to gain a deeper understanding of the genetic mechanisms of kiwifruit, making breeding more targeted. Methods such as MAS and GS have also achieved remarkable results in improving the target traits. Interspecific hybridization and cis-genetic engineering and other methods have brought new possibilities for the breeding of superior varieties.

Future research should focus on protecting and making good use of the existing genetic resources. Establishing a core germplasm resource bank can better preserve and manage diverse resources. Continuing to promote and optimize technical means such as genomic selection is helpful for making breeding work more efficient. In the face of climate change and the constantly changing demands of the market, breeding goals should give priority to new varieties with strong disease resistance and high environmental adaptability.

The combination of traditional breeding methods and modern genomic tools has led kiwifruit production onto a sustainable development path. Only by breeding more new varieties with good taste, attractive color, rich nutrition and strong stress resistance in the future can the kiwifruit industry continue to grow and develop, and maintain its competitiveness and influence in the global market.

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Conflict of Interest Disclosure

The author affirms that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

References

- Cheng C., Datson P., Hilario E., Deng C., Manako K., McNeillage M., Bomert M., and Hoeata K., 2019, Genomic predictions in diploid *Actinidia chinensis* (kiwifruit), *European Journal of Horticultural Science*, 84(4): 213-217.
<https://doi.org/10.17660/ejhs.2019/84.4.3>
- Ferguson A., 2007, The need for characterisation and evaluation of germplasm: kiwifruit as an example, *Euphytica*, 154: 371-382.
<https://doi.org/10.1007/s10681-006-9188-2>
- Fraser L., Tsang G., Datson P., De Silva N., Harvey C., Gill G., Crowhurst R., McNeillage M., 2009, A gene-rich linkage map in the dioecious species *Actinidia chinensis* (kiwifruit) reveals putative X/Y sex-determining chromosomes, *BMC Genomics*, 10: 102.
<https://doi.org/10.1186/1471-2164-10-102>
- Hanley Z., 2018, Kiwifruit (*Actinidia* spp.) breeding, In: Al-Khayri J., Jain S., and Johnson D. (eds.), *Advances in plant breeding strategies: fruits*, Springer, Cham, Switzerland, pp.377-401.
https://doi.org/10.1007/978-3-319-91944-7_10
- Hu G., Jiang Q., Wang Z., Li Z., Liao W., Shen D., and Zhong C., 2022, Genetic diversity analysis and core collection construction of the *Actinidia chinensis* complex (kiwifruit) based on SSR markers, *Agronomy*, 12(12): 3078.
<https://doi.org/10.3390/agronomy12123078>
- Li D., Liu Y., Li X., Rao J., Yao X., and Zhong C., 2014, Genetic diversity in kiwifruit polyploid complexes: insights into cultivar evaluation, conservation, and utilization, *Tree Genetics and Genomes*, 10: 1451-1463.
<https://doi.org/10.1007/s11295-014-0773-6>
- Li D.W., Zhong C.H., and Bulley S.M., 2022, Kiwifruit MYBS1-like and GBF3 transcription factors influence l-ascorbic acid biosynthesis by activating transcription of *GDP-L-galactose phosphorylase 3*, *New Phytologist*, 235(6): 2497.
<https://doi.org/10.1111/nph.18097>
- Li Y.W., Zhang J., Liang L.Y., Chen B.L., Huang Y.W., Jiang X., Liu Y., Huang J.K., and Wang X., 2024, Rhizosphere microbial interactions and their impact on kiwifruit health, *Molecular Microbiology Research*, 14(5): 248-258.
<https://doi.org/10.5376/mmr.2024.14.0027>
- Liao G., Li Z., Huang C., Zhong M., Tao J., Qu X., Chen L., and Xu X., 2019, Genetic diversity of inner quality and SSR association analysis of wild kiwifruit (*Actinidia eriantha*), *Scientia Horticulturae*, 248: 241-247.
<https://doi.org/10.1016/j.scienta.2019.01.021>
- Liu C., Li D., Zhou J., Zhang Q., Tian H., and Yao X., 2017, Construction of a SNP-based genetic linkage map for kiwifruit using next-generation restriction-site-associated DNA sequencing (RADseq), *Molecular Breeding*, 37: 139.
<https://doi.org/10.1007/s11032-017-0729-2>
- Nazir M., Lou J., Wang Y., Zou S., and Huang H., 2024, Kiwifruit in the omics age: advances in genomics, breeding, and beyond, *Plants*, 13(15): 2156.
<https://doi.org/10.3390/plants13152156>
- Oh S., Lee M., Kim K., Han H., Won K., Kwack Y., Shin H., and Kim D., 2018, Genetic diversity of kiwifruit (*Actinidia* spp.), including Korean native *A. arguta*, using single nucleotide polymorphisms derived from genotyping-by-sequencing, *Horticulture, Environment, and Biotechnology*, 60: 105-114.
<https://doi.org/10.1007/s13580-018-0106-z>
- Pinheiro L.A.M., Pereira C., Barreal M.E., Gallego P.P., Balcão V.M., and Almeida A., 2020, Use of phage $\phi 6$ to inactivate *Pseudomonas syringae* pv. *actinidiae* in kiwifruit plants: in vitro and ex vivo experiments, *Applied Microbiology and Biotechnology*, 104: 1319-1330.
<https://doi.org/10.1007/s00253-019-10301-7>
- Qi B., Wang F., Ye K., Mo Q., Gong H., Liu P., Jiang Q., and Li J., 2023, Genetic diversity of 52 species of kiwifruit (*Actinidia chinensis* Planch.), *Horticulturae*, 9(7): 753.
<https://doi.org/10.3390/horticulturae9070753>
- Scaglione D., Fornasiero A., Pinto C., Cattonaro F., Spadotto A., Infante R., Meneses C., Messina R., Lain O., Cipriani G., and Testolin R., 2015, A RAD-based linkage map of kiwifruit (*Actinidia chinensis* Pl.) as a tool to improve the genome assembly and to scan the genomic region of the gender determinant for the marker-assisted breeding, *Tree Genetics and Genomes*, 11: 115.
<https://doi.org/10.1007/s11295-015-0941-3>
- Sekhon J., Hoeata K., Borgers V., Paterson T., Taufan N., Herrick J., Kaji R., McNeillage M., Cheng C., and Datson P., 2019, Conservation of *Actinidia chinensis* alleles in a Psa environment, *Acta Horticulturae*, 1243: 109-114.
- Shu P., Zhang Z., Wu Y., Chen Y., Li K., Deng H., Zhang J., Zhang X., Wang J., Liu Z., Xie Y., Du K., Li M., Bouzayen M., Hong Y., Zhang Y., and Liu M., 2023, A comprehensive metabolic map reveals major quality regulations in red-flesh kiwifruit (*Actinidia chinensis*), *New Phytologist*, 238(5): 2064-2079.
<https://doi.org/10.1111/nph.18840>
- Wang R., Xing S., Bourke P., Qi X., Lin M., Esselink D., Arens P., Voorrips R., Visser R., Sun L., Zhong Y., Gu H., Li Y., Li S., Maliepaard C., and Fang J., 2022, Development of a 135K SNP genotyping array for *Actinidia arguta* and its applications for genetic mapping and QTL analysis in kiwifruit, *Plant Biotechnology Journal*, 21: 369-380.
<https://doi.org/10.1111/pbi.13958>
- Wu J., 2018, Establishment of in vitro culture systems for breeding new types of kiwifruit and for *Actinidia* genomics studies, *Acta Horticulturae*, 1224: 195-201.

- Zhang Q., Liu C., Liu Y., VanBuren R., Yao X., Zhong C., and Huang H., 2015, High-density interspecific genetic maps of kiwifruit and the identification of sex-specific markers, DNA Research, 22: 367-375.
<https://doi.org/10.1093/dnares/dsv019>
- Zhong C.H., Huang W.J., Li D.W., Zhang Q., and Li L., 2021, Dynamic analysis of global kiwifruit and industry development and fresh fruit trade, China Fruits, 7(7): 101-108.



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