Advances in Kiwifruit Canker Disease Resistance Breeding: Postprint

Authors: Wang Faming, Mo Quanhui, Ye Kaiyu, Gong Hongjuan, Jiang Qiaosheng, Liu Pingping, Li Jiewei

Date: 2018-12-19T00:00:00+00:00

Abstract

Kiwifruit bacterial canker disease is a devastating disease that threatens global kiwifruit production. Currently, there are no effective control methods, and breeding resistant varieties represents one of the important approaches to ensure the healthy development of the kiwifruit industry. Consequently, resistance breeding against kiwifruit canker disease has become a research hotspot in recent years. However, the resistance of most kiwifruit germplasm resources to canker disease remains unknown, which limits the exploration and utilization of superior resistant germplasm resources. Although several identification and evaluation methods for kiwifruit canker disease resistance have been developed, their effectiveness is not ideal, with significant limitations, and the accuracy and stability of identification need improvement. This paper reviews several aspects of kiwifruit canker disease resistance breeding, such as the selection of resistant materials (resistance of existing varieties, research on resistant rootstocks, and wild resistant resources, etc.), resistance identification and evaluation techniques (field identification, in vivo or in vitro identification, etc.), and resistance mechanism research, and proposes constructive recommendations for existing problems. It is argued that the most critical aspect in the process of kiwifruit canker disease resistance breeding is to establish a scientific and systematic evaluation system for canker disease resistance to conduct large-scale resistance surveys and assessments of kiwifruit germplasm resources. On this basis, interspecific hybridization and genetic engineering breeding techniques should be fully utilized to accelerate the resistance breeding process, thereby driving in-depth research on the resistance mechanisms of kiwifruit canker disease and the mining and utilization of disease resistance genes. The ultimate aim is to fundamentally solve the key problem of canker disease plaguing kiwifruit production and promote the green, healthy, and sustainable development of the kiwifruit industry.

Full Text

Research Progress on Kiwifruit Resistance Breeding to Pseudomonas syringae pv. actinidiae

WANG Faming, MO Quanhui, YE Kaiyu, GONG Hongjuan, JIANG Qiaosheng, LIU Pingping, LI Jiewei*

(Guangxi Key Laboratory of Plant Conservation and Restoration Ecology in Karst Terrain, Guangxi Institute of Botany, Guangxi Zhuang Autonomous Region and Chinese Academy of Sciences, Guilin 541006, Guangxi, China)

Abstract

Kiwifruit bacterial canker is one of the most destructive diseases threatening global kiwifruit production, and currently no effective cure exists. Developing resistant cultivars represents one of the most important approaches to ensure the healthy development of the kiwifruit industry, making resistance breeding a hot topic in recent kiwifruit research. However, the resistance levels of most kiwifruit germplasm resources remain unknown, limiting the discovery and utilization of elite resistant materials. Although several methods for identifying and evaluating kiwifruit resistance to bacterial canker have been developed, their effectiveness has been suboptimal with significant limitations, and the accuracy and stability of these assessments require improvement. This review addresses several aspects of kiwifruit bacterial canker resistance breeding, including the selection of resistant materials (resistance of existing cultivars, resistant rootstock research, and wild resistant resources), resistance identification and evaluation techniques (field evaluation, in vivo and in vitro assays), and resistance mechanism studies. Constructive suggestions are proposed to address existing problems. The establishment of a scientific and systematic evaluation system for bacterial canker resistance is considered the most critical step, enabling large-scale resistance screening and assessment of kiwifruit germplasm resources. Based on this foundation, interspecific hybridization and genetic engineering technologies should be fully utilized to accelerate resistance breeding progress, which will in turn drive in-depth research on resistance mechanisms and facilitate the mining and utilization of resistance genes. The ultimate goal is to fundamentally solve the key problem of bacterial canker 困扰 in kiwifruit production and promote green, healthy, and sustainable development of the kiwifruit industry.

Keywords: kiwifruit, bacterial canker, resistance breeding, identification and evaluation, resistance mechanism

---

Kiwifruit bacterial canker is a devastating disease threatening global kiwifruit production (Chapman et al, 2012). First discovered in Japan in 1984 (Takikawa et al, 1989), the disease erupted on a large scale in Italy in 2008 and rapidly spread to other countries worldwide (Balestra et al, 2009; Balestra et al, 2010;

Mazzaglia et al, 2011). Within just a few years, it became an international epidemic endangering nearly all kiwifruit production regions. Characterized by sudden outbreaks, recurrence, rapid transmission, devastating impact, and difficulty in eradication, the disease has caused severe economic losses and become the most challenging problem in kiwifruit production globally, seriously affecting the healthy and sustainable development of the industry (Khandan et al, 2013).

The disease is caused by *Pseudomonas syringae* pv. *actinidiae* (Psa) (Takikawa et al, 1989), which infects trunks, branches, shoots, leaves, and flowers, causing leaf spots, shoot dieback, and various canker symptoms (Ferrante & Scortichini, 2010; Bull et al, 2011). Psa exhibits strong ecological adaptability, acquiring resistance to local environments and hosts through mobile genetic elements and gain or loss of virulence factors, or by modifying effector gene types and levels. For instance, one globally pandemic Psa variant has developed Cu and antibiotic resistance (Scortichini et al, 2012), greatly increasing control difficulty.

Numerous studies have reported on kiwifruit bacterial canker control (李淼等, 2009; 易盼盼, 2014; 张慧琴等, 2013; 李聪, 2016). However, once the disease occurs, no cure currently exists. While rain shelters and biochemical agents such as copper compounds, antibiotics, and activators can provide some protection, these measures are primarily preventive. Moreover, they increase production costs, and some countries have banned certain chemical agents due to potential health and ecological concerns.

Based on years of production experience, breeding resistant cultivars has proven to be an effective approach for controlling kiwifruit bacterial canker. Currently, there are hundreds of kiwifruit cultivars or lines and dozens of wild species worldwide, some of which show strong resistance to bacterial canker, but the resistance levels of most cultivars remain unknown. This paper provides a comprehensive review of recent progress in kiwifruit bacterial canker resistance breeding, including resistant cultivar selection, resistance identification and evaluation techniques, and resistance mechanism studies, and offers suggestions to address existing problems, aiming to provide references for future breeding efforts.

1.1 Resistance of Existing Cultivars

According to the latest classification standards, the genus *Actinidia* comprises 55 species and 76 taxa (Li, 2009), with the vast majority native to China. Except for some recently developed "soft jujube" type kiwifruit cultivars, most current cultivars are derived from *Actinidia chinensis* (including the "delicious" variety), primarily due to its superior horticultural traits. However, most "Chinese" type kiwifruit have proven susceptible or moderately resistant to bacterial canker. For example, major domestic cultivars such as Hongyang, Donghong, Wanhong, Qihong, Jinyan, Hort16A, Jinyang, Jintao, Jinxia, Chuhong, and Lushanxiang have been confirmed as susceptible or highly susceptible (Beatson R, 2014; 刘娟, 2015; 石志军等, 2014; 易盼盼, 2014; 张慧琴等, 2013). Cultivars includ-

ing Hayward, Huayou, Zaoxian, Kuimi, Qinmei, Chenguang, Bruno, Miliang No. 1, Jinshi, Cuiyu, Cuixiang, and Qinmei are considered moderately resistant or moderately susceptible (李淼等, 2009; 石志军等, 2014; 易盼盼, 2014; Beatson R, 2014; 刘娟, 2015). Only a few cultivars such as Huate (hairy flower type), Xuxiang, and Jinkui are considered resistant or highly resistant (李淼等, 2009; 石志军等, 2014; 易盼盼, 2014). However, even for these resistant or moderately resistant cultivars, inconsistent evaluation results exist. For instance, studies by 李聪 (2016) and 易盼盼等 (2014) considered "Xuxiang" as moderately resistant, while 李淼等 (2009) classified "Qinmei" as susceptible, contrary to other studies (石志军等, 2014; 易盼盼, 2014; 刘娟, 2015). Although Jinkui is widely recognized as highly resistant, our investigations found approximately 20% disease incidence in some high-altitude, high-humidity areas of Jiangshan City, Zhejiang Province. These inconsistent conclusions may result from different regional climate and environmental conditions, evaluation methods, artificial inoculation techniques, or disease index assessment methods.

New Zealand has long been committed to kiwifruit bacterial canker resistance breeding. Through extensive intraspecific and interspecific hybridization and seedling selection, they have screened excellent resistant cultivar materials such as G3 and G14 from large progeny populations to replace or supplement susceptible mainstream cultivars like Hort16A. They have also identified strongly resistant male pollinator cultivars through field and artificial inoculation screening, including M33, M56, Chieftain, King, Matua, and M.series (http://www.kvh.org.nz/vdb/document/91188). Except for M33 being tetraploid, all others are hexaploid.

1.2 Resistant Rootstock Research

Rootstock usage significantly influences early fruiting, high yield, fruit quality, and disease resistance improvement in scion cultivars, playing a positive role in fruit production. Studies have shown that appropriate kiwifruit rootstocks can promote flower bud differentiation (Cruz-Castillo et al, 1991; Wang et al, 1994), increase yield (Cruz-Castillo et al, 1991), improve soluble solids content (Cruz-Castillo et al, 1991; 李洁维等, 2004), enhance growth vigor (Cruz-Castillo et al, 1991; 蒋桂华等, 1998; 李洁维等, 2004; 王莉等, 2001; Clearwater et al, 2006), and improve stress and pest/disease resistance (Stewart et al, 1991; 王莉等, 2001; Erper et al, 2013). However, research specifically targeting bacterial canker resistance remains relatively limited. 邵卫平和刘永立等 (2015) screened resistant plants "Xuxiang" Seedling No. 2 and "Bruno" Seedling No. 3 from 13 seedling lines of Xuxiang and Bruno for use as bacterial canker-resistant rootstocks, verifying their resistance through CAT and POD enzyme activities. Lei et al (2015) obtained an excellent resistant rootstock YZ310 through hybridization between QM91136 and SX45872, validating its resistance through in vitro branch and leaf inoculation methods. New Zealand and other countries initiated kiwifruit resistant rootstock research earlier (Beatson, 2014). In recent years, a rootstock cultivar "Bounty" has been verified to possess strong bacterial canker

resistance. Compared with the commonly used rootstock "Bruno," Bounty not only significantly enhances scion tolerance to bacterial canker but also exhibits good drought and waterlogging tolerance, and can induce flowering about one week earlier than Bruno-grafted plants. However, due to its lower yield potential, dense planting is required in cultivation (New Zealand Kiwifruit Book, 2016). Appropriate rootstock selection and utilization significantly impact kiwifruit production, but current research on bacterial canker-resistant rootstocks remains insufficient. One major reason is that breeders generally lack resistant rootstock resources. Existing rootstock selection primarily derives from hybrid progeny or seedlings of current cultivars, most of which have proven non-resistant to bacterial canker, making selection difficult. However, other wild *Actinidia* species contain strongly resistant individuals. Targeted research on these resources would undoubtedly accelerate the breeding process for excellent bacterial canker-resistant kiwifruit rootstocks.

1.3 Wild Actinidia Resources for Resistance Breeding

China possesses extremely rich wild kiwifruit germplasm resources. Through long-term natural selection, wild kiwifruit have developed strong adaptability and stress-resistance genes with abundant genetic variation, serving as important foundational resources for cultivar improvement. Selecting elite germplasm from wild resources, particularly those with excellent fruit quality and stress/disease resistance, has become an important approach for cultivar breeding. Current domestic research has demonstrated that certain wild species show significant resistance to kiwifruit bacterial canker, such as *A. eriantha* (易盼盼, 2014), *A. arguta* (易盼盼, 2014), *A. tetramera* (刘娟, 2015), and *A. callosa* (刘娟, 2015). Taking advantage of the large-scale bacterial canker outbreak, New Zealand conducted resistance screening on extensive *Actinidia* germplasm collections at the PFR (Plant & Food Research Limited) Te Puke germplasm repository. From 3,500 accessions representing 24 different species, they identified a series of strongly resistant wild species belonging to the *Leiocarpae* section, including *A. arguta*, *A. macrosperma*, *A. valvata*, *A. polygama*, *A. melanandra*, and *A. purpurea* (Datson et al, 2015). Our institution, Guangxi Institute of Botany, has conducted taxonomic research and wild germplasm investigation, collection, and preservation since 1976. We have established the largest kiwifruit germplasm repository in South China, collecting core germplasm of over 40 species, more than 10 of which are native to Guangxi, representing rich genetic diversity. In addition to previously reported resistant resources (Li et al, 2013), we have continued to screen individual plants with resistant or highly resistant responses to bacterial canker from species including *A. eriantha*, *A. valvata*, *A. tetramera*, *A. macrosperma*, *A. latifolia*, *A. guilinensis*, *A. arguta*, and *A. callosa* through field observation combined with in vitro identification (to be published separately). Therefore, if we can fully utilize our domestic resource advantages and conduct comprehensive, systematic studies on bacterial canker resistance in wild germplasm, we can discover more elite resistant resources, reduce the blindness of disease resistance

breeding, and conduct targeted cultivar improvement.

2.1 Field Evaluation

Currently, kiwifruit bacterial canker resistance evaluation primarily relies on field surveys, which provide the most direct method for cultivar resistance assessment. 王振荣等 (1998) and 李瑶等 (2001) established grading standards based on the number of diseased branches and the proportion of trunk canker circumference, typically dividing resistance into five categories: highly resistant, moderately resistant, moderately susceptible, highly susceptible, and whole-plant death. This system has been gradually adopted by others (申哲等, 2009; 易盼盼, 2014; 刘娟, 2015). Additionally, some researchers have calculated disease incidence and index based on leaf lesion number and area. 李聪等 (2016) used this method and found that *A. eriantha* was highly resistant; Xuxiang, Jinkui, Jinnong No. 2, and Hayward were moderately resistant; Qinmei and Jinxiang were moderately susceptible; and Chuhong and Golden Fruit were highly susceptible. However, these results differ from other studies, indicating that domestic field evaluation methods for bacterial canker resistance have not yet reached consensus. Even in New Zealand and other countries, systematic methods for field resistance evaluation are lacking, with assessments primarily based on plant mortality rates, shoot infection rates, and branch infection rates (http://www.kvh.org.nz/vdb/document/91188).

2.2 In Vivo or In Vitro Evaluation

Although field evaluation provides the most intuitive method for kiwifruit bacterial canker resistance assessment, results are often inconsistent due to various factors including pathogen transmission, annual climate, geography, and management practices, requiring lengthy observation periods. In vivo inoculation evaluation during the seedling stage has become another relatively intuitive identification method. In vivo evaluation typically employs stem or leaf inoculation. For stem inoculation, methods include drilling (石志军等, 2014; 易盼盼, 2014; Lei et al, 2015) or needle puncture (石志军等, 2014; 邵卫平和刘永立, 2015; Datson et al, 2015). After inoculation, plants are cultured under controlled temperature and humidity for a period, and resistance is evaluated based on disease symptoms (易盼盼, 2014; 邵卫平和刘永立, 2015) and lesion size (Lei et al, 2015), length (Datson et al, 2015), or bacterial ooze near the wound (石志军等, 2014). Leaf inoculation also typically uses wounding (Lei et al, 2015) or subcutaneous injection (张慧琴等, 2014), with resistance evaluated based on lesion size (Lei et al, 2015) or disease incidence (张慧琴等, 2014) after inoculation. Compared with natural field evaluation, in vivo inoculation can better control disease conditions and more closely reflects the plant' s natural resistance response. However, in vivo inoculation requires strict laboratory environments and complex procedures, making large-scale, batch processing difficult. It also risks pathogen spread, and seedling resistance may differ from adult plant resistance, resulting in discrepancies with field evaluation results.

In addition, in vitro branch and leaf inoculation techniques have been widely applied in disease resistance evaluation of other fruit trees (Tynan et al, 1998; Cao et al, 1999; Abe et al, 2007; Wan et al, 2015; Gonçalves-Zuliani et al, 2016) and have been adapted for kiwifruit. In vitro branch inoculation primarily uses drilling or needle puncture methods, followed by in vitro culture under controlled temperature and humidity, with resistance evaluated based on lesion length, radius, or bacterial ooze status at the inoculation site (张慧琴等, 2014; 易盼盼, 2014; Lei et al, 2015). However, in vitro leaf inoculation methods (张慧琴等, 2014) have proven ineffective. Although kiwifruit research has borrowed in vitro identification methods from other fruit trees, specific procedures for material processing, inoculation timing, culture temperature, humidity, and resistance evaluation criteria are not standardized, leading to inconsistent results for the same cultivar. As a bacterial disease, kiwifruit bacterial canker has particular pathogen characteristics, and evaluation methods suitable for fungal diseases may not be applicable. Therefore, establishing a suitable, operationally simple, and unified in vitro identification technology system for bacterial canker resistance is imperative. New Zealand' s PFR (Hoyte et al, 2015) developed hard branch and tender shoot inoculation techniques for kiwifruit germplasm evaluation, using WSBI (woody stem bioassay index) and GSSBI (green stem-stab bioassay index) to assess disease levels. These methods have been applied to some cultivars and large intraspecific and interspecific hybrid populations, showing certain positive correlations with field resistance evaluation. However, the evaluation method is somewhat complex, with lesion length measurements at millimeter-level resolution providing low discrimination, and has not been widely adopted by others, possibly indicating it is still in early development stages.

3. Resistance Mechanism Studies

Early domestic and international research on kiwifruit bacterial canker resistance mechanisms primarily focused on morphology (李淼等, 2002; 李淼等, 2003; 李淼等, 2005; 张小桐, 2007; 李聪, 2016; 李庚飞等, 2008) and physiology/biochemistry (李淼等, 2005; 张小桐, 2007; 李淼等, 2009; 石志军等, 2014; 易盼盼, 2014; 李聪, 2016), as reviewed in previous papers by 李黎 (2013) and 高小宁 (2012). Recent years have seen progress in molecular mechanisms of bacterial canker resistance. 文欢等 (2016) compared structural differences in NBS-LRR resistance genes between susceptible cultivar "Hongyang"and resistant cultivar "Xuxiang,"finding through amino acid alignment and phylogenetic analysis that Xuxiang' s NBS domain was more complete and potentially associated with resistance, and identified two pairs of resistance-related primers. Petriccione et al (2013; 2014) used proteomic two-dimensional electrophoresis to study protein expression differences in kiwifruit shoots and leaves at different times after Psa infection, identifying a series of pathogenesis-related differentially expressed proteins that contribute to understanding the molecular interaction mechanisms between Psa and kiwifruit. However, due to limitations of two-dimensional electrophoresis technology, only a minority of differentially expressed proteins could be identified. Michelotti et

al (2015) used RNA-seq technology to study gene expression patterns in benzothiadiazole (ASM, a plant activator)-treated kiwifruit leaves and controls at different times during early Psa infection, analyzing the molecular mechanisms of Psa-kiwifruit interaction and ASM resistance regulation mechanisms. However, using ASM to study resistance through hormone regulation may differ significantly from the resistance pathways and expression patterns regulated by kiwifruit' s own resistance genes, presenting certain limitations. Wang et al (2018) studied the molecular mechanisms of kiwifruit-Psa interaction through transcriptome sequencing, identifying 8,255 differentially expressed genes and finding significant expression differences in terpenoid metabolism genes that may play roles in plant defense. Wang et al (2017) used whole transcriptome sequencing to study interspecific expression patterns of LncRNA, Circular RNA, and coding genes in three *Actinidia* species ("Chinese" ["Hongyang" and "Jinyan"], "hairy flower," and "soft jujube") after Psa infection. Results showed that both protein-coding genes and LncRNA or Circular RNA transcripts exhibited species-specific expression, and that pattern-triggered immunity (PTI) was the main cause of interspecific differences in kiwifruit response to Psa infection. Through weighted gene co-expression network analysis, both LncRNA and circular RNA were found to participate in host immune defense against Psa, and the resistance of hairy flower and soft jujube kiwifruit may result from Psa' s inability to anchor to their receptor genes, thus failing to suppress host PTI resistance responses. These findings provide a theoretical foundation for breeding bacterial canker-resistant kiwifruit cultivars through interspecific hybridization or new gene editing techniques. Resistance mechanism studies can provide theoretical bases for kiwifruit resistance breeding, particularly accelerating the breeding process through resistance gene mapping and molecular marker development. However, no formal reports on bacterial canker resistance gene mapping and cloning have been published. During a 2017 visit to New Zealand' s PFR, Dr. Zac Hanley introduced their progress in mapping bacterial canker resistance genes, indicating they had localized the resistance gene to a relatively small interval.

4.1 Large-Scale Resistance Screening and Evaluation of Kiwifruit Germplasm Resources

In recent years, numerous new kiwifruit cultivars have emerged, but most have been short-lived. Besides lacking obvious advantages in major horticultural and economic traits over current mainstream cultivars, another important reason is the lack of bacterial canker resistance identification during cultivar registration. As a key factor affecting kiwifruit production, the resistance level of an excellent kiwifruit cultivar to bacterial canker determines its potential for large-scale promotion and sustainable development. The recent extensive planting and promotion of the relatively resistant cultivar "Xuxiang" is primarily based on this reason. However, only a few cultivars have relatively clear resistance levels, and resistant cultivars are generally lacking. This is mainly because most cultivars were developed through intraspecific hybridization or seedling selection from

Chinese-type kiwifruit, which generally lack bacterial canker resistance genes and have relatively narrow genetic backgrounds. Furthermore, even fewer studies have examined bacterial canker resistance in other kiwifruit species. Only a few species have been confirmed to have general resistance, while most species have unknown resistance levels with limited targeted research. Numerous elite wild resistant germplasm resources await discovery, limiting their further development and utilization. We recommend accelerating bacterial canker resistance evaluation of kiwifruit germplasm resources and incorporating resistance evaluation as an essential component in new cultivar registration or approval processes.

4.2 Establishing More Scientific and Systematic Kiwifruit Bacterial Canker Resistance Identification and Evaluation Technology Systems

The unclear resistance status of most kiwifruit germplasm resources primarily results from the long-term lack of effective resistance identification methods. Field evaluation remains the main approach for determining cultivar resistance, but it requires specific disease conditions and lengthy observation periods. Furthermore, disease survey methods themselves directly affect evaluation results. For example, many researchers habitually use disease indices calculated from the number of diseased leaves or lesions to evaluate resistance levels, but practice has proven this approach unscientific for kiwifruit. Studies by Vanneste et al (2014) and Nardozza et al (2015) showed that the resistant species *A. arguta* exhibited faster and more severe symptom responses after leaf inoculation compared with susceptible cultivars. Similarly, during in vivo leaf inoculation of resistant material "Jiangdicun Maohua" and susceptible material "Hongyang" in our research, we observed the same phenomenon: although Hongyang died completely 5-6 weeks after removal from the culture chamber while Jiangdicun Maohua grew normally, it was Jiangdicun Maohua, not Hongyang, that showed obvious leaf disease symptoms one week after inoculation. Therefore, using this disease index calculation method to determine bacterial canker resistance levels may yield completely opposite results. In vivo and in vitro artificial identification technologies also remain immature, with chaotic identification methods and evaluation standards. For instance, some researchers use disease incidence rates to evaluate resistance levels in in vivo or in vitro assays. More scientifically speaking, under completely consistent inoculation materials, environments, and operations, the disease severity of the same type of material should be consistent, and disease incidence should not exist, which conversely demonstrates the instability of this method. Current resistance identification methods all have certain limitations. We recommend improving and unifying kiwifruit bacterial canker resistance identification and evaluation methods, particularly establishing more scientific and reliable in vitro rapid identification and evaluation technology systems.

4.3 Accelerating Resistance Breeding Through Interspecific Hybridization and Genetic Engineering

Currently, most major cultivar breeding programs in China and New Zealand use existing cultivars as parents through intraspecific hybridization. Only a few cultivars have been developed through interspecific hybridization. For example, "Jinyan" kiwifruit (Zhong et al, 2012) is an excellent cultivar developed by Wuhan Botanical Garden through interspecific hybridization between "hairy flower" and "Chinese" type kiwifruit, but unfortunately, its bacterial canker resistance was not significantly improved (易盼盼, 2014; Wang et al, 2017). This demonstrates that even when using resistant species for hybridization, segregation of progeny traits must be considered. Although previous interspecific hybridization efforts produced some specific materials (王圣梅等, 1989; 朱鸿云等, 1994; 安和祥等, 1995; 范培格等, 2004), the primary purpose was not to obtain resistant cultivars, and comprehensive resistance evaluation was not conducted. While wild *Actinidia* species generally have poor comprehensive horticultural traits, certain species possess excellent characteristics not found in *A. chinensis*, such as disease and stress resistance (*A. eriantha*, *A. arguta*, *A. polygama*, *A. macrosperma*, *A. valvata*), easy peeling (*A. eriantha*), high yield (*A. latifolia*, *A. guilinensis*), evergreen habit (*A. cylindrica*, *A. albiflora*, *A. liangguangensis*, *A. carnosifolia*), attractive flowers (*A. eriantha*, *A. carnosifolia*, *A. rubus*), and unique flavors (*A. sorbifolia*, *A. chrysantha*, *A. henryi*), representing important breeding values and application prospects. If we can utilize these resistant species with unique horticultural traits for pyramiding breeding, developing excellent new resistant cultivars through interspecific hybridization and gene introgression would have broad application prospects. Additionally, genetic engineering breeding technologies should be fully utilized to shorten the breeding process and improve efficiency. Current kiwifruit transgenic breeding involves development and physiological regulation, nutritional and quality improvement, pest and disease resistance, stress tolerance, and plant architecture modification. Domestic kiwifruit transgenic technology application started relatively late, focusing primarily on establishing and verifying transgenic technology systems, mainly concerning plant stress tolerance, fruit storage, and fruit disease resistance. Research specifically targeting bacterial canker through transgenic approaches is relatively limited. 周月等 (2014) used "Red Sun" kiwifruit as material to transform the LJAMP2 gene under CaMV35S promoter control into Red Sun via *Agrobacterium*-mediated transformation, successfully obtaining transgenic plants, though no further verification has been reported. In recent years, with the maturation and improvement of kiwifruit transgenic and efficient gene editing technology systems (Wang et al, 2018), new opportunities have emerged for bacterial canker-resistant cultivar breeding. We recommend fully utilizing modern engineering breeding technologies, including transgenesis, gene editing, embryo rescue, ploidy breeding, and physical/chemical mutagenesis, to accelerate resistance breeding progress.

4.4 Fully Utilizing Domestic Resource Advantages and Establishing Scientific and Orderly Resource Exchange and Sharing Mechanisms

China is the country with the richest kiwifruit germplasm resources, possessing unique advantages for bacterial canker-resistant cultivar breeding. However, only a few research institutions have established relatively complete living gene banks of germplasm resources, many of which took decades and generations of effort through arduous field investigation and collection to reach their current scale. As the most valuable scientific strategic resources, "cherishing one' s own broom" is understandable. However, "closed-door policy" and "working behind closed doors" are not conducive to full resource development and utilization. This requires a reasonable and effective resource exchange and utilization mechanism based on respecting and recognizing intellectual property rights while innovating cooperation mechanisms. Several national-level kiwifruit industry alliances established in China encompass most domestic kiwifruit research institutions and major enterprises, with promoting resource exchange and cooperative development as major agenda items, but no effective sharing and win-win cooperation mechanisms or binding contractual documents have been formed. We recommend using national kiwifruit industry systems or industry alliances as platforms for top-level planning and design, establishing guaranteed long-term cooperation and win-win mechanisms that respect and balance concerns of all parties, promoting rational resource sharing and utilization, accelerating kiwifruit bacterial canker resistance breeding progress, and promoting healthy and orderly development of China' s kiwifruit industry.

5. Outlook

Progress in kiwifruit bacterial canker resistance breeding has been relatively slow, primarily due to immature resistance identification and evaluation methods, resulting in unclear resistance status of most kiwifruit germplasm resources. This prevents effective utilization of resistant resources for disease resistance breeding and limits the mining and utilization of resistance gene resources. Therefore, establishing a scientific and highly accurate rapid identification method is key to accelerating kiwifruit bacterial canker resistance breeding. We believe that with continuous development and improvement of bacterial canker resistance identification technologies and evaluation methods, more and more excellent bacterial canker-resistant cultivars or highly resistant wild germplasm will be discovered and utilized, fundamentally solving the key problem of bacterial canker 困扰 in kiwifruit production and promoting green, healthy, and sustainable development of the kiwifruit industry.

References

ABE K, KOTODA N, KATO H, et al, 2007. Resistance sources to Valsa canker (*Valsa ceratosperma*) in a germplasm collection of diverse *Malus* species[J]. *Plant Breed*, 126(4): 449-453.

AN HX, CAI DR, MU XJ, et al, 1995. New germplasm of interspecific hybridization in *Actinidiae* [J]. *Acta Hort-amsterdam Sinica*, (2): 133-137.

BALESTRA G M, RENZI M, MAZZAGLIA A, 2010. First report of bacterial canker of *Actinidia deliciosa* caused by *Pseudomonas syringae* pv. *Actinidiae* in Portugal [J]. *New Dis Rep*, 22: 10.

BALESTRA GM, MAZZAGLIA A, QUATTRUCCI A, et al, 2009. Occurrence of *Pseudomonas syringae* pv. *actinidiae* in Jin Tao kiwi plants in Italy[J]. *Australas Plant Dis Notes*, 48(2): 299-301.

BULL CT, CLARKE CR, CAI R, et al, 2011. Multilocus sequence typing of *Pseudomonas syringae* sensu lato confirms previously described genomospecies and permits rapid identification of *P. syringae* pv. *coriandricola* and *P. syringae* pv. *apii* causing bacterial leaf spot on parsley[J]. *Phytopathology*, 101(7): 847.

CAO T, SAYLER RJ, DEJONG TM, et al, 1999. Influence of Stem Diameter, Water Content, and Freezing-Thawing on Bacterial Canker Development in Excised Stems of Dormant Stone Fruit[J]. *Phytopathology*, 89(10):962-966.

CHAPMAN JR, TAYLOR R K, WEIR BS, et al, 2012. Phylogenetic Relationships Among Global Populations of *Pseudomonas syringae* pv. *actinidiae*[J]. *Phytopathology*, 11(102): 1034-1044.

CLEARWATER MJ, SELEZNYOYA AN, THORP TG, et al, 2006. Vigor-controlling rootstocks affect early shoot growth and leaf area development of kiwifruit[J]. *Tree Physiol*, 26(4): 505-515.

CRUZ-CASTILLO J G, LAWES G S, WOOLLEY D J, et al, 1991. Rootstock influence on kiwifruit vine performance[J]. *N Z J Crop Hortic Sci*, 4(19): 361-364.

DATSON P, NARDOZZA S, MANAKO K, et al, 2015. Monitoring the *Actinidia* germplasm for resistance to *Pseudomonas syringae* pv. *actinidiae*[J]. *Acta Hortic*, (1095): 181-184.

ERPER, ISMAIL, TUNALI, et al, 2013. Characterization of root rot disease of kiwifruit in the Black Sea region of Turkey[J]. *Eur J Plant Pathol*, 136(2):291-300.

FAN PG, AN HX, CAI DR, et al, 2004. Interspecific hybridization between species of *Actinidiae* L. and breeding of superior selection [J]. *J Fruit Sci*, (3): 208-211.

FERRANTE P, SCORTICHINI M, 2010. Molecular and phenotypic features of *Pseudomonas syringae* pv. *actinidiae* isolated during recent epidemics of bacterial canker on yellow kiwifruit (*Actinidia chinensis*) in central Italy[J]. *Plant Pathol*, 59(5): 954-962.

GAO X, ZHAO ZB, HUANG QL, Qin H, et al, 2012. Research progress on bacterial canker disease of kiwifrui [J]. *J Fruit Sci*, (02): 262-268.

GONCALVES-ZULIANI AO, NANAMI DSY, BARBIERI BR, et al, 2016. Evaluation of Resistance to Asiatic Citrus Canker among Selections of Pêra Sweet Orange (*Citrus sinensis*)[J]. *Plant Dis*, 100(10): 1994-2000.

HOYTE S, REGLINSKI T, ELMER P, et al, 2015. Development and using bioassays to screen for Psa resistance in Neaw Zealand kiwifruit[J]. *Acta Horticulturae Hort-amsterdam*, (1095): 171-180.

JIANG GH, XIE M, CHEN XX, et al, 1998. Rootstock effects on growth and fruiting in kiwifruit [J]. *Acta Agric Zhejiangensis*, (03): 50-51.

KHANDAN HAN, WORNER SP, JONES EE, et al, 2013. Predicting the potential global distribution of *Pseudomonas syringae* pv. *actinidiae* (Psa)[J]. *N Z Plant Protect*, (66): 184-193.

LEI YS, JING ZB, LI L, 2015. Selection and Evaluation of a New Kiwifruit Rootstock Hybrid for Bacterial Canker Resistance[J]. *Acta Hort*, (1096).

LI C, 2016. Correlation of the relationship between resistance of branch leaves structure and inclusion and kiwifruit canker[D]. Northwest A & F University.

LI GF, ZHOU SB, LI Y, 2008. A preliminary study on the relationship between dermal pore characteristics of kiwifruit and resistance to ulcer disease [J]. *Chin Plant Prot*, (05): 30-31.

LI JW, WANG XG, MO L, et al, 2004. Study on the selection of rootstocks for the good clone 'Shimei' of *Actinidia deliciosa* [J]. *Guihaia*, (1): 43-48.

LI L, ZHONG CH, LI DW, et al, 2013. Research progress on bacterial canker disease of kiwifrui [J]. *Huazhong J Agr University*, (5): 124-133.

LI M, TAN G, LI Y, et al, 2003. Relationship between the shoot tissue structure of kiwifruit cultivars and bacterial canker disease resistance [J]. *Anhui J Agr University*, (3): 240-245.

LI M, TAN GJ, LI Y, et al, 2002. Study ON the Leaf Tissue Structure of Kiwifrit Culivars in Relation to Bacterial Canker Disease Restance [J]. *Anhui J Agric Sci*, (5): 740-742.

LI M, TAN GJ, LI Y, et al, 2005. Resistance mechanism of kiwifruit cultivars to *Pseudomonas syringae* pv. *actinidiae* [J]. *J Plant Prot*, (01): 37-42.

LI M, TAN GJ, LI Y, et al, 2009. A Study on the Relationship beween Isozyme and the Resistance of Kiwifruit Cultivars to Bacterial Canker by *Pseudomonas syringae* pv *actinidiae* [J]. *Acta Laser Biol Sinica*, (02): 218-225.

LI X, LI J, Soejarto DD, 2009. Advances in the study of the systematics of *Actinidia* Lindley[J]. *Chin Front Biol*, 4(1).

LI Y, CHENG HY, FANG SM, et al, 2001. Prevalent forecast of kiwfruit bacterial canker caused by *Pseudomonas syringae* pv. *actinidiae* [J]. *Chin J Appl Ecol*, (3): 355-358.

LIU J, 2015. Evaluation of Resistant Varieties on Kiwifruit Bacterial Canker and Cluster Analysis of Genetic Relations by ISSR Markers[D]. Sichuan Agr University.

MAZZAGLIA A, RENZI M, BALESTRA GM, 2011. Comparison and utilization of different PCR-based approaches for molecular typing of *Pseudomonas syringae* pv. *actinidiae* strains from Italy[J]. *Can J Plant Pathol*, 1(33): 8-18.

MICHELOTTI V, LAMONTANARA A, BURIANI G, et al, 2015. RNAseq analysis of the molecular initeraction between *Pseudomonas syringae* pv. *actinidiae* (Psa) and the kiwifruit[J]. *Acta Hort-amsterdam*, (1096): 357-362.

NARDOZZA S, MARTINEZ-SANCHEZ M, CURTIS C, et al, 2015. Screening *Actinidia* Germplasm for Different Levels of Tolerance, or Resistance, to Psa (*Pseudomonas syringae* pv. *actinidiae*)[J]. *Acta Hortic*, (1096): 351-356.

PETRICCIONE M, CECCO ID, ARENA S, et al, 2013. Proteomic changes in *Actinidia chinensis* shoot during systemic infection with a pandemic *Pseudomonas syringae* pv. *actinidiae* strain[J]. *J Proteomics*, 78: 461-476.

PETRICCIONE M, SALZANO AM, CECCO ID, et al, 2014. Proteomic analysis of the *Actinidia deliciosa* leaf apoplast during biotrophic colonization by *Pseudomonas syringae* pv. *actinidiae*[J]. *J Proteomics*, 101: 43-62.

SCORTICHINI M, MARCELLETTI S, FERRANTE P, et al, 2012. *Pseudomonas syringae* pv. *actinidiae*: a re-emerging, multi-faceted, pandemic pathogen[J]. *Mol Plant Pathol*, 13(7): 631-640.

SHAO WP, LIU YL, 2015. Sedection and Inoculative ldentification of Kiwifruit Resistance Rootstock [J]. *Anhui J Agric Sci*, (35): 214-245.

SHEN Z, HUANG LL, KANG ZS, 2009. The Investigation of Kiwifruit Bacterial Canker in Guanzhong Zone of Shaanxi Province[J]. *Acta Agri Boreali-occidentalis Sin*, (01): 191-193.

SHI ZJ, ZHANG HQ, XIAO JP, et al, 2014. The resistance evaluation of different kiwifruit varieties to canker[J]. *Acta Agric Zhejiang*, 3(26): 752-759.

STEWART A, MCCARRISON AM, 1991. Pathogenicity and relative virulence of seven *Phytophthora* species on kiwifruit[J]. *N Z J Exp Agric*, 19(1):73-76.

TAKIKAWA Y, SERIZAWA S, ICHIKAWA T, et al, 1989. *Pseudomonas syringae* pv. *actinidiae* pv. nov: The Causal Bacterium of Canker of Kiwifruit in Japan[J]. *Ann Phytopath Soc Japan*, 4(55): 437-444.

TYNAN K M, SCOTT E S, SEDGLEY M, 1998. Development of excised shoot and root assays for in vitro evaluation of *Banksia* species for response to *Phytophthora* species[J]. *Plant Path*, (47): 456-462.

VANNESTE J, CORNISH D, Yu J, et al, 2014. First Report of *Pseudomonas syringae* pv. *actinidiae* the Causal Agent of Bacterial Canker of Kiwifruit on *Actinidia arguta* Vines in New Zealand[J]. *Plant Dis*, (98): 418.

WAN R, HOU X, WANG X, et al, 2015. Resistance evaluation of Chinese wild *Vitis* genotypes against *Botrytis cinerea* and different responses of resistant and susceptible hosts to the infection[J]. *Front Plant Sci*, 6:854.

WANG L, WANG SM, HUANG HW, 2001. Graft compatibility among *Actinidia* species and screening, rootstocks resistant to root-knot Nematodes [J]. *Plant Sci J*, (1): 47-51.

WANG SM, WU XW, HUANG R, et al, 1989. Preliminary report of fructuation in interspecific cross of Chinese gooseberries [J]. *Wuhan Plant Sci J*, (4): 399-402.

WANG T, WANG G, JIA Z, et al, 2018. Transcriptome Analysis of Kiwifruit in Response to *Pseudomonas syringae* pv. *actinidiae* Infection[J]. *Int J Mol Sci*, 19(2): 373.

WANG Z Y, PATTERSON K J, GOULD K S, et al, 1994. Rootstock effects on budburst and flowering in kiwifruit[J]. *Sci Hort-amsterdam*, 57(3), 187-199.

WANG Z, GAO T, GU J, et al, 1998. Main Factors Affecting KiwiFruit Canker [J]. *Anhui J AgrIC Sci*, 8(4): 59-60.

WANG Z, LIU Y, LI D, et al, 2017. Identificationof Circular RNAs in Kiwifruit and Their Species-Specific Response to Bacterial Canker Pathogen Invasion[J]. *Front Plant Sci*, 8:413.

WANG Z, LIU Y, LI L, et al, 2017. Whole transcriptome sequencing of *Pseudomonas syringae* pv. *actinidiae*-infected kiwifruit plants reveals species-specific interaction between long non-coding RNA and coding genes[J]. *Sci Rep*, 7(1).

WANG Z, WANG S, LI D, et al, 2018. Optimized paired-sgRNA/Cas9 cloning and expression cassette triggers high-efficiency multiplex genome editing in kiwifruit[J]. *Plant Biotech J*.

WANG ZR, GAO TC, GU JT, et al, 1998. Research on the prevention and treatment of kiwifruit ulcer disease[J]. *Anhui J AgrIC Sci*, 4(26): 349-351.

WEN H,2016. Research progress on bacterial canker disease of kiwifruit [D]. Zhejiang University.

YI PP, 2014. Different Of Kiwifruit V arieties eacterical canker resistant identification and pathogenesis-related enzymes research [D]. Northwest A & F University.

YI PP, 2014. Resistance identificaiton of different kiwifruit varieties to bacterial canker and the study of pathogenesis-related enzymes[D]. Northwest A & F University.

ZHANG HQ, LI HM, FENG JJ, et al, 2013. Investigation and analysis of infection caused by *Pseudomonas syringae* pv. *Actinidiae* and itsaffecting factors in Zhejiang province [J]. *Acta Agric Zhejiang*, (4): 832-835.

ZHANG HQ, MAO XQ, XIAO JP, et al, 2014. Rapid molecular identification of *Actinidia* bacterial canker and preliminary screening of resistant materials in kiwifruit [J]. *J Nucl Agric Sci*, (7): 1181-1187.

ZHANG HQ, MAO XQ, XIAO JP, et al, 2014. Rapid molecular identification of *Actinidia* bacterial canker and preliminary screening of resistant materials in kiwifruit[J]. *J Nucl Agric Sci*, (7): 1181-1187.

ZHANG XT, 2007. Study on the resistance indexes of kiwifruit to *Pseudomonas syringae* pv. *actinida* [D]. Anhui Agricultural University.

ZHONG C, WANG S, ZHENGWANG, 2012. 'Jinyan' , an interspecific hybrid kiwifruit with brilliant yellow flesh and good storage quality[J]. *Hortscience*, 8(47): 1187-1190.

ZHOU Y, ZHAO X, WU X, et al, 2014. *Agrobacterium*-mediated transformation of LJAMP2 gene into 'Red Sun' kiwifruit and its molecular identification[J]. *Chin J Biotechnol*, (6): 931-942.

ZHU HY, DU RM, LI SL, et al, 1994. A preliminary study on the distant hybridization of kiwifruit[J]. *Henan J Agric Sci*, (01): 25-27.

Note: Figure translations are in progress. See original paper for figures.