Research Progress on Disease Resistance Genes and Breeding in Banana *(Musa spp.)*

Fuxin Liu
Shenzhen Middle School, Shenzhen 518000, China

Abstract. Banana (Musa spp.), the fourth most important staple crop and a vital economic commodity globally, faces severe threats from Fusarium wilt tropical race 4 (TR4), leaf spot diseases, and viral infections. TR4 has spread to 25 countries, endangering 50% of banana cultivation areas. This review systematically summarizes recent advances in disease resistance gene exploration and molecular breeding technologies: (1) Functional studies of resistance genes reveal that NBS-LRR-type genes recognize pathogen effectors to activate immune responses. Overexpression of RGA2 enhances TR4 resistance in Cavendish bananas by up to 82%. (2) Precise editing of signaling regulatory genes and physical barrier-related genes significantly improves disease resistance. CRISPR-mediated editing of the MaNPR1 promoter triples TR4 resistance. (3) Breakthroughs in molecular breeding—including gene editing (CRISPR/Cas9), synthetic biology (inducible resistance circuits), and marker-assisted selection (MaACS markers)—have shortened breeding cycles from 15 to 8 years while enabling pyramiding of multi-gene resistance. However, challenges persist, such as genetic uniformity, pathogen co-evolution, and technological implementation barriers. Future efforts should integrate multi-omics technologies, develop broad-spectrum resistance strategies, and establish global germplasm innovation platforms to ensure sustainable banana production.

Keywords: Banana disease resistance genes; tropical race 4 (TR4); NBS-LRR; molecular breeding.

1. Introduction

Bananas (Musa spp.) are a vital crop that was domesticated around 8000 BC in the highlands of Papua New Guinea. Over the millennia, bananas have risen to prominence and now stand as the fourth most important global food crop, recognized not only for their nutritional value but also for their significant economic contributions. By the year 2023, global banana production reached an impressive 128 million tons annually. This remarkable figure encompasses a wide array of products beyond just fresh fruit sales; it includes processed goods such as banana flour and pectin, pharmaceutical extracts like polyphenolic antioxidants, and environmentally friendly materials, including bioplastics made from banana fibers (Alzate Acevedo et al., 2021).

In many tropical developing countries, bananas serve as a cornerstone of food security. The annual per capita consumption of bananas in countries such as Uganda and Rwanda exceeds 200 kilograms. Bananas contribute over 30% of the daily caloric intake for these populations (Kilwenge et al., 2023). However, this heavy reliance on bananas brings with it significant challenges. Approximately 70% of global commercial banana production is based on the monoculture of Cavendish cultivars. The lack of biodiversity makes them more vulnerable to pests and diseases. Consequently, disease threats have emerged as the foremost challenge facing sustainable development within the banana industry. Historically, the evolution of pathogens and the replacement of banana varieties have been intricately linked. In the mid-20th century, a devastating fungal pathogen known as *Fusarium oxysporum* race 1 (Foc1) led to the near-collapse of the disease. This crisis prompted a global shift towards Cavendish cultivars as growers sought to protect their crops from these threats. However, the emergence of Tropical Race 4 (TR4) in the 21st century has reignited concerns within the industry (Mejías Herrera et al., 2023). First identified in Malaysia in 1990, TR4 has since spread to 25 countries, resulting in yield reductions ranging from 40% to an alarming 100% in major Chinese production regions such as Guangxi and Yunnan (Zhan et al., 2022). The International Banana and Plantago Asiatica Improvement Network (INIBAP) predicts that within the next few years, TR4 could endanger up to 50% of the world's banana-growing areas. At the same time, pathogen infestation exacerbates the environment for banana pathogenicity: for example, black leaf disease is a severe leaf disease that farmers in Latin America apply a fungicide every two weeks to suppress the progression of the disease, and it is expensive, costing around $300 per hectare per treatment. In addition, the banana bunch-top virus (BBTV) destroyed up to 90% of banana plants on Indian Ocean islands (Soares et al. 2021). Overall, the current disease management system for bananas faces three key issues: the unsustainability of chemical controls, the marginal effects of agronomic practices, and the inherent inefficiencies of traditional breeding methods. Therefore, the mining of disease resistance genes and the advancement of molecular breeding technology have become key strategies to address these challenges.

This article reviews the latest research progress on the resistance mechanism of bananas in recent years, summarizes the common infectious diseases of bananas and their molecular mechanisms, and finally, based on the existing molecular breeding techniques, summarizes the coping strategies to enhance the disease resistance of bananas to ensure the sustainability of this important crop. This article will provide a theoretical basis for improving the disease resistance of bananas.

2. Major Banana Diseases and Pathogenic Characteristics

2.1 Banana Fusarium Wilt

Fusarium wilt Wilt is a devastating plant disease caused by soil-borne pathogens and is one of the most significant threats to banana production. Fusarium wilt is mainly caused by the infection of fusarium wilt pathogen. Fusarium wilt (Foc) belongs to the Ascomycota phylum and has a high host specificity, mainly infecting bananas. Focs are divided into four distinct physiological races, of which tropical race 4 (TR4) is considered the most harmful, with TR4 being able to infect all banana genotypes and has the potential to cause widespread agricultural destruction (Bragard et al. 2022). TR4 penetrates plant tissues by secreting a series of cell wall-degrading enzymes (pectinate lyase), which helps it penetrate plant tissues. In addition, TR4 produces plant toxins such as Fusarium acid to disrupt the vascular bundles of bananas, leading to severe physiological damage. Genomic studies have revealed 12 effector genes specific for TR4, especially Focr4_10101 that enable pathogens to successfully establish infection, and play a crucial role in inhibiting the host's immune response (Castillo et al., 2019). Once infected with TR4, banana plants exhibit several distinct symptoms. Initial signs usually include yellowing and wilting of old leaves, and bananas may also produce reddish-brown exudate from split pseudostems as the infection progresses, showing brownish vascular bundles. However, due to the already emerging resistance of TR4 to commonly used fungicides, there is a lack of effective chemical controls that can be used to combat this pathogen. Therefore, the development of resistant banana varieties has become the only viable solution to mitigate the impact of TR4 on global banana production (Wang et al., 2024).

The prevention and control of banana wilt disease requires a comprehensive variety of prevention and control methods to get better results. Although the prevention and control of banana wilt-resistant varieties are pushed wide play a key role, the diversification of pathogenic physiological races will also accelerate the product loss of disease resistance. The performance in the field is often not as good as it can be, and it is difficult to apply it in production and promotion. Traditional chemical control is easy to flow in soil and water due to small molecule fungicides. It is easy to develop resistance and has not achieved good results in the control of banana wilt fungus effect, while biological control, crop rotation, and intercropping due to high economic costs, none. The method of continuous planting and labor costs are high, and it is difficult to be limited by factors such as economic benefits and real implementation.

2.2 Black Sigatoka

Black leaf spot disease is particularly common in tropical regions. Usually, fungicides need to be used regularly every two weeks, with each treatment costing about 300 US dollars per hectare, causing a serious financial burden (Noar et al., 2022). Therefore, it is becoming increasingly important to find sustainable control measures to protect banana cultivation. Black Sigatoka is another key foliar disease affecting bananas, caused by the ascomycete fungus Mycosphaerella. Genomic analysis of P. fijiensis revealed the presence of 56 candidate effector genes, such as Mf_CRN1, which are involved in the disruption of host defense signaling pathways (Mbo Nkoulou et al., 2022). P. fijiensis invades banana leaves through the stomata, where a toxin called fijiensin is secreted to attack and disrupt the membranes of chloroplasts, thereby reducing the plant's photosynthetic capacity and stunting the development of the fruit. The initial symptom of black leaf spot infection is the appearance of green spots on banana leaves, which gradually expand into spindle-shaped necrotic lesions and eventually lead to extensive leaf charring.

2.3 Viral Diseases

Banana Bunchy Top Virus (BBTV): Its DNA-S-encoded movement protein (MP) hijacks host plasmodesmata to facilitate cell-to-cell transport (Venkataraman et al., 2022). Transmitted persistently by the banana aphid (Pentalonia nigronervosa), BBTV induces leaf yellowing, plant stunting, and "pencil-like" pseudostem deformities. In Kerala, India, BBTV outbreaks have resulted in 90% of crop loss in banana plantations (Ximba et al., 2022). Banana Streak Virus (BSV): BSV, a member of the genus Badnavirus, integrates its genome into the host DNA (endogenous BSV, eBSV) and reactivates under stress conditions (e.g., high temperatures) (Iskra-Caruana et al., 2014). Infection causes yellow streaks or necrotic spots on leaves and fruit development arrest. In Cameroon, BSV has reduced banana export eligibility to 60% (Ricciuti et al., 2021).

3. Mining and Functional Characterization of Banana Disease Resistance Genes

3.1 NBS-LRR-Type Genes

The NBS-LRR (Nucleotide-Binding Site Leucine-Rich Repeat) gene family represents a fundamental aspect of plant immune systems, playing a pivotal role in triggering disease resistance responses through the recognition of pathogen effectors. These genes are necessary for plants to identify and respond to various pathogens. For example, the genomes of wild banana germplasms such as Musa acuminata and Musa balbisiana contain abundant NBS-LRR gene resources. The evolutionary characteristics of the NBS-LRR gene are closely related to the specificity of the anti-pathogen (DeYoung & Innes, 2006). The RGA2 gene encodes a protein containing the canonical CC-NBS-LRR domain, which plays a key role in plant immunity. Notably, the LRR domain of RGA2 can specifically bind to the C-terminal 34-amino acid motif (motif 3) AVRRGA2 the TR4 effector, and this interaction activates ATPase activity within the RGA2 NBS domain, resulting in a conformational change that is essential for initiating a defense response (Amir et al., 2016). Once activated, the RGA2 protein triggers a series of signaling events, including the MAPK signaling pathway, hypersensitivity reaction (HR), and systemically acquired electrical resistance (SAR). Together, these interconnected processes enhance the resilience of plants to pathogen attacks. In practice, overexpression of the RGA2 gene in the transgenic Cavendish banana increased the drug resistance rate of TR4 infection by 82%, suggesting that the use of this gene can enhance the potential of banana disease management strategies (García-Bastidas et al., 2022). Another important gene is MARGC10, which MARGC10 located on the Musa Balbisiana chromosome, and has a TIR-NBS-LRR domain. The MARGC10 TIR domain is particularly adept at binding the N-terminal secretory signal peptide of the leaf spot pathogen effector PFJ_EFF3, effectively preventing its translocation into the host cytoplasm (Wöhle &Gebhard, 2020), suggesting that MARGC10 genes can prevent the establishment of pathogenic infection in early defense mechanisms. In addition, MARGC10 also plays an important regulatory role by inducing the expression of the salicylic acid (SA) synthase gene ICS1. The results of the study showed an eightfold increase in SA levels in leaves MARGC10 overexpression and expanded plant defenses by upregulating genes associated with pathogenesis, such as PR1 and PR5 (Janda et al., 2020). Increasing the expression of Margc10 in the planted variety "Gros Michel" can significantly reduce the incidence of black leaf spot disease (Bebber, 2019).

3.2 Signaling Regulatory Genes

NPR1 plays an important role in plant defense strategies. For instance, CRISPR-mediated editing of the MANPR1 promoter region has been employed to drive pathogens to induce NPR1 overexpression, thereby significantly enhancing the resistance of tropical Subspecies 4 (TR4) strains of thyroid wilt disease (Lin et al., 2021). NPR1 is widely recognized as a central regulator within the salicylic acid (SA) signaling pathway and plays a vital role in plant immunity. Under non-stressful conditions, NPR1 usually maintains a stable conformation in the cytoplasm with oxidative trimers as the cytoplasm to prevent premature activation of the defense response. However, when plants are challenged by stress or pathogens, fluctuations in SA levels trigger significant conformational changes in NPR1. These changes occur by modulating its nuclear localization signal, allowing NPR1 to transfer it into the nucleus, allowing it to exert its regulatory function more efficiently (Zavaliev et al., 2020). Once activated by salicylic acid, NPR1 interacts with other signaling molecules to fine-tune the plant's defense mechanisms: a significant interaction occurs between SA-activated NPR1 and MYC2, which are core transcription factors involved in jasmonic acid (JA) signaling. When NPR1 interacts with MyC2, it inhibits MyC2's ability to bind to the G-Box element in the target gene, thereby regulating the expression of JA response genes. This interaction is critical to balancing the trade-off between disease resistance and insect defense (Kallenbach et al., 2010).

3.3 Physical Barrier-Associated Genes

The overexpression of cytochrome P450 enzyme significantly thickens the cuticle of banana leaves, thereby reducing the penetration efficiency of pathogens (Waring, 2020). However, this thickened cuticle delays attachment formation (Chong et al., 2019). Therefore, silencing keratin monomer transporter genes using RNAi can damage the integrity of the stratum corneum and increase the invasion rate of TR4 (Beisson et al., 2012). The cellulose synthase gene CesA reinforces cell wall structure. CRISPR knockout of CesA3 reduces cell wall thickness by 40%, doubling TR4 hyphal expansion rates(Hu et al., 2019). Introducing the disease-tolerant rice allele OsCESA9 into bananas elevates vascular bundle lignin content by 25%, boosting TR4 resistance to 75%(Ye et al., 2021).

4. Advances in Banana Disease Resistance Breeding Technologies

Molecular markers have undergone the development process from linkage markers and gene markers (functional markers) to associated markers. In the early stage, the main purpose of using separate groups is to find chain marks. The disadvantage of chain marks is that they are not universal, and the accuracy may change after changing the group. Gene markers have developed with the improvement of gene isolation technology. Gene markers are highly versatile, not affected by population sources, and have extremely high accuracy.

4.1 Conventional Hybrid Breeding

Due to the triploid and sterile nature of most cultivated bananas, traditional breeding relies on wild diploid or diploid relatives as pollen donors. For example, crossing *M. acuminata* with cultivated varieties has yielded TR4-resistant lines like ‘GCTCV-219’. However, challenges such as extended breeding cycles (10–15 years) and linkage drag persist. Integrating phenomics (high-throughput photosynthetic phenotyping) with greenhouse-based accelerated generation cycling (2.5 generations/year) has reduced the breeding cycle from 15 to 8 years (Chen et al., 2019). A representative workflow includes: using TR4-resistant wild M. acuminata ssp (AA) as the male parent and susceptible cultivar ‘Williams’ (AAA) as the female parent, generating tetraploid (AAAA) intermediates via embryo rescue, followed by chromosome doubling to produce fertile hexaploids (AAAAAA), and finally backcrossing to develop triploid GCTCV-219 (AAA).

4.2 Marker-Assisted Selection (MAS)

Molecular Marker-assisted selection (MAS) is a breeding technology that uses molecular markers of target traits to select banana offspring strains, and then obtains a single plant containing excellent target genes. MAS is popular in banana breeding for accurately transferring target gene fragments of interest to breeders and accelerating the recovery of genomes of reincarnation parents and is widely used. Therefore, traditional banana breeding must be combined with MAS, such as applying MAS to early-generation selection crops. The efficiency of molecular labeling and whether the detection method is high throughput are key factors in determining MAS efficiency. With the development of DNA sequencing technology, high-throughput SNP has become the preferred marker for genetic research and crop breeding, and has been widely used in genetic resource identification, MAS-based KASP typing technology can meet the requirements of low, medium and high-throughput genotyping, and can detect SNP insertions and deletions. This technology can effectively identify banana polymorphic sites. MAS leverages molecular markers derived from banana microsatellite sequences, such as the MaACS marker (flanking the ACS1 gene), which exhibits a high correlation with Foc resistance phenotypes(Rocha et al., 2021). Developing trait-linked markers (e.g., SSRs and SNPs) accelerates the selection of superior genotypes. For instance, the MaACS marker has been successfully deployed to breed Fusarium wilt-resistant lines(Nakkeeran et al., 2021).

4.3 Transgenic Technology

Transgenic approaches involve introducing antifungal protein genes (e.g., chitinase gene Chit42) into bananas to enhance resistance against leaf spot diseases (Sreeramanan et al., 2008). RNA interference (RNAi) technology, targeting viral genes with RNAi constructs, significantly suppresses BBTV replication(Jekayinoluwa et al., 2020).

4.4 Genome Editing

The CRISPR/Cas9 system is part of the bacterial and archaeal immune system in the CRISPR/Cas system, and has the protection function to prevent the invasion of phages and plasmid DNA from prokaryotes. Genome editing tools were developed to effectively solve this problem and quickly became a conventional means of crop improvement. Genome editing technology is to cut DNA in specific regions of the genome, realize specific changes in DNA and introduce new repair mechanisms. Genome editing technology can accurately realize the effect of deleting, replacing or inserting specific sequences at the target location of the crop genome, ultimately producing new target traits. In terms of fruit quality, gene editing technology is used to regulate the synthesis of fruit nutrients in bananas, apples and grapes. The banana MaPDS gene was edited using the modified CRISPR/Cas9 multi-target vector system, and it was found that most plants showed an albino mutant phenotype. In addition, the editing efficiency of delivering polycistronic gRNAs targeting PDS gene exons in bananas using the CRISPR/Cas9 gene editing system is as high as 100%. In bananas, CRISPR/Cas9 technology is used to increase the content of β-carotene in bananas, and a banana variety rich in β-carotene was created. The accumulation of β-carotene in the flesh of the edited strain was 6 times higher than that of the unedited strain. For example, knocking out some susceptibility genes increases banana resistance to powdery mildew (Wang et al., 2021), while editing MaNPR1 confers broad-spectrum resistance to a wide range of pathogens (Tripathi et al., 2017).

5. Summary and Prospects

In this paper, the main banana diseases and their pathogenic characteristics, the functional research of disease resistance genes, and the research progress of disease resistance breeding technology in recent years are reviewed. In terms of disease resistance genes, NBS-LRR genes (such as RGA2 and MaRGC10) activate immune responses by recognizing pathogenic effector proteins, and significantly improve resistance to TR4 and black leaf spot. The signaling regulatory gene NPR1 balances disease resistance and growth by coordinating the salicylic acid (SA) and jasmonic acid (JA) signaling pathways. Physical barrier-related genes (e.g., cytochrome P450, CesA) limit pathogen invasion by strengthening the stratum corneum and cell wall structure. Among the disease resistance breeding technologies, traditional hybridization combined with phenomics accelerated the breeding of TR4-resistant varieties, molecular marker-assisted selection (MAS) and transgenic technologies (such as RNAi and antifungal protein genes) improved the accuracy of target traits, while CRISPR/Cas9 gene editing technology achieved broad-spectrum resistance by knocking out susceptible genes or regulating immune pathways. Despite the remarkable progress in research, banana disease resistance breeding still faces multiple challenges: the genetic variation of TR4 may weaken the efficacy of existing resistance genes, and adaptive disease resistance strategies need to be designed through multi-gene superposition or dynamic monitoring of pathogenic effector variants; Bananas are often co-infected by a variety of pathogens, and it is necessary to analyze the interaction mechanism of different disease resistance signaling pathways in the future, and develop multi-resistant varieties with antifungal, antiviral and stress resistance. Finally, the overexpression of disease resistance genes may affect the yield and quality of bananas, and it is necessary to use tissue-specific promoters or conditional expression systems to finely regulate the temporal and temporal expression of resistance genes.

References

[1] Alzate Acevedo, S., Díaz Carrillo Á, J., Flórez-López, E., & Grande-Tovar, C. D. (2021). Recovery of Banana Waste-Loss from Production and Processing: A Contribution to a Circular Economy. Molecules, 26(17). https://doi.org/10.3390/molecules26175282

[2] Amir, M., Dar, M. A., Wahiduzzaman, Islam, A., Ahmad, F., & Imtaiyaz Hassan, M. (2016). Purification and characterization of RGA2, a Rho2 GTPase-activating protein from Tinospora cordifolia. 3 Biotech, 6(1), 85. https://doi.org/10.1007/s13205-016-0400-3

[3] Bebber, D. P. (2019). Climate change effects on Black Sigatoka disease of banana. Philos Trans R Soc Lond B Biol Sci, 374(1775), 20180269. https://doi.org/10.1098/rstb.2018.0269

[4] Beisson, F., Li-Beisson, Y., & Pollard, M. (2012). Solving the puzzles of cutin and suberin polymer biosynthesis. Curr Opin Plant Biol, 15(3), 329-337. https://doi.org/10.1016/j.pbi.2012.03.003

[5] Bragard, C., Baptista, P., Chatzivassiliou, E., Di Serio, F., Gonthier, P., Jaques Miret, J. A., Justesen, A. F., MacLeod, A., Magnusson, C. S., Milonas, P., Navas-Cortes, J. A., Parnell, S., Potting, R., Stefani, E., Thulke, H. H., Van der Werf, W., Civera, A. V., Yuen, J., Zappalà, L.,…Reignault, P. L. (2022). Pest categorisation of Fusarium oxysporum f. sp. cubense Tropical Race 4. Efsa j, 20(1), e07092. https://doi.org/10.2903/j.efsa.2022.7092

[6] Castillo, A. G., Puig, C. G., & Cumagun, C. J. R. (2019). Non-Synergistic Effect of Trichoderma harzianum and Glomus spp. in Reducing Infection of Fusarium Wilt in Banana. Pathogens, 8(2). https://doi.org/10.3390/pathogens8020043

[7] Chen, A., Sun, J., Matthews, A., Armas-Egas, L., Chen, N., Hamill, S., Mintoff, S., Tran-Nguyen, L. T. T., Batley, J., & Aitken, E. A. B. (2019). Assessing Variations in Host Resistance to Fusarium oxysporum f sp. cubense Race 4 in Musa Species, With a Focus on the Subtropical Race 4. Front Microbiol, 10, 1062. https://doi.org/10.3389/fmicb.2019.01062

[8] Chong, P., Vichou, A. E., Schouten, H. J., Meijer, H. J. G., Arango Isaza, R. E., & Kema, G. H. J. (2019). Pfcyp51 exclusively determines reduced sensitivity to 14α-demethylase inhibitor fungicides in the banana black Sigatoka pathogen Pseudocercospora fijiensis. PLoS One, 14(10), e0223858. https://doi.org/10.1371/journal.pone.0223858

[9] DeYoung, B. J., & Innes, R. W. (2006). Plant NBS-LRR proteins in pathogen sensing and host defense. Nat Immunol, 7(12), 1243-1249. https://doi.org/10.1038/ni1410

[10] García-Bastidas, F. A., Arango-Isaza, R., Rodriguez-Cabal, H. A., Seidl, M. F., Cappadona, G., Segura, R., Salacinas, M., & Kema, G. H. J. (2022). Induced resistance to Fusarium wilt of banana caused by Tropical Race 4 in Cavendish cv Grand Naine bananas after challenging with avirulent Fusarium spp. PLoS One, 17(9), e0273335. https://doi.org/10.1371/journal.pone.0273335

[11] Hu, Z., Zhang, T., Rombaut, D., Decaestecker, W., Xing, A., D'Haeyer, S., Höfer, R., Vercauteren, I., Karimi, M., Jacobs, T., & De Veylder, L. (2019). Genome Editing-Based Engineering of CESA3 Dual Cellulose-Inhibitor-Resistant Plants. Plant Physiol, 180(2), 827-836. https://doi.org/10.1104/pp.18.01486

[12] Iskra-Caruana, M. L., Chabannes, M., Duroy, P. O., & Muller, E. (2014). A possible scenario for the evolution of Banana streak virus in banana. Virus Res, 186, 155-162. https://doi.org/10.1016/j.virusres.2014.01.005

[13] Janda, T., Szalai, G., & Pál, M. (2020). Salicylic Acid Signalling in Plants. Int J Mol Sci, 21(7). https://doi.org/10.3390/ijms21072655

[14] Jekayinoluwa, T., Tripathi, L., Tripathi, J. N., Ntui, V. O., Obiero, G., Muge, E., & Dale, J. (2020). RNAi technology for management of banana bunchy top disease. Food Energy Secur, 9(4), e247. https://doi.org/10.1002/fes3.247

[15] Kallenbach, M., Alagna, F., Baldwin, I. T., & Bonaventure, G. (2010). Nicotiana attenuata SIPK, WIPK, NPR1, and fatty acid-amino acid conjugates participate in the induction of jasmonic acid biosynthesis by affecting early enzymatic steps in the pathway. Plant Physiol, 152(1), 96-106. https://doi.org/10.1104/pp.109.149013

[16] Kilwenge, R., Adewopo, J., Manners, R., Mwizerwa, C., Kabirigi, M., Gaidashova, S., & Schut, M. (2023). Climate-Related Risk Modeling of Banana Xanthomonas Wilt Disease Incidence in the Cropland Area of Rwanda. Plant Dis, 107(7), 2017-2026. https://doi.org/10.1094/pdis-07-22-1672-re

[17] Lin, P., Dong, T., Chen, W., Zou, N., Chen, Y., Li, Y., Chen, K., Wang, M., & Liu, J. (2021). Expression Analysis of MaTGA8 Transcription Factor in Banana and Its Defence Functional Analysis by Overexpression in Arabidopsis. Int J Mol Sci, 22(17). https://doi.org/10.3390/ijms22179344

[18] Mbo Nkoulou, L. F., Ngalle, H. B., Cros, D., Adje, C. O. A., Fassinou, N. V. H., Bell, J., & Achigan-Dako, E. G. (2022). Perspective for genomic-enabled prediction against black sigatoka disease and drought stress in polyploid species. Front Plant Sci, 13, 953133. https://doi.org/10.3389/fpls.2022.953133

[19] Mejías Herrera, R., Hernández, Y., Magdama, F., Mostert, D., Bothma, S., Paredes Salgado, E. M., Terán, D., González, E., Angulo, R., Angel, L., Rodríguez, Y., Ortega, R., Viljoen, A., & Marys, E. E. D. (2023). First report of Fusarium wilt of Cavendish bananas caused by Fusarium oxysporum f. sp. cubense Tropical Race 4 in Venezuela. Plant Dis. https://doi.org/10.1094/pdis-04-23-0781-pdn

[20] Nakkeeran, S., Rajamanickam, S., Saravanan, R., Vanthana, M., & Soorianathasundaram, K. (2021). Bacterial endophytome-mediated resistance in banana for the management of Fusarium wilt. 3 Biotech, 11(6), 267. https://doi.org/10.1007/s13205-021-02833-5

[21] Noar, R. D., Thomas, E., & Daub, M. E. (2022). Genetic Characteristics and Metabolic Interactions between Pseudocercospora fijiensis and Banana: Progress toward Controlling Black Sigatoka. Plants (Basel), 11(7). https://doi.org/10.3390/plants11070948

[22] Ricciuti, E., Laboureau, N., Noumbissié, G., Chabannes, M., Sukhikh, N., Pooggin, M. M., & Iskra-Caruana, M. L. (2021). Extrachromosomal viral DNA produced by transcriptionally active endogenous viral elements in non-infected banana hybrids impedes quantitative PCR diagnostics of banana streak virus infections in banana hybrids. J Gen Virol, 102(11). https://doi.org/10.1099/jgv.0.001670

[23] Rocha, A. J., Soares, J., Nascimento, F. D. S., Santos, A. S., Amorim, V. B. O., Ferreira, C. F., Haddad, F., Santos-Serejo, J. A. D., & Amorim, E. P. (2021). Improvements in the Resistance of the Banana Species to Fusarium Wilt: A Systematic Review of Methods and Perspectives. J Fungi (Basel), 7(4). https://doi.org/10.3390/jof7040249

[24] Soares, J. M. S., Rocha, A. J., Nascimento, F. S., Santos, A. S., Miller, R. N. G., Ferreira, C. F., Haddad, F., Amorim, V. B. O., & Amorim, E. P. (2021). Genetic Improvement for Resistance to Black Sigatoka in Bananas: A Systematic Review. Front Plant Sci, 12, 657916. https://doi.org/10.3389/fpls.2021.657916

[25] Tripathi, L., Atkinson, H., Roderick, H., Kubiriba, J., & Tripathi, J. N. (2017). Genetically engineered bananas resistant to Xanthomonas wilt disease and nematodes. Food Energy Secur, 6(2), 37-47. https://doi.org/10.1002/fes3.101

[26] Venkataraman, S., Selvarajan, R., Subramanian, S. S., & Handanahalli, S. S. (2022). Insights into the capsid structure of banana bunchy top virus. 3 Biotech, 12(7), 144. https://doi.org/10.1007/s13205-022-03204-4

[27] Wang, Y., Myers, G., Yu, L., Deng, K., Balbin-Cuesta, G., Singh, S. A., Guan, Y., Khoriaty, R., & Engel, J. D. (2024). TR4 and BCL11A repress γ-globin transcription via independent mechanisms. Blood, 144(26), 2762-2772. https://doi.org/10.1182/blood.2024024599

[28] Waring, R. H. (2020). Cytochrome P450: genotype to phenotype. Xenobiotica, 50(1), 9-18. https://doi.org/10.1080/00498254.2019.1648911

[29] Wöhle, L., & Gebhard, M. (2020). SteadEye-Head-Improving MARG-Sensor Based Head Orientation Measurements Through Eye Tracking Data. Sensors (Basel), 20(10). https://doi.org/10.3390/s20102759

[30] Ximba, S. P. F., Tshabalala, J., Gubba, A., & Jooste, A. E. C. (2022). Monitoring the distribution of banana bunchy top virus in South Africa: a country-wide survey. Arch Virol, 167(6), 1433-1441. https://doi.org/10.1007/s00705-022-05451-5

[31] Ye, Y., Wang, S., Wu, K., Ren, Y., Jiang, H., Chen, J., Tao, L., Fu, X., Liu, B., & Wu, Y. (2021). A Semi-Dominant Mutation in OsCESA9 Improves Salt Tolerance and Favors Field Straw Decay Traits by Altering Cell Wall Properties in Rice. Rice (N Y), 14(1), 19. https://doi.org/10.1186/s12284-021-00457-0

[32] Zavaliev, R., Mohan, R., Chen, T., & Dong, X. (2020). Formation of NPR1 Condensates Promotes Cell Survival during the Plant Immune Response. Cell, 182(5), 1093-1108.e1018. https://doi.org/10.1016/j.cell.2020.07.016

[33] Zhan, N., Kuang, M., Li, C., Liu, S., Deng, G., Viljoen, A., Yi, G., & Sheng, O. (2022). First Report of Fusarium Wilt of Iholena Banana (Musa spp.) Caused by Fusarium oxysporum f. sp. cubense Tropical Race 4 in China. Plant Dis. https://doi.org/10.1094/pdis-11-21-2621-pdn