AGRI MAGAZINE
(International E-Magazine for Agricultural Articles)
Volume: 03, Issue: 02 (February, 2026)
Available online at http://www.agrimagazine.in
©Agri Magazine, ISSN: 3048-8656

Use of Genomics to Fight against Citrus Greening Disease

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Genomics is playing a transformative role in the fight against citrus greening disease, or Huanglongbing (HLB), one of the most destructive diseases threatening citrus production worldwide (Bové, 2006). By decoding the genetic makeup of citrus plants, the HLB-causing bacterium *Candidatus Liberibacter asiaticus*, and its insect vector, the Asian citrus psyllid, scientists are gaining critical insights into disease spread and host responses (Wang et al., 2017; Duan et al., 2009). Advanced genomic approaches such as pan-genome analysis have enabled the identification of resistance and tolerance genes in citrus and its wild relatives (Yu et al., 2022; Huang et al., 2021), while CRISPR-based gene editing is being explored to enhance plant defense pathways and disrupt pathogen infection processes (Zhang et al., 2023; Peng et al., 2020). Collectively, these genomics-driven strategies provide new hope for sustainable citrus cultivation and long-term protection of global citrus industries.

What is Citrus Greening?

Citrus greening disease, caused by the phloem-limited bacterium *Candidatus Liberibacter asiaticus* (CLas), disrupts the vascular system of citrus trees, blocking nutrient transport and ultimately leading to leaf drop, bitter and misshapen fruits, tree decline, and death (Bové, 2006; Gottwald, 2010). The disease was first detected in Florida in 2005 and has since devastated the U.S. citrus industry, reducing citrus production by more than 80 percent within two decades (Singerman and Rogers, 2020). Despite its economic and agricultural impact, no complete cure for citrus greening is currently available. However, advances in genomics are providing new opportunities to combat the disease by targeting its genetic foundations. Genomic studies are revealing how CLas survives and spreads within the host, how citrus plants respond at the molecular level, and how resistance or tolerance can be enhanced through modern breeding, gene editing, and other biotechnological approaches (Duan et al., 2009; Wang et al., 2017; Huang et al., 2021).

Key Genomic Strategies

Researchers are sequencing entire citrus genomes to construct comprehensive "pan-genomes" that enable comparisons among susceptible, tolerant, and resistant citrus varieties, including wild relatives such as Australian limes (*Microcitrus* spp.) (Huang et al., 2021; Yu et al., 2022). This comparative genomic approach has been instrumental in identifying key immune-related genes, particularly nucleotide-binding site–leucine-rich repeat (NBS-LRR) proteins, which play a crucial role in pathogen recognition and defense against *Candidatus Liberibacter asiaticus* infection (Wang et al., 2017; Rawat et al., 2015). In parallel, genome-wide association studies (GWAS) have successfully pinpointed genetic variants and loci associated with HLB tolerance in wild and non-commercial citrus species, offering valuable molecular targets for genomics-assisted breeding and biotechnological interventions aimed at developing more resilient citrus cultivars (Yu et al., 2022; Huang et al., 2023).

CRISPR: Precision Editing: CRISPR/Cas9 gene-editing technology is increasingly being used to precisely modify citrus genes associated with disease susceptibility and immune defense, thereby interfering with *Candidatus Liberibacter asiaticus* infection without the introduction of foreign DNA (Peng et al., 2020; Zhang et al., 2023). By knocking out susceptibility-related genes or enhancing immune-responsive pathways, researchers have successfully developed non-transgenic citrus plants exhibiting improved resistance to Huanglongbing (HLB). Recent studies have also demonstrated multiplex gene editing, in which multiple target genes are edited simultaneously to reinforce plant defenses against oxidative stress and pathogen effector proteins (Jia et al., 2022; Huang et al., 2023). Notably, large-scale field evaluations conducted in Florida, involving more than 120 CRISPR-edited citrus trees, have reported the absence of visible HLB symptoms even after pathogen exposure, underscoring the strong potential of gene-editing technologies as durable and long-term solutions for citrus greening management (Dutt et al., 2024).

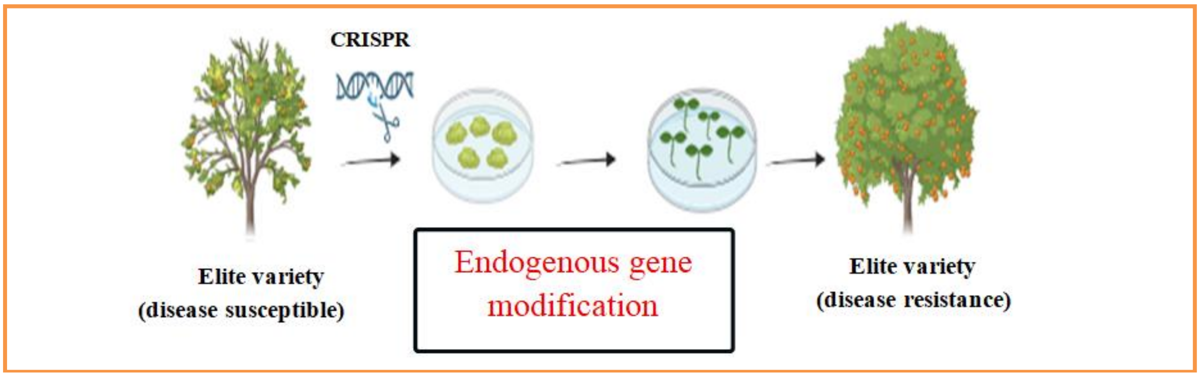

Fig 1: Disease resistance was developed through CRISPR-Cas9 mediated gene editing

Bt Gene Innovation: Scientists at the University of Florida are also investigating transgenic strategies to manage citrus greening by introducing genes from *Bacillus thuringiensis* (Bt) into citrus plants (Dutt et al., 2015; Killiny et al., 2021). These Bt genes enable citrus trees to express insecticidal proteins directly in the phloem tissue, the primary feeding site of the Asian citrus psyllid. Consequently, juvenile psyllids ingest the toxin during feeding and are killed before they can mature and transmit *Candidatus Liberibacter asiaticus*. Laboratory and greenhouse studies have demonstrated near-complete mortality of early instar psyllids, effectively suppressing population growth and interrupting disease transmission (Dutt et al., 2016; Hall et al., 2020). Field trials are anticipated in the near future, and this approach holds strong promise for reducing dependence on chemical insecticides while contributing to sustainable management of citrus greening disease.

Promising Results

Wild citrus relatives such as Australian limes (*Microcitrus* spp.), along with HLB-tolerant hybrids like ‘Sugar Belle,’ are emerging as valuable sources of natural resistance genes that are now being exploited through genomics-assisted breeding programs (Albrecht et al., 2017; Huang et al., 2021). By identifying, introgressing, or enhancing these resistance-associated traits in commercial citrus backgrounds, researchers are developing trees capable of surviving longer and maintaining productivity under sustained HLB pressure (Ramadugu et al., 2016; Yu et al., 2022). In parallel, genomically improved and gene-edited citrus varieties are undergoing large-scale field evaluations across multiple locations, with several research programs accelerating progress toward commercial deployment by 2025 (Dutt et al., 2024; Zhang et al., 2023). Collectively, these advances represent a major turning point in HLB management, offering realistic hope for revitalizing citrus industries and ensuring long-term global citrus production.

Conclusion

Citrus greening disease has long been viewed as an unstoppable threat to the global citrus industry, but genomics is rapidly changing that narrative. By uncovering the genetic interactions between citrus plants, the HLB pathogen, and its insect vector, scientists are moving beyond symptom management toward true, long-term solutions. From genomics-assisted breeding and CRISPR-based gene editing to innovative vector control strategies, these advances are reshaping how citrus greening is understood and managed. While challenges remain, the integration of genomics into citrus research marks a decisive shift from crisis response to prevention and resilience. With continued research, responsible field testing, and farmer adoption, genomics-driven innovations have the potential to restore productivity, reduce chemical dependence, and secure a sustainable future for citrus cultivation worldwide.

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