



Genomics Enabled Surveillance for Emerging Plant Pathogens

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Emerging and re-emerging plant pathogens are intensifying risks to crop productivity and food security. Climate variability, expanded trade and movement of planting materials, changing vector ecology, and high-density monoculture systems collectively accelerate the introduction, establishment, and adaptation of pathogens. As a result, outbreaks are increasingly characterized by rapid spread, mixed infections, and faster erosion of host resistance and chemical efficacy. This shifting landscape demands a transition from reactive disease control to preparedness built on rapid detection, precise pathogen identification, and durability-focused breeding.

A central limitation in plant health management is the delay between initial infection and actionable diagnosis. Conventional symptom-based scouting and culture-based identification remain valuable, but they often arrive after the epidemic has gained momentum. Current diagnostic trends emphasize speed and specificity through molecular workflows that enable earlier confirmation and improved discrimination among closely related taxa. In parallel, sequencing-informed approaches, such as metabarcoding and metagenomics, strengthen our capacity to detect unexpected pathogens and resolve complex disease syndromes, particularly when classical assays fail due to pathogen novelty or mixed microbial backgrounds.

Importantly, identification is no longer restricted to naming the species. For many pathosystems, management and resistance outcomes are determined by population structure, pathotypes, effector repertoires, and fungicide resistance alleles. Pathogen

population genomics and pangenome frameworks are therefore emerging as essential tools for risk assessment supporting lineage tracking, introduction inference, and prediction of resistance breakdown. When integrated into regional surveillance, genomics shifts diagnostics from case confirmation to epidemiological intelligence.

Breeding remains the most sustainable route to disease control; however, emerging pathogens highlight the fragility of single-gene major solutions under strong selection pressure. Durable resistance strategies are increasingly prioritized, including pyramiding of resistance genes, deployment of quantitative resistance loci, and integration of pathogen-informed selection. Accelerated breeding platforms-assisted selection, genomic prediction, and speed breeding can shorten release cycles, but long-term success depends on aligning resistance deployment with evolving pathogen populations rather than relying on static resistance sources.

Artificial intelligence is contributing as an integrative layer across detection and breeding. Machine learning models can support the early detection of stress and disease from imaging and sensor data, prioritize sampling for confirmatory diagnostics, and enhance the prediction of resistance performance across environments when combined with genomic and phenotypic datasets. However, broad adoption requires rigorous field validation, clear reporting of uncertainties, and explainability to ensure that model outputs translate into reliable decisions for breeders, agronomists, and growers. Key bottlenecks include the harmonization of phenotyping and metadata standards, limited surveillance coverage in many

regions, and weak interoperability between diagnostic outputs and breeding pipelines. Addressing these gaps will require coordinated surveillance networks, standardized reporting frameworks, and sustained collaboration among plant pathologists, breeders, bioinformaticians, and extension systems.

In summary, the emerging pathogen era necessitates integrated plant health systems centered on rapid detection, population-aware identification, and durable resistance breeding. Establishing these linkages, diagnostics to surveillance, surveillance to breeding, and breeding to deployment, will be essential for resilient crop production under accelerating biological and climatic change.