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MOLECULAR DETECTION, GENETIC DIVERSITY, AND INTEGRATED MANAGEMENT OF VIRAL DISEASES AFFECTING TOMATO CROPS

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Abstract. Tomato (Solanum lycopersicum L.) is one of the most economically important vegetable crops worldwide. Viral diseases represent a significant constraint to tomato production because they can cause severe reductions in plant growth, fruit quality, and yield. The identification and monitoring of viral pathogens are therefore essential for developing effective disease-management strategies. Traditional methods of virus diagnosis based mainly on symptom observation are often insufficient because different viruses can produce similar symptoms, while environmental conditions may influence symptom development. Molecular diagnostic techniques, including reverse transcription polymerase chain reaction (RT-PCR), quantitative PCR, and sequencing-based approaches, provide more reliable tools for the detection and identification of tomato viruses.

This study discusses the molecular detection, genetic diversity, and phylogenetic characterization of important viruses associated with tomato production. Molecular approaches can be used to determine the genetic relationships among virus isolates and to identify potentially emerging or genetically distinct variants. Phylogenetic analysis based on viral genomic sequences provides valuable information about the evolutionary relationships and geographical distribution of viral populations. In addition, integrated disease management, including the use of healthy planting material, resistant or tolerant cultivars, vector management, sanitation, and regular molecular monitoring, can reduce the spread and economic impact of viral diseases. The combination of molecular diagnostics, genetic analysis, and integrated management represents a promising approach for sustainable tomato production.

Keywords:tomato, plant viruses, molecular detection, RT-PCR, genetic diversity, phylogenetic analysis, disease management, Solanum lycopersicum.

Introduction. Tomato is an important vegetable crop cultivated in many regions under open-field and protected production systems. Its high nutritional and economic value makes the crop an important component of agricultural production. However, tomato cultivation is affected by numerous biotic stresses, among which viral diseases are particularly difficult to manage.

Tomato plants infected with viruses may exhibit symptoms such as mosaic patterns, chlorosis, leaf deformation, necrotic lesions, stunting, curling, and abnormal fruit development. In some cases, infected plants may remain asymptomatic during the early stages of infection, making visual diagnosis unreliable. Furthermore, mixed infections involving two or more viruses can produce complex symptoms and complicate pathogen identification.

Molecular diagnostic methods provide an opportunity to overcome many limitations of conventional disease diagnosis. Detection of viral nucleic acids through PCR- and sequencing-based techniques can confirm infection even when symptoms are weak or absent

The objective of this study is to review the application of molecular methods for detecting tomato viruses, evaluate the importance of genetic and phylogenetic analyses, and discuss approaches for improving the integrated management of viral diseases in tomato production.

Materials and methods. For molecular identification of tomato viruses, symptomatic and apparently healthy tomato leaf samples can be collected from different production areas. Samples should be appropriately labelled and transported under conditions that preserve the integrity of viral nucleic acids.

Total RNA or DNA can be extracted from plant tissues using commercial extraction kits or validated laboratory protocols, depending on the target virus. For RNA viruses, complementary DNA (cDNA) can be synthesized using reverse transcriptase. Specific primers targeting conserved genomic regions of the suspected viruses can then be used for PCR or RT-PCR amplification.

The resulting amplification products can be visualized by agarose gel electrophoresis. Positive samples can subsequently be subjected to nucleotide sequencing. Obtained sequences can be compared with publicly available sequences using nucleotide-sequence databases. Multiple sequence alignment can be performed to identify conserved and variable regions.

Phylogenetic relationships among virus isolates can be reconstructed using appropriate phylogenetic methods, such as Neighbor-Joining, Maximum Likelihood, or Bayesian approaches. Statistical support for individual branches can be evaluated using bootstrap analysis or other appropriate methods.

Molecular identification of tomato viruses. Molecular identification is particularly important because symptoms caused by different tomato viruses can be very similar. RT-PCR is one of the commonly used techniques for detecting RNA viruses, while PCR can be applied to DNA viruses.

The selection of appropriate primers is an important component of molecular diagnostics. Primers designed against conserved genomic regions can provide broad detection, whereas primers targeting variable regions may be useful for differentiating closely related virus isolates.

Sequencing of PCR products provides additional confirmation of virus identity. Compared with symptom-based diagnosis, sequence information can provide direct evidence of the genetic identity of a pathogen. High-throughput sequencing can also be useful when the causative virus is unknown or when mixed infections are suspected.

Genetic Diversity and Phylogenetic Analysis. Viral populations can contain considerable genetic variation. Mutation, recombination, selection pressure, and movement of infected plant material may contribute to the emergence and distribution of genetically different virus isolates.

Phylogenetic analysis enables researchers to determine the evolutionary relationships among isolates collected from different geographical regions. Closely related isolates may form distinct phylogenetic groups, while genetically divergent isolates may indicate independent evolutionary histories or the introduction of viruses from different sources.

The analysis of nucleotide sequences can therefore provide information that is useful not only for taxonomy but also for epidemiological studies. Monitoring genetic variation is particularly important because newly emerging variants may possess altered biological characteristics, including differences in host range, transmissibility, or resistance to control measures.

Integrated Management of Tomato Viral Diseases. There is generally no single control method that can completely eliminate viral diseases from tomato production systems. Therefore, an integrated approach should be adopted.

The production and use of virus-free or pathogen-tested planting material is one of the most important preventive measures. Resistant or tolerant tomato cultivars should also be incorporated into disease-management programs whenever suitable varieties are available.

Vector management is another critical component. Depending on the virus, insect vectors such as aphids, whiteflies, or thrips may contribute to disease transmission. Monitoring vector

populations and implementing appropriate integrated pest-management practices can reduce the probability of virus spread.

Field sanitation is also essential. Infected plants and crop residues can serve as sources of inoculum. Removal of infected plants, control of alternative hosts and weeds, disinfection of tools, and proper management of crop residues can help reduce pathogen pressure.

Regular molecular monitoring should complement conventional field inspection. Early detection of viral pathogens can facilitate rapid implementation of control measures and prevent the establishment and spread of economically important virus populations.

Improvement of disease-control strategies. Future disease-management programs should integrate molecular diagnostics with epidemiological monitoring. Establishing systematic surveillance programs would allow researchers to identify the most common viruses and monitor changes in their genetic composition.

The development of rapid and sensitive diagnostic assays could improve early detection at both laboratory and production levels. Portable molecular diagnostic technologies may eventually allow some pathogens to be detected directly in the field.

Breeding programs should also consider information obtained from molecular and phylogenetic studies. Identification of genetically diverse virus populations can help researchers evaluate whether available resistant cultivars are likely to remain effective against locally circulating isolates.

An integrated strategy combining resistant cultivars, healthy planting material, vector management, sanitation, molecular surveillance, and farmer education is likely to provide more sustainable protection than reliance on a single control method.

Conclusion. Tomato viral diseases are among the most important biological factors limiting the productivity, quality, and sustainability of tomato production worldwide. The increasing diversity of viruses, their rapid genetic variability, the occurrence of mixed infections, and the involvement of different insect vectors make the diagnosis and management of viral diseases increasingly complex. Therefore, effective protection of tomato crops requires the integration of modern molecular diagnostic methods, genetic and phylogenetic analysis, and environmentally sustainable disease-management strategies.

Molecular identification plays a fundamental role in the accurate detection of tomato viruses. Conventional symptom-based diagnosis is often insufficient because different viral pathogens can cause similar symptoms, while the severity and appearance of symptoms may vary depending on tomato cultivar, environmental conditions, plant age, and the presence of mixed infections. Techniques such as PCR, RT-PCR, real-time PCR, and nucleotide sequencing provide more sensitive and specific methods for detecting viral pathogens. These approaches allow viruses to be identified at an early stage of infection and can also detect pathogens in plants that show weak or no visible symptoms.

Phylogenetic analysis is an important complementary approach for understanding the genetic diversity and evolutionary relationships of tomato viruses. Analysis of nucleotide sequences obtained from different geographical regions makes it possible to compare virus isolates, identify genetically distinct groups, and monitor the emergence and spread of new variants. Such information is valuable for epidemiological studies and can contribute to the development of appropriate diagnostic assays and disease-control programs. Continuous monitoring of viral genetic diversity is particularly important because genetically different isolates may vary in their pathogenicity, host range, transmission efficiency, and interaction with resistant tomato cultivars.

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