

Identification of Genetic Diversity of Cucumber Mosaic Virus in Pepper Fields in Şanlıurfa, Turkey

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Aim of the Study: Understanding genetic structures of virus populations with their genetic diversities and their evolutionary mechanisms is an important aspect of controlling viral diseases. Cucumber mosaic virus (CMV) is common in most pepper fields in Turkey. CMV infections have been frequently reported from Turkey on different plant families showing mild to severe symptoms. Genetically CMV may be divided into two major subgroups, I and II, based on genetic diversities on some sequence structure, and subgroup I can be further divided into subgroups IA and IB. The aim of this study is to determine the genetic diversity of CMV in pepper fields in the Şanlıurfa province.

Material and Methods: In 2013-2014, surveys were performed in 36 different pepper fields in Şanlıurfa. Leaf samples showing virus-like symptoms were taken from pepper plants and placed in polyethylene bags and stored at -20 °C until use. DAS-ELISA test was used first to identify viruses. CMV-positive samples were then tested by RT-PCR according to two different CMV-specific gene region (RNA1 and RNA2). The PCR product fragments were digested by *Mlu*I endonuclease restriction enzyme. The bands observed on agarose gel after restriction fragment length polymorphism assay (RFLP).

Results: In this study, the presence of CMV virus in field grown pepper plants was determined by DAS-ELISA and RT-PCR methods. The PCR products of the RNA1 and RNA2 gene regions were not cut by the *Mlu*I enzyme in RFLP process. This indicates that all of the tested pepper plants infected with CMV virus subgroup IA. The result of the study is consistency with previous studies carried out in the region however with this study subgroup-based diagnosis was made. CMV is transmitted by aphids from infected plants to healthy plants. The detection of genetically the same CMV strain from different regions suggests that the pathogen-vector-host relationship is preserved.

Keywords: Genetic diversity, CMV, RNA1, RNA2, Subgroup IA, RT-PCR.