DESCRIPTION FOR THE GENERAL PUBLIC (IN ENGLISH)

The role of the genetic diversity of 3′-UTR of RNA1 in processes of transmission and replication of tomato torrado virus

Tomato torrado virus belongs to *Torradovirus* genus in *the Secoviridae* family. ToTV infects Solanaceae plants, mainly tomatoes, causing considerable losses in their production. The typical symptom of ToTV disease constitute necrosis beginning at the base of leaves that develop to whole plants leading to its death. The virus is transmitted by whiteflies *Trialeurodes vaporariorum*, *T. abutilonea* and *Bemisia tabaci*.

Up to now ToTV has been identified in Europe, America, Australia and Africa. In Poland, so far, three isolates Kra, Wal'03 and Ros ToTV have been reported, that on the basis of greenhouse observations differ in the symptoms expression on infected plants. The comparative sequence analyses showed very high similarity within the coding regions of known ToTV isolates, simultaneously indicating very high genetic diversity in the untranslated region localized at the 3′-end of RNA1 strand. The observed genetic diversity resulted from the insertion/deletion mutations encompassing 6 to 163 nucleotides. These mutations have been observed not only between isolates, but also within the population of the same isolate. Additionally the unique organization of this region was observed, indicating the variable region (VR), conserved region (CR) as well the presence of characteristic direct repeats (DR). The discovery of such heterogeneity in ToTV genome is thought to be an atypical phenomenon among known plants viruses. In the light of these data this project is focused on the explanation of the importance and the role of identified genetic variability within discussed region. The viral 3′-UTR regions are thought to contain the signal sequences regulating the virus replication, gene expression, translation, and RNA stability. Moreover, in some cases (e.g. among human viruses) it was proved that the presence of DRs is essential for replication as well virus transmission by the vector. Despite the fact that the origin of pool of genetic variants of 3′-UTR RNA1 strand of Polish ToTV isolates remain still unknown, it was hypothesized that their presence may be an effect of virus adaptation to the environment depending on the presence or lack of the vector – greenhouse whitefly. On the other hand the heterogeneity may be crucial for the regulation of the replication process, affecting the virus accumulation in host plant cells, thus modulating (exacerbation / attenuation) of the infection symptoms. So far, the mechanism of the replication process has not been an object of the studies for any torradovirus species, hence the viral and host factors taking part in this process and involved in host-virus interactions remain also unknown. Therefore the main purpose of this project is analysis of the impact of the identified variability in analyzed region on the replication rate of particular genetic variants. The approach to indicate dominant 3′-UTR mutated sequence among the pool od deletion variants, in relation to the way of transmission will be undertaken. It is also planned to indicate the deletion variant that accumulates at the highest level during the viral transmission by vector or transmitted mechanically. In consequence the analysis of 3′-UTR variant of RNA1 that is preferably acquired by whiteflies during feeding on the ToTV infected plants, and then subsequently transmitted to the healthy plant hosts will be also carried out. Additional aim is the identification of plant host factors interacting with viral RNA polymerase (RdRp) that are important in the formation of the replication complex, in relation to the type of genetic variant of 3'-UTR RNA1 present in infected cells.

We hope that results of this project will explain the significance of genetic variability within regulatory region of RNA1 in the ToTV epidemiology, expanding the knowledge of plant viruses, primarily *Tomato torrado virus* species, as well as torradoviruses.