

Plant viruses are distributed worldwide, infecting economically important and ornamental plant species. The viral infection often results in yield and quality losses. Viral diseases cannot be directly controlled by chemical application on infected plants. Therefore, control strategies are based on the use of certified virus-free plant material, eradication of diseased plants and control of vectors populations. The virus infection can be accompanied by additional, defective RNA particles (D RNAs) which can be derived from parental virus genomes through rearrangements, deletions, or recombination events. D RNAs can modulate helper virus accumulation and symptoms observed on infected plants, often weakening them, or even completely eliminating them (defective interfering RNAs, DI RNAs). This unique feature makes them a potential innovative tool to protect plants against viruses. Therefore, it is extremely important to expand the knowledge about DI RNAs formation and their influence on virus replication in plants. The goal of the following project is to examine the role of specific sequence regions/motifs in *Tomato black ring virus* (TBRV) genome and the impact of between-host transmission on DI RNAs formation. TBRV infects a wide range of economically important plants (potatoes, tomatoes, artichokes) as well as ornamental plants and trees. Previous studies conducted in the Institute of Plant Protection – National Research Institute have demonstrated that several TBRV isolates are capable of DI RNAs formation *de novo* during extended passages in one host. Moreover, these particles interfere drastically with virus accumulation and attenuate the disease phenotype elicited by the helper virus. The two types of DI RNAs were described and comparison of DI RNA and helper virus nucleotide sequences revealed the motifs/regions potentially involved in the generation of additional RNA particles.

The goal of the following project is to investigate the role of specific regions/motifs in the TBRV genome in the formation of DI RNAs. Therefore, the particular mutations in these sequences/motifs will be introduced and the effect of the changes of DI RNAs generation will be verified. Moreover, the impact of between-host transmission (host-jumping) on DI RNAs generation will be investigated. The previous studies revealed that DI RNAs are formed as a result of serial passages in the same host. Hence, the question is: whether the between-host transmission will force the induction or rather will stop the process of DI RNAs generation? The research will be performed in the context of analysis of DI RNAs formation and their influence on virus accumulation.

The realization of the following project will allow to expand the knowledge about the impact of specific regions/motifs in the TBRV genome as well as between-host transmission on the formation, structure and properties of DI RNAs. It will be also a step towards development of new, innovative tools to protect plants against viruses. Results of this research will be disseminated through presentations at relevant scientific meetings and published in international journals within the fields of phytopathology, virology, and evolutionary biology.