

The characteristic future of many of plant viruses is a high level of genetic variability, which determines their evolutionary success. The factors responsible for diversity of viral populations are point mutations and recombination. Characterization of the genetic variation of viral populations provides relevant information on the processes involved in virus evolution and epidemiology and it is crucial for designing reliable diagnostic tools and developing efficient and durable disease control strategies. The range of genetic variability of RNA viruses often correlates with the amount of infected species and can be greater if more species may be a potential host of the virus. Spread from the reservoirs into a new environment and establishing productive infections and effective between-host transmission mechanism are steps require for emergence to occur. One of the viruses which infect a wide range of economically important plants worldwide is *Tomato black ring virus* (TBRV). For multihost pathogens, adaptation to multiple hosts has important implications as it is one of the main factors determining the probability and the severity of emerging disease outbreaks. The goal of the following project is to analyze evolution of TBRV and its ability to adapt to different hosts. The virus is spread worldwide and infects many crops, ornamentals and perennial plants belonging to different botanical families. However, little is known about its variability, evolutionary dynamics and rate of replication. Moreover, only a limited number of complete TBRV genomes have been sequenced. Obtaining knowledge on virus evolvability to adapt to a new host and on the factors that favor or constrain host adaptation is one of the most important tasks of efficient plant protection. We planned to analyze the structure and level of diversity of virus population within the country and from other geographical regions. This will allow us to trace the phylogenetic relationships between isolates acquired from different locations and hosts, variability and dynamics of the virus. These studies will also enable the analysis of the virus population of perennial and annual plants. In the case of perennial crops, the virus species inhabited their hosts for several years in relatively stable environmental conditions. This could favor such a course of evolution, which would lead to produce a stable virus-host system enabling the long existence of both partners. Such plants can also serve as a reservoir for the virus. The situation is different in the case of annual plants, where intensive multiplication of the virus would give more evolutionary advantage. The full-length genome sequences of isolates collected from the hosts representing different families: tomato, marigold and black locust will be obtained. The sequences will be compared with other described to date. This will allow predicting conserved and variable regions in the genome TBRV and analysis of mutations. The potential recombination events will be also analyzed. This knowledge is crucial to design efficient and fast methods for virus detection and control. For a deeper insight into the interactions between TBRV and its hosts, infectious cDNA clones will be constructed. The fast evolution and small genomes of RNA viruses make them excellent models for experimental evolution. Different TBRV isolates will be subjected to multiple passages in a variety of hosts. The symptoms and structure of created viral population will be compared with the initial ones. It will allow to gain knowledge on the ability of the virus to adapt to specific host plants. In addition the presence of additional particles in the viral genome called defective RNAs that may affect the type of disease symptoms on plants will be verified. The planned research will broaden our understanding of the evolution and epidemiology of the virus. 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. The participation and scholarship for the student has been planned in the project and research will be carried out as part of a master of sciences thesis.