

Cucurbits are among the most cultivated vegetables worldwide, and their global production is estimated at approx. 151 million tons. The incidence of viral diseases and the damage caused to economically important crops are increasing every day. More than 70 virus species belonging to the major plant virus genera are now described as infecting cultivated cucurbits in nature. Viruses infecting cucurbit crops are efficiently transmitted by aphids. In recent years, the increasing occurrence of various aphid species has been noticed, many of which can very effectively transmit viruses over long distances. This phenomenon is significantly influenced by climatic changes, which affect the dynamics and structure of the aphid population and their life cycle. Changes in insect vector populations that might result from climate change (geographical distribution range, densities, migration potential, and phenology) could affect the spread of plant viruses. Zucchini (*Cucurbita pepo* var. *giromontiina*) is one of the major cultivated cucurbit species in Poland and, over the last few years, several severe outbreaks of different viruses have been reported, leading to losses of approx. 95%. To make the situation more dramatic, in the fields, plants are commonly infected by more than one virus (mixed infections), thereby leading to synergistic combinations that result in the development of very severe symptoms on infected plants and their fruits, which do not possess market and consumable value. Whatsoever, the research conducted by our team has allowed us to detect new viral species, not previously recorded in our country. One of the most important challenges and tasks of efficient plant protection is the early detection and identification of plant pathogens in order to prevent the further spreading of the disease. Moreover, the characterization of the genetic variation of viral populations provides key 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 aim of this project is to carry out the comprehensive analysis of: (i) the incidence, distribution, and population structure of viruses infecting zucchini and their aphid vectors (ii) the occurrence of viruses in wild plants and weeds on and in the neighbourhood of cultivated fields that can act as alternative hosts and virus reservoirs; (iii) the frequency and effect of mixed infections both on symptoms severity, virus accumulation and the dynamics of virus evolution; (iv) the genetic diversity of watermelon mosaic virus (WMV) as one of the most prevalent viruses infecting cucurbit crops in Poland. We will also try to analyse factors that contribute virus emergence including climate change and local host diversity. Moreover, we are going to identify and highlight the network of ecological interactions that are expected from co-infection and compare it to a baseline of single infection only. These analyses will contribute to the understanding of the community structure of viruses in the agroecological landscape. The research planned in the project will be conducted using the most modern molecular biology techniques, including high throughput sequencing (HTS) which will enable the detection of various virus species in plant material and in the aphids. HTS technologies allow for *de novo* virus identification and do not require any prior knowledge on the targeted pathogens. Studies on the genetic diversity of WMV populations will be carried out using the WMV isolates collected by our research team in previous years (95 isolates), sequences obtained during the proposed project and those available in GenBank. The evolutionary analysis will be performed using bioinformatic tools that allow for establishing the phylogenetic relationships among isolates, the occurrence of recombination events, and the correlation between the genetic diversity and geographical distribution and host species. With this data, we will be able to shed light on the epidemiological and evolutionary dynamics of WMV in Poland and worldwide, especially considering the growing distribution of plant material across the globe. In this project, we are going to analyze the occurrence of mixed infections in zucchini and wild plants and their impact on symptoms severity and virus accumulation especially since numerous synergistic interactions have been described resulting in an enhancement of disease symptoms. The presence and occurrence of recombinant viral variants that can be created during mixed infections will be also analyzed using bioinformatic softwares. Understanding the role of genetic diversity in controlling the patterns of pathogen emergence and the impact in nature has the potential to provide new insights into crop management. The realization of this project will be an important step into expanding knowledge about the host-vector-pathogen-interactions and analyzing the factors that affect the virus emergence. The predictive models developed during this project will highlight key risk factors for virus outbreaks and crop damage. This knowledge is crucial in developing plant protection strategies against these pathogens. The project will be performed in the framework of international cooperation with scientists from the Netherlands and Spain that have vast experience in ecology, epidemiology and evolution of viruses. A student will be hired as a scholar within the project, and his/her contribution will be a part of an MS thesis. The results on the distribution of the viruses and aphids will be posted on the Agrophage Signaling Platform (<https://www.agrofagi.com.pl/>), which allows for monitoring the occurrence of threats in crops. Systematic monitoring of pests is a very important element of Integrated Pest Management.