

## „Studies on *Ribes* plants, *Cecidophyopsis* mites and Blackcurrant Reversion virus for sustainable resistance breeding and cultivation of *Ribes*”

1.1.1.1/18/A/026

### Progress of the project (01.03.2021. – 31.05.2021.)

Within **Activity No.1**, the morphometric data analysis was continued. Phylogenetic analyses of ITS/5.8S/28S and COX1 sequences was started. In parallel, the literature studies were performed for possibilities to include morphological parameters of mite genitalia for species discrimination. It was concluded that these parameters are more suitable for delineation among the genera rather than the species; therefore, studies on this aspect were not continued.

To obtain samples for sequencing, all previously detected BRV positive samples were retested with BRV coat protein-specific primers. For sequencing, samples from redcurrants, blackcurrants, alpine currants, golden currants, gooseberry and their hybrids were chosen. Overall, 26 samples were sequenced at BMC on a genetic analyzer ABI PRISM 3130xl. Obtained BRV sequences covered BRV coat protein gene from position 3480 nt - 3643 nt (based on GenBank reference sequence AF020051).

Within **Activity No.2** the corrections according to the reviewer's comments were made in the review article on resistance of *Ribes* to *Cecidophyopsis* and BRV, and their interactions, and the manuscript was resubmitted to *Annals of Applied Biology*.

The work was completed on the study on genotyping analysis of *Ribes* genetic resources using SSR markers, paper “Evaluation of blackcurrant (*Ribes nigrum*) germplasm structure by microsatellite-based fingerprinting for the diversification of the breeding material” (authors: Gunārs Lācis, Katrīna Kārklīņa, Irita Kota-Dombrovska, Sarmīte Strautiņa) has been accepted for publication in the “*Journal of Berry Research*” (<https://www.iospress.nl/journal/journal-of-berry-research/>). Work was continued on the analysis of genotyping data of chloroplast molecular markers (cpSSR) of *Ribes* plant material, development of a resistance gene *P* identification method and analysis and processing of NGS data. Work has begun on the isolation of total RNA from infested and control samples of blackcurrants (cultivar “Mara Eglite”) harvested in August 2019 and stored at -80°C. The complete genome sequence of Black currant-associated rhabdovirus 1 (BCaRV) isolate Māra Eglite was inserted into the European Nucleotide Archive database under accession number OU015520-OU015520. The prepared manuscript of the article “First report of black currant-associated rhabdovirus 1 in blackcurrants in Latvia” has been submitted to the journal “*Plant Disease*”.

The work was continued for PCR amplification of TEF 1- $\alpha$ , and HSP70 genes and their possible use for establishment of diagnostic method for *Cecidophyopsis* species on *Ribes* hosts. Evaluation of COX1 sequences for design of species specific primers for diagnostic purposes was continued.

For the improvement of resistance evaluation method, various *Ribes* genotypes were evaluated in the field by counting of invaded and no-invaded buds of each plant in the experimental plot. New experiment was set up to study possibility of mites invade different groups of *Ribes* using in-vitro propagated plants and mites from different *Ribes* groups for invasion.

The evaluation of *Ribe's* genetic resources field collections was continued, describing genotypes according to RIBESCO descriptors. The third year data set on plant phenological and vegetative development, flowering, frost resistance was collected. The collection in Pūre was assessed for the prevalence and symptoms of BRV. A report on the resistance of

blackcurrant cultivars to gall mites was provided at the information day "Spring 2021" organized by the Institute of Horticulture, which presented the results collected during the project. Samples of red and white currants were collected from the Pūre`s collection for the determination of BRV in laboratory tests in order to clarify the visual signs of the disease. In the tissue culture laboratory, 14 *Ribes* genotypes from different species were propagated for laboratory resistance studies. 9 blackcurrant, 2 red currant and 5 gooseberry genotypes are currently introduced and maintained *in vitro* to create a virus and pest free core collection. Preserved blackcurrants and gooseberries were tested for viruses in the laboratory.

*Information prepared 1.03.2021.*