

## „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 (01.12.2020. – 28.02.2021.)

Within **Activity No.1** measurements of mite morphological parameters based on SEM images were completed, and the morphometric data analysis was started. Quality controls of ITS/5.8S/28S and COX1 sequences and alignment preparation was continued for the further analysis. The testing of BRV in single mites after the electron microscopy was continued to study involvement of mite species in BRV transmission. Design and testing of primers for BRV CP amplification was continued.

Within **Activity No.2** the writing of article on resistance of *Ribes* to *Cecidophyopsis* and BRV, and their interactions was completed, and the review manuscript was submitted to *Annals of Applied Biology*.

The work was continued on the improvement of the analysis of the *Ribes* genetic resources SSR marker genotyping results and supplementing the draft of the publication. Analysis of genotyping data of chloroplast molecular markers (cpSSR) of *Ribes* plant material has been started, evaluation of the applicability of markers with the aim to explain the possible species structure of *Ribes* interspecific crosses. Within Action No.2, work on the analysis and processing of NGS data was continued. Work continued on the preparation and sequencing of NGS libraries of infected and control samples of currants [cultivar ‘Kodu Suur Valge’ (‘Hele’)] and '*Ribes alpinum*' harvested in May 2019 and stored at -80 °C. After analysis of NGS transcriptome data, Black currant-associated rhabdovirus 1 (BCaRV) was identified in blackcurrant samples (cultivar ‘Mara Eglite’) collected in May 2019, which has not been identified in Latvia so far. Based on these results, a manuscript of the article was prepared for submission to the journal "Plant Disease", as well as the viral genome sequence was inserted into the GenBank database.

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 started.

Evaluation of local genetic resources and analysis of data from season of 2020 was continued. The propagation and maintaining of *in vitro* plants required for industrial research and the establishment of genetic resources core collection was continued, and the testing of plants for presence of viruses and elimination efficiency was started.