

„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 (01.06.2020. – 31.08.2020.)

Within **Activity No.1**, the amplification and cloning of the ITS/5.8S region of mites was done for the samples from UK and after electron microscopy. The prepared samples were sent for sequencing to the project partner BMC. Sequencing of the ITS/5.8S region of mites transferred by the Leading Partner was performed by the Sanger method. Fragment Length analysis (FLA) was performed on new mite multiplex PCR samples on the genetic analyser ABI PRISM 3130xl for the species determination, using the previously developed automated analysis protocol. The research on mite morphology by an electron microscopy and testing of BRV in single mites after the electron microscopy and plant material was continued.

Within **Activity No.2** the writing an article on resistance of *Ribes* to *Cecidophyopsis* and BRV, and their interactions was continued.

The analysis of the sequences obtained from resistance *Ce* gene-specific amplification fragments was continued. A draft of the publication on the results of SSR marker genotyping of *Ribes* genetic resources has been prepared, and experts from different project activities have been involved to start the improvements of draft publication. The chloroplast molecular markers (cpSSR) adapted in the previous stages of the project were used to start the genotyping of *Ribes* plant material in order to explain the possible species structure of interspecific crosses. The cpSSR genotyping was performed on 126 samples of blackcurrants (including samples of *Ribes* species used in blackcurrant breeding), as well as 13 samples of red currants, 3 gooseberries, 8 *Ribes alpinum* and 10 other *Ribes* species. At the BMC, length analysis for 23 chloroplast molecular markers, selected in the previous stages of the project, of FLA samples (3812 samples) transferred by the Leading Partner were started on the genetic analyzer ABI PRISM 3130xl, and development of automated analysis protocols.

NGS libraries were prepared of blackcurrant (cultivar ‘Mara Eglite’) mite-infested and control samples for sequencing on MGISEq2000. Work continued on the preparation of NGS libraries of mite-infested and control samples of *Ribes alpinum* and red currant (cultivar ‘Kodu Suur Valge’ (‘Hele’)) harvested in May and stored at -80°C. The evaluating of experimental infestation of *Ribes* plants with several bud mite species was undertaken. a new infestation experiment was set up using several species of *Ribes* in-vitro propagated plants and mites collected from various host plants.

Protocols for PCR amplification of COX1, TEF 1- α , and HSP70 genes were established and practical testing in the laboratory was started using the newly designed primers.

The evaluation of *Ribes* genetic resources field collections and genotype describing according to RIBESCO descriptors was continued. The second year data set on genotype yield, berry quality, pest and disease resistance was collected, and phenotypic berry characterization and photography was performed. In the Tissue Culture Laboratory, the propagation and maintenance *in vitro* of plants required for industrial research, which was started in 2019, was continued, as well as the *in vitro* propagation of another 16 genotypes required for research was started. The maintenance of 10 blackcurrant and 5 gooseberry genotypes *in vitro* for the creation of virus and pest free genetic resource core collection was continued and the samples were collected and tested. Additionally, 6 currants and 1 gooseberry genotype of Latvian origin were introduced *in vitro*.