NACIONĀLAIS ATTĪSTĪBAS PLĀNS 2020
EIROPAS SAVIENĪBA
Eiropas Reģionālās attīstības fonds
IEGULDĪJUMS TAVĀ NĀKOTNĒ

„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 (01.12.2021. – 28.02.2022.)

Within **Activity No.1,** the data analysis was continued and the first draft of the manuscript was prepared about the *Cecidophyopsis* species concept and genetic diversity based on four gene sequence and morphometric data analysis. The testing of viruses in mite individuals was completed. The analysis of obtained data was completed and preparation of scientific publication about mite involvement in virus transmission on *Ribes* was started.

Within the framework of **Activity No.2**, the work on the analysis of genotyping data of chloroplast molecular markers (cpSSR) of *Ribes* plant material was continued, the plan of the article manuscript was developed, the preparation of the first version was started. An analysis of information was performed and a summary prepared about *Ribes* genes, differential expression of which was observed in the results of the NGS experiment on infested and control genotypes.

NGS library preparation optimization was performed and according to established optimization protocol NGS libraries were prepared of *Ribes alpinum*, redcurrant (cv. ‘Kodu Suur Valge’ (‘Hele’)) and blackcurrant meristema cultures – cv. ‘Mara Eglite’, *Ribes dikuscha*, *R. ussurience*, mite-infested and control samples for sequencing on DNBSEQ-G400. The NGS libraries were sequenced on DNBSEQ-G400. Primary statistical analysis of RNA-Seq data of samples was performed. The first version of the manuscript on the method of RNA extraction from blackcurrants, *Ribes alpinum* and redcurrants for downstream applications – cDNA synthesis for NGS libraries preparation for the acquisition and analysis of transcriptome data has been prepared.

The monitoring of bud mite damages was continued in the experiment established in 2019 and counting of damaged and healthy buds on experimental plants was completed. Since the virus infection symptoms and bud damages were not clearly visible during the previous season on *in-vitro* propagated plants used in the experiment established in 2021, the vegetation of plants was forced in January in the greenhouse. Counting of damaged and healthy buds and evaluation of virus infection symptoms on experimental plants was completed.

The practical development and testing of diagnostic method for differentiating *Cecidophyopsis* species on *Ribes* plants was completed by using the sequence information of several genes and developed primers. For testing of method efficiency and comparison other species from eriophyid mites that can be present on *Ribes* plants were included in the tests.

At the final of the project, the evaluation data for three years of observations was completed for *Ribes* genotypes of local origin, which are preserved in the collection of genetic resources of Latvia, and for newly acquired genotypes, for which the evaluation had not been previously performed or was performed incompletely. The descriptors developed during the international RIBESCO project were used in the evaluation. In total, 31 blackcurrant, 14 currant and 23 gooseberry genotypes were evaluated. The evaluation payed particular attention to the resistance of genotypes to gall mites and BRV, which is most relevant for blackcurrants. Blackcurrant genotypes VI-2, GEN 233A, GEN 264, 30B1, 8872 and 5/8/2/23 showed the highest resistance to both gall mites and BRV during the evaluation years. In the frame of the project, the list of Latvia genetic resources for *Ribes* plants has been finalised and submitted to the National Contact Point for Genetic Resources and included in the International European Database on genetic resources EURISCO. A total of 31 blackcurrant, 22 gooseberry and 11 currant genotypes are included in the list. All *Ribes* genotypes included in the list of genetic resources of Latvia have been described according to EURISCO descriptors. A list of the core collection of *Ribes* plants of native origin has been created by selecting the most valuable genotypes. Core collection includes 10 blackcurrant, 5 gooseberry and 5 redcurrant genotypes. The selected genotypes have already been introduced *in vitro* in the previous stages of the project and are currently stored in the LatHort Tissue Culture Laboratory, but some of the genotypes have also been planted in the *in situ* collection of the recovered plants established by the LatHort.

The popular scientific publication about blackcurrant resistance mechanisms and cultivar resistance to gall mites is prepared and published to inform society about the project and research results: Laugale V., Lācis G. (2022). Upeņu rezistences mehānismi un šķirņu izturība pret pumpurērcēm. Agro Tops, Nr.2 (294), 64.-66.lpp.

Information prepared 28.02.2022.