

***Cecidophyopsis* mites and blackcurrant reversion virus on *Ribes* hosts**

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Keywords: breeding, diversity, gall mites, resistance, viral diseases

Currants (*Ribes*) occupy a significant niche in the Latvian horticulture sector. *Ribes* (host) production in all growing regions is severely constrained by *Cecidophyopsis* mites (pest and pathogen vector) and blackcurrant reversion virus (BRV) (pathogen). Host resistance is a key factor for *Cecidophyopsis* and blackcurrant reversion disease (BRD) control. In the ERDF project Nr.1.1.1.1/18/A/026 (<https://www.darzkopibasinstituts.lv/en/projects/studies-on-ribes-plants-cecidophyopsis-mites-and-blackcurrant-reversion-virus-for>), we studied the *Cecidophyopsis* species concept and role in BRV transmission, genetic diversity and host resistance and performed evaluation and maintenance of local *Ribes* germplasm.

Comprehensive literature studies showed that *Cecidophyopsis* is a poorly studied mite group with limited sampling. Species identification based on host and host misnaming in the literature complicates the interpretation of the distribution and species data. BRV transmission is still not completely clear, and the biology studies behind the different BRD forms and host resistance are needed. Field observations in different locations indicate the imperfection in the existing *Ribes* resistance concept (*Ce* and *P* gene dominant heredity), which is not fully supported by the cultivar evaluation or crossing experiments. Although there is an association between mite infestations and BRV, the interaction mechanisms between plant, pest, and pathogen seem distinct and indirect.

Cecidophyopsis taxa on *Ribes* were reassessed; their genetic diversity and role in BRV transmission were analysed based on an extensive collection from Latvia, Finland, Poland, Lithuania, and the United Kingdom, including type hosts and localities. Comparative sequence and phylogenetic analysis of *ITS/28S*, *EF1-alpha*, *COI*, *HSP70* showed that *ITS1* used for species differentiation was highly variable and confirmed closed genetic relatedness of several taxa. BRV presence was confirmed by PCR in individuals of all studied *Cecidophyopsis* taxa.

Development and application of methods for specific molecular markers for *Ce* and *P* resistance genes, cloning and sequencing of specific amplicons, and genotyping data analysis were done to characterise *Ce* and *P* gene role in *Ribes* resistance. A hypothesis was raised about the possible effect of species composition on the resistance response rather than the specific resistance of *P* or *Ce* genes. Therefore, the evaluation of the composition of blackcurrant interspecific hybrid species using cpSSR (chloroplast simple sequence repeat) markers was performed, allowing the adaptation of a new approach for the discrimination and identification of *Ribes* species.

To facilitate *Ribes* resistance studies using NGS technologies, suitable RNA isolation methods were adapted for blackcurrants, redcurrants and *R.alpinum* based on lysis matrix technology with low sample input, preventing contamination and RNA degradation risks. During blackcurrant resistance studies with NGS approach, additional RNA-seq data analysis was performed due to the difference in heatmap pattern between experimental samples, resulting in BCaRV (black currant-associated rhabdovirus) detection for the first time in Latvia.

Inventory of existing phenotyping and genotyping data of local *Ribes* germplasm was performed. Recently obtained accessions were evaluated with emphasis on resistance to *Cecidophyopsis* and BRD. The improved assessment methodology of mite damages was developed allowing to obtain more precise statement on resistance. Most valuable native

accessions were selected and virus-free germplasm core collection established. The updated list of local *Ribes* germplasm was created and data renewed in Nordic-Baltic genetic resource (<https://nordic-baltic-genebanks.org/gringlobal/search.aspx>) and EURISCO (https://eurisco.ipk-gatersleben.de/apex/eurisco_ws/r/eurisco/) databases.