

Analysis of selected *Ribes* genotypes diversified in their resistance to blackcurrant gall mite (*Cecidophyopsis ribis*) using SSR markers

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Gall mite is one of the major problems in cultivation of blackcurrant. *Ribes* pest, being a vector of *Black currant reversion virus* (BRV), causes deformation and damages of buds, and in consequence yield reduction.

The aim of presented study was to recognise genome regions linked to the resistance to gall mite in *Ribes* plants (Institute of Horticulture field collection) using SSR markers.

The study was carried out on DNA template extracted from young leaves of 15 genotypes. PCRs with 25 microsatellite primers, chosen from the blackcurrant maps, developed by Scottish (SCRI S36/1/100 × EMRS B1834) and Lithuanian (No 93-169-2 × ‘Dainiai’) research groups, were performed.

Correlation between the DNA polymorphism and plants resistance was evaluated by multiple correspondence analyzes (MCA). Performed studies allowed to group tested genotypes in two clusters: resistant (‘Vir’, ‘Kroma’, ‘Dlinnokistnaja’, ‘Tisel’, ‘Ruben’, ‘Tihope’, ‘Karry’) and susceptible (‘Ben Sarek’, ‘Ben Alder’, ‘Blizgiai’, ‘Ben Kilbreg’, ‘Gofert’, ‘Ben Hope’, ‘Lentaj’, ‘Ben Garin’) to gall mite.

In the genomes of tested plants, identified alleles linked to gall mite resistance, derived from LG2 (seven genotypes) and LG4 (five genotypes), corresponding to Scottish map, as well as from LG1 (five genotypes) and LG2 (six genotypes), corresponding to Lithuanian genetic *Ribes* map.

Keywords: *Cecidophyopsis ribis*, diversity, *Ribes*, segregation, SSR marker, tolerance