O7.1 Fine mapping of the *RBPG1* locus which controls the response to *Botrytis cinerea* endopolygalacturonases in *Arabidopsis thaliana*

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During infection, *Botrytis cinerea* secretes endopolygalacturonases (BcPGs) that are able to degrade pectin in the cell walls of host plants. Previous research has demonstrated that infiltration of purified BcPGs, produced in the yeast *Pichia pastoris*, into the leaf apoplast could cause tissue maceration, collapse and necrosis development in several plant species. However, not all BcPGs caused similar damage and also not all plant species responded similarly to the same BcPG. We investigated the natural variation in the response of *Arabidopsis thaliana* to four different BcPGs by infiltrating leaves of different *A. thaliana* accessions with the pure enzymes. Considerable variation in responses was observed, ranging from no visible symptoms to full necrosis of the entire infiltrated leaf area. Of the 47 *A. thaliana* accessions tested, Br-0 and Est-0 showed a significantly lower response to the infiltration with BcPGs than any of the other accessions tested. Chemical analysis of cell wall composition and architecture revealed several differences in sugar composition and modification between ecotypes Col-0 (sensitive) and Br-0 (resistant).

Quantitative trait locus (QTL) mapping was performed in a segregating F2 progeny from the cross between accessions Col-0 (total tissue collapse and necrosis upon BcPG infiltration) and Br-0 (no symptoms). A single QTL controlling the response to BcPGs was detected. The Br-0 allele at this locus is recessive and significantly diminishes the response to the BcPGs. The locus was designated RBPG1 and was positioned on chromosome 3 of the *A. thaliana* genome in a 12 cM interval, containing 366 predicted genes. Several new markers were generated based on the single nucleartide polymophisms (SNPs) between Col-0 and Br-0, and a new population was generated to further map the RBPG1 locus, which reduced the interval to 0.15 Mbp, containing 44 predicted genes. We studied the expression pattern of the candidate genes in Col-0 and Br-0 leaves. T-DNA insertion lines of the candidate genes in Col-0 background (sensitive to BcPGs) were infiltrated with BcPGs in order to find mutants that are resistant. We will present the latest progress in our attempts to identify the RBPG1 gene.