Use of two genomic approaches to identify QTLs for common bacterial blight resistance in *Phaseolus vulgaris* L. in the cranberry type market class

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Common bacterial blight (CBB), caused by *Xanthomonas phaseoli* pv. *phaseoli* and *Xanthomonas citri* pv. *fuscans*, is one of the most widespread diseases of common bean (*Phaseolus vulgaris* L.). CBB reduces yield and seed quality by up to 50% under favorable conditions. The cranberry type market class is characterized by large seed size and is highly valued by consumers but it is particularly susceptible to CBB. Despite the availability of resistance sources and progress in breeding through disease screening and marker-assisted selection, genetic studies specific to cranberry beans remain limited, and markers tailored to this background are lacking.

The objective of this research is to identify and characterize quantitative trait loci (QTLs) conferring resistance to CBB in this market class and to develop molecular markers that can be directly applied in breeding programs. Two complementary next-generation sequencing (NGS) approaches were used on populations that inherited resistance from a shared *Phaseolus acutifolius* resistance donors. First, a recombinant inbred line (RIL) population at the F_4:F_5 stage, developed within the PIC project, was genotyped by whole-genome sequencing (WGS). A high-density linkage map was constructed, and disease response was evaluated under controlled greenhouse conditions using a 1–9 severity scale and the area under the disease progress curve (AUDPC) was calculated. Second, an F_2 population was screened with the same phenotyping protocol, and bulked segregant analysis (BSA/QTL-seq) was performed by sequencing DNA pools from the 30 most resistant and 30 most susceptible individuals. SNP-index and ΔSNP-index calculations were conducted using the QTLseqr package to identify candidate genomic intervals.

The two methods identified three major QTLs on chromosomes Pv06, Pv08, and Pv11, having the QTLs on Pv06 and Pv08 shared between the two approaches. Notably, loci on Pv06 and Pv11 appear to be novel in the cranberry background, highlighting possible unexplored sources of resistance. Ongoing work includes validation of candidate INDEL and SNP mutations by PCR and development of markers.