

Leaf Bacteriome in Sugar Beet Shows Differential Response against Beet curly top virus during Resistant and Susceptible Interactions

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ABSTRACT

Beet curly top virus (BCTV) significantly reduces sugar beet yield in semi-arid production areas. Genetic resistance to BCTV is limited; therefore, identification of additional resistance-associated factors is highly desired. Using 16S rRNA sequencing and BCTV resistant (R) genotypes (KDH13, KDH4-9) along with a susceptible (S) genotype (KDH19-17), we investigated leaf bacteriome changes during BCTV post inoculation (pi). At day 6 (~6-week-old plants), Cyanobacteria were predominant (~90%); whereas, at week 4 (~10-week-old plants) Firmicutes (11–66%), Bacteroidetes (17–26%), and Verrucomicrobia (12–29%) were predominant phyla and genotype dependent. Both Bacteroidetes and Verrucomicrobia, increased post infection only in the R lines. The bacterial genera *Brevibacillus* increased at 6 dpi, and *Akkermansia* and *Bacteroides* at 4 wkpi in the R lines. Linear discriminant analysis effect size (LEfSe) identified potential biomarkers in the R vs. S lines. Functional profiling revealed bacterial enrichment associated with the TCA cycle, polyisoprenoid, and L-methionine biosynthesis pathways only in KDH4-9 at 6 dpi. At 4 wkpi, bacteria associated with tryptophan and palmitate biosynthesis in the R lines, and uridine monophosphate, phosphatidyl glycerol, and phospholipid biosynthesis in the S line, were enriched. Future characterization of bacterial genera with antiviral properties will help establish their use as biocontrol agents/biomarkers against BCTV.

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