EUJAYL, IMAD A.*, and CARL A. STRAUSBAUGH, USDA-ARS, Northwest Irrigation and Soils Research Laboratory, Kimberly, ID 83341. **Identification of differentially expressed genes induced by *Beet curly top virus* infection in sugarbeet.**

Resistance to *Beet curly top virus* (BCTV) in commercial varieties grown in Western USA is a requirement for approval. Currently the disease is controlled with pesticides that provide protection for the first two month of growth. Host resistance is integral to the chemical control and provides control throughout the growing season. There is very limited public knowledge of the mode of inheritance of BCT trait, and there are no DNA markers that can be used in selection breeding. This research was designed to provide an insight into the genetic responses induced by the three BCTV strains: Cal/Logan (Cal), Worland (Wor), and severe and to identify the genes that differentially expressed in response to the infections. Gene expression was studied using transcriptomics approach via RNA-sequencing of a highly resistant doubled haploid line (KDH13-PI663862) compared to a highly susceptible line (K19-19). KDH13 was subjected to 7 treatments: infested with non-infectious leafhoppers, infections with leafhoppers population carrying a single, two, or three strains, and control healthy leaf, but K19-19 was infected with the three strains in one treatment. Total RNA was extracted from leaves of the 8 treatments (3 biological replications, 24 mRNA libraries), was sequenced in a HiSeq2500 and analyzed using TopHat and Cufflinks software. All sequences were aligned to the reference genome RefBeet-1.2. Significantly differentially expressed genes (DEGs) were identified, based on 28 pair-wise comparisons, at a false-discovery-rate (*FDR*) lower than 0.01 and at least a 4 fold change in expression level (LogFC> 2.0 or <-2.0). Important pathogen defense genes such as *DND1* (defense no death), that is known to be involved in innate immune response to pathogens, was found up-regulated (*FDR = 5.43E-6*) in KDH13 when infected with the three strains compared to infestation with non-infections leafhoppers, but no response of *DND1* was observed in K19-19. This gene transcript of 6.6Kb size is located on chromosome 1 of the genetic map. Additionally, transcripts of *IDH1* gene were totally absent in K19-19 infected with the three strains. There was a pattern of some defense gene families, including *ERF* genes subunits that were up-regulated when KDH13 was infected with Wor only and down-regulated when its infected with both Cal and Wor, an evidence of strain-specific and strain interaction differential gene expression. Additionally, no significant differential expression of genes/transcripts detected in the comparison between a treatment infected with the three strains and treatment infected with Cal and Wor combination. The sequence of DEGs transcripts will be used to design qPCR assays for confirmation in these lines as well as in parental lines and segregating populations, to develop reliable DNA markers for marker assisted selection for BCT resistance. This research is the first to reveal gene transcriptional profiles associated with resistance as well as susceptibility to BCTV.