IMAD A. EUJAYL * and CARL A. STRAUSBAUGH, USDA-ARS-Northwest Irrigation and Soils Research Laboratory, 3793 N. 3600 E. Kimberly, ID 83341. **CRK8 Gene family expression is upregulated in Beet Curly Top Resistant sugar beet line.**

Resistance to *Beet curly top virus* (BCTV) is an essential trait for cultivars to be grown in arid and semi-arid areas worldwide. Currently neonicotinoid insecticides are used to compensate for low to moderate levels of resistance in cultivars. USDA-ARS publicly releases germplasm with economically important traits such as the line KDH13 (PI663862) which has exceptional resistance to BCTV. KDH13 has been further utilized to identify genes regulating resistance via gene expression profiling (RNA-sequencing). KDH13 was subjected to 7 treatments: an un-infested control treatment, a second control with non-infectious leafhoppers, and leafhoppers infested with one of three BCTV strains (California/Logan, Worland, and Severe) or a combination of the three strains. The transcriptomic sequence data from KDH13 was digitally analyzed against sequence of susceptible line (K19-19) that was infected with the three strains. The sequences were aligned to the reference genome sequence (RefBeet-1.2). Based on 28 pair-wise comparisons, the differentially expressed transcripts/genes were identified at threshold of False-Discovery-Rate (FDR) of <0.05 and a LogFC (fold change) >±2.0. The analysis revealed that Cysteine-rich Receptor-like protein Kinase-8 (CRK8; AT4G23160) was the most differentially expressed transcripts in the comparisons between the two lines. In KDH13, 4 transcripts/members of the CRK8 super-family showed consistent overexpression caused by and infection with the three BCTV strains at LogFC of 2.3 and FDR $<1.0^{-4}$. The sequence of CRK8 were used to design quantitative PCR analyses. The qPCR validated these 4 CRK8 transcripts are a key regulator of CT resistance through overexpression as a defense system and can be used to screen progenies for BCTV resistance.