EUJAYL, IMAD[1*], CARL STRAUSBAUGH[1], WOLFGANG MECHELKE[2], DIETRICH BORCHARDT[2] and ANDRZEJ KILIAN[3], [1]USDA-ARS, Northwest Irrigation and Soils Research Laboratory, 3793 N. 3600 E. Kimberly, ID 83341, USA, [2]KWS-SAAT AG, Grimsehlstr 31 37555 Einbeck, Germany and [3]Diversity Array Technology PL, 1 Wilf Crane Crescent, Yarralumla, ACT 2600, Australia. **DArT based genetic linkage map of sugarbeet and mapping of beet curly top.**

ABSTRACT

Developing varieties with genetic resistance to beet curly top is crucial to the sugarbeet industry. Determining the mode of inheritance and identification of markers linked to beet curly top (BCT) resistance genes are imperative to developing resistant germplasm and deployment of markers assisted breeding. The objectives of this study were to construct a high-density genetic linkage map so as to identify DNA markers tightly linked to BCT resistance genes and explore its heritability. Diversity Arrays Technology (DArT) markers, a relatively new high-throughput marker system provided an opportunity to obtain species-specific large number of markers. DArT were developed for sugar beet providing 7,680 specific clones publically available. These markers were produced from genomic representations from genetically diverse panel of a total of 92 genotypes comprised commercial varieties, germplasm accessions, *Beta maritima,* and *Beta macrocarpa*. Parental lines with extreme reactions to curly top were used to produce an F_2 mapping population segregating for BCT. The seed parent is a doubled haploid line produced by KWS that is originated from C773/C46 germplasm released by USDA-ARS which is highly resistant to BCT. The pollinator parent is an elite line from KWS-Germany that is highly susceptible to BCT. These parents were crossed to obtain an F_1 hybrid which was inbred (selfed) to produce the F_2 population. The parents and the population (181 individuals) were inoculated with the BCTV using 5 viruliferous hoppers en-caged and allowed to feed on a single leaf of each plant. Leaf samples were collected from all plants for ELISA analysis. The population was genotyped with 641 polymorphic markers comprised 592 DArT, 33 SNP, and 16 SSR. A genetic linkage map was constructed using JoinMap/MapQTL calculation models that counted for markers in the maternal and paternal phases as observed in DArT markers data. The number of co-dominant markers (SNP and SSR) is limited a fact that dictated construction of separate preliminary maternal and paternal maps. The two maps identified nine linkage groups that correspond to the haploid number of chromosomes which spanned 763 cM. The two maps fitted very well and markers were well distributed with an average interval length of 2.5cM. The SNP and SSR markers were mapped as expected in the known published chromosomes. The phenotypic data of BCT visual rating and virus accumulation quantified by ELISA were significantly correlated at r= 0.797. The quantitative phenotypic data was analyzed to detect QTLs. A single QTL was detected in chromosome 7, which explains limited phenotypic variability of 9.8% at LOD score of 5.9. Three markers; 2 SNP and 1 EST-SSR were detected linked to this QTL. This study is the first to develop DArT markers for sugar beet as well as first public BCT focused genetic linkage map. The current genetic map will be enriched with more co-dominant markers to join the maternal and paternal maps in a complete map with high density of co-dominant markers.