

Identification of QTL Region(s) for Studying the Development Rate in Stevia

Prabhjot Kaur*, ; Ryan Warner, and Keivan Bahmani,

Abstract: The rate at which plants produce new nodes (development rate) is one of the primary factors controlling crop production time or time to first yield of agricultural crops. *Stevia rebaudiana* is a crop grown for the extraction of sweet-tasting steviol glycosides produced in the leaves for use as a non-caloric sugar substitute. Breeding stevia cultivars that develop faster will facilitate multiple harvests during its annual production season and increase biomass production. Understanding the genetic factors controlling vegetative development rate will facilitate breeding of faster developing cultivars. A stevia F1 mapping population consisting of 200 individuals (population MSU18-02) planted in triplicate was evaluated at two field locations in Michigan. Plants were phenotyped for node number, plant height, maximum plant width, minimum width, primary and secondary branching, leaf length, leaf width, stem caliper, flowering stage, plant vigor and steviol glycoside profile. Our initial data analysis indicated that no significant correlation ($\alpha = 0.05$) was found between number of nodes and any other morphological traits except that node number was found to be positively correlated with maximum and minimum plant width at one out of the two locations, suggesting that node number could be independently studied. Genotyping-by sequencing was used to generate SNP markers for genetic mapping. A novel significant QTL for node number on linkage group 4, explaining 9% of the phenotypic variation, was identified. Two more peaks falling just below the threshold were identified on linkage groups 3 and 4. The population will be evaluated again this year to evaluate the robustness of the identified QTL regions across years.

Evaluation of Fine-Scale Genetic Diversity of *Pyrus Calleryana* Populations

Shiwani Sapkota*, *University of Tennessee - Knoxville*; Sarah L. Boggess, *University of Tennessee - Knoxville*; Robert Trigiano, ; William E. Klingeman, *University of Tennessee*; Denita Hadziabdic, *University of Tennessee - Knoxville*; David R Coyle, *Clemson University* and Marcin Nowicki,

Abstract: *Pyrus calleryana* Decne., commonly known as Callery pear, is a pear species native to eastern and southern China, Taiwan, Korea, and Japan. Callery pear was initially brought to the United States (U.S.) for breeding with *P. communis* (European pear) to create fire blight-resistant fruit tree selections. Several *P. calleryana* selections exhibited desirable horticultural traits for urban use, which led to the development and release of several hybrid cultivars. The species and its hybrid progeny typically present a rounded to conical crown and sharp spurs on the branches, though the species shows considerable phenotypic plasticity. 'Bradford' is the most widely planted and a commonly known cultivar of Callery pear in the U.S. In the landscape, *P. calleryana* and its cultivars are used as deciduous shade and flowering trees. Now, Callery pear is one of the most common invasive plants across the eastern U.S., raising concern about the transformation of a once popular landscape tree into an aggressive invader in just a few decades. Because the mechanisms contributing to its invasiveness are not well understood, our study was undertaken to assess the genetic diversity and population structure of invasive Callery pear populations presented within a narrow geographic range. We hypothesized there would be high genetic diversity among Callery pear trees distributed across smaller areas of Tennessee, Georgia, and South Carolina. Using 15 microsatellite markers, a total of 180 naturalized population samples collected across six naturally occurring sites in Tennessee, Georgia, and South Carolina were used for the study. Results supported our hypothesis and revealed the presence of population structure

with high genetic diversity among the collection sites. Results from AMOVA showed the majority of variance identified was attributed within the populations, which validates the presence of population structure in the study dataset. Our data suggests that Callery pear populations across smaller geographic areas have been able to maintain high levels of genetic diversity making them more adaptable to the given environment. This study helps broaden the existing knowledge on genetic diversity patterns, origins, and spread of the species. To control the invasive species, we suggest to limit gene flow by creating some barriers between invasive populations, and to maintain smaller effective population size by using periodic management practices such as fire, chemicals, etc., that may help to prevent the maintenance of incurred genetic diversity limiting their evolutionary potential.

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Genetic Diversity and Population Structure of *Spinacia turkestanica*, a Wild Progenitor of Cultivated Spinach, *Spinacia oleracea*

Sanjaya Gyawali, *Mount Vernon Northwestern Washington Research and Extension Center*; Gehendra Bhattarai*, ; Ainong Shi, ; Chris Kik, *Wageningen University and Research* and Lindsey J. du Toit, *Mount Vernon Northwestern Washington Research and Extension Center*

Abstract: Genotype-by-sequencing (GBS) was employed to identify single nucleotide polymorphism (SNP) markers in 76 *Spinacia turkestanica*, 16 *S. oleracea*, and 4 *S. tetrandra* accessions. The genetic diversity, population differentiation, and population structure of the 96 *Spinacia* accessions were investigated using 1,730 SNPs. Furthermore, 7,065 SNPs were employed to compare the 76 *S. turkestanica* and 16 *S. oleracea* accessions. The polymorphic information content of the 1,730 and 7,065 SNPs ranged from 0.09 to 0.375, respectively, suggesting the SNPs could be useful in genetic studies. The *S. tetrandra* accessions were highly differentiated from the *S. oleracea* accessions ($F_{st} = 0.142$, $N_m = 1.40$) compared to the genetic relationship of *S. turkestanica* and *S. oleracea* accessions ($F_{st} = 0.037$, $N_m = 6.56$). In addition, *S. turkestanica* accessions had greater genetic identity to *S. oleracea* accessions ($I_d = 0.972$) compared to the relationship of *S. tetrandra* with *S. oleracea* accessions ($I_d = 0.875$). The results suggest that *S. turkestanica* was the more immediate progenitor of modern cultivated spinach, *S. oleracea*, than *S. tetrandra*. The *S. turkestanica* accessions collected from Central Asia comprised two distinct subpopulations (Q2 and Q3), with one subpopulation sharing greater genetic identity to the *S. oleracea* population (Q1). Likewise, the Q1 had a smaller F_{st} (0.008) and greater N_m (31.89) with the Q2 than with the Q3 subpopulation ($F_{st} = 0.013$, $N_m = 18.47$). The distribution of *S. turkestanica* subpopulations collected in Uzbekistan and Tajikistan suggests that Q2 accessions originated primarily in Uzbekistan. In contrast, Q3 accessions originated mostly in Tajikistan, with the Zarafshan Mountain Range providing a physical barrier that largely separated the Q2 and Q3 subpopulations of *S. turkestanica*. Admixtures of Q2 and Q3 were found primarily among spinach accessions collected at the lower elevations along the western end of the Zarafshan Mountain Range, near the Uzbekistan and Tajikistan border. The high level of genetic diversity found in the Q2 and Q3 subpopulations may be valuable for identifying novel, agronomically important traits in *S. turkestanica* that can be incorporated into *S. oleracea* breeding programs.

Genomics-Guided Breeding for Mechanical Harvest Traits in Green Chile

Franchesca A. Ortega*, *New Mexico State University*; Bradley W. Tonnessen, ; Theresa A. Hill, *University of California*; Allen Van Deynze, *University of California* and Stephanie Walker,

Abstract: Chile pepper (*Capsicum annum*) is a valuable veg-