WASHINGTON TURFGRASS SEED COMMISSION

PROGRESS REPORT FORMAT FOR 2018 PROJECTS

Project No.: WSU ACCOUNT# 13C-3019-6780

Title: Characterization of vernalization genes and flowering in Kentucky Bluegrass

Personnel: Michael M. Neff Ph.D. (PI), Gaganjot Sidhu (Postdoc) and Xin Xin (Graduate Student)

Reporting Period: 7/16/18 – present (4.0 months)

Accomplishments: In the first year of this project, John Hadish, a rotating Molecular Plant Sciences (MPS) graduate student cloned fragments of two flowering time genes, *VRN1* and *VRN3*, from the KBG genome. A new postdoc, Dr. Gaganjot Sidhu, and a MPS graduate student, Xin Xin joined the Neff lab in July and August 2018, respectively and began working on this project. Xin is supported by a scholarship from the China Scholarship Council, requiring only $2500/semester plus summer salary coming from this project. As a result, this project can now support two scientists, working as a team. In the past three months, Gaganjot has identified nine publicly available KBG transcriptomic/genomic studies. With this resource, Gaganjot has performed *in-silico* studies to identify *VRN* genes from KBG using wheat *VRN1*, *2* and *3* coding sequence as a reference. Gaganjot, Xin, and Evan Stowe (an undergraduate student working in the Neff lab) have identified a total of eight copies of *VRN1*, three copies of *VRN2*, and two copies of *VRN3* genes in KBG. Gaganjot and Xin have also designed primers to perform wet lab experiments to validate the *in-silico* studies. They have also started both growth chamber and vernalization chamber/greenhouse experiments to examine the expression of these flowering genes as outlined in this proposal.

Results: Using the transcriptomic reads ranging from 41 to 555 million in individual studies, eight structural copies of *VRN1* were identified. Unlike *VRN1*, only three copies of *VRN2* and two copies of *VRN3* were identified, most probably due to reduced number of reads available for these genes. These results also suggest that *VRN1* has a higher expression level compared to the other two genes. Gaganjot and Xin are using *in-silico* and wet lab experiments to validate the sequence and copy numbers of these genes. This will also facilitate in creating an expression atlas of *VRN* genes in KBG for different developmental stages and biotic as well as abiotic stress treatments. In addition, Gaganjot and Xin will continue to clone these and other known flowering related genes from varieties Jumpstart and Barsweet as well as the wild Alaskan accession described in our proposal in order to compare their sequences with the identified sequences from other KBG accessions. The *in-silico* and cloned sequences share high degrees of similarity with orthologous gene sequences previously characterized from *Hordeum vulgare* and several *Triticum* species. This is in accordance with past research that indicates there is a high degree of conservation in VRN1 (Shinozuka et al. (2013). A growth chamber study consisting of Jumpstart, Barsweet and an Alaskan accession was also initiated along with control accessions Aspen, Midnight, Park, and Trenton. After giving a start chamber treatment of 6 and 8 weeks, the plants are now in the vernalization chamber and the data and tissue collection is in progress.

Publications: None at this time.