



## Validation of Seed Size Variants Identified in the University of Minnesota Pennycress Genetics Program

Marshah Menos, 2021 Integrated Plant Systems – Undergraduate Research Experience<sup>1</sup>, Eva Serena Gjesvold<sup>1</sup>, M. David Marks<sup>1</sup> and Ratan Chopra<sup>1,2</sup>

<sup>1</sup>Department of Plant and Microbial Biology, University of Minnesota, Saint Paul, MN 55018

<sup>2</sup>Department of Agronomy and Plant Genetics, University of Minnesota, Saint Paul, MN 55018

Internship advisor: Dr. [Ratan Chopra](#)

**Abstract:** *Thlaspi arvense* (field pennycress) is domesticated as a new winter oilseed cash cover crop for northern climates of the world. Despite its potential to intensify agricultural productivity without new land displacement, the challenge remains to identify pennycress varieties with bigger seed size for post harvest handling and processing. Over the last six years, UMN pennycress genetics program has utilized several approaches to identify genetic control for seed size related traits. These approaches included the use of EMS mutagen to induce variation and the use of Oryzalin to induce ploidy. During the internship, I was involved in validating three lines that were discovered using these methods, respectively, as this trait is highly influenced by the environment. For the ploidy induced seed size variants, I looked at heritability of the seed pod fill and 1,000 seed weights. Previously it was found that this tetraploid line had about 1.63g per 1000 seeds and 8 seeds per pod and during the 2020-2021 growing season, I found that this line was stable and produced about 1.51g per 1000 seeds and 7 seeds per pod. Although there was some variation from the last year, we did not see any plants with poor seed fill and any impact on plant development. For the EMS-induced alleles, I was validating the translational genomics study in progress that was evaluating the effect of mutations in the SWEET4 and SWEET11 genes for seed related traits. To do this, I isolated DNA from the plants growing in the field and genotyped them using KASP markers to confirm the homozygous mutants for sweet4-1 and sweet11-1. Once the genotype was confirmed, I selected 6 plants from each of the wild-type (MN106), sweet4-1, and sweet11-1 to evaluate seed pod fill, 1,000 seed weight and plant height. We found that there were no significant differences in the plant height and pod fill among these lines but the 1,000 seed weight was significantly lower in sweet4-1 (0.74g) and no significant differences in sweet11-1 (0.93g) compared to the wild-type (0.96g). These results are consistent with the reports in *A. thaliana* and validate the findings from the previous years. In conclusion, I was able to validate the stability of this trait in the lines identified and was able to confirm the genetic control using SWEET genes as an example.