

Winter Oilseed Quarterly Update #11: Evaluating genetic diversity in field pennycress

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Field pennycress (*Thlaspi arvense* L.) is a new cash cover crop under development by the Forever Green Initiative at the University of Minnesota. The objective of our pennycress breeding program is to develop high yielding and early maturing pennycress lines. Wild pennycress collections are important resources for these agronomic traits and can also provide traits for environmental adaptation and biotic and abiotic stress tolerance. Genetic diversity must be present to select for these traits. Therefore, understanding the genetic variation present in our pennycress collections was a crucial step to creating a strong breeding program that can advance pennycress as a new cash cover crop for cold climates.

The pennycress germplasm used in the creation of the UMN pennycress breeding program includes 121 wild collections made in the U.S., Canada, Europe, and Armenia (Figure 1). Our objective was to use genetic markers to evaluate the diversity present in these collections and determine if more collections should be made to expand the gene pool. We also determined if pennycress lines collected in close geographic locations were more related to each other than those collected from distant locations or if pennycress lines collected in regions with similar environments were genetically similar. This knowledge could help us identify pennycress collections with traits that could improve yield or stress tolerance in Minnesota growing conditions. For example, pennycress lines collected in European countries with harsh winter may be able to provide traits like cold and freeze tolerance.

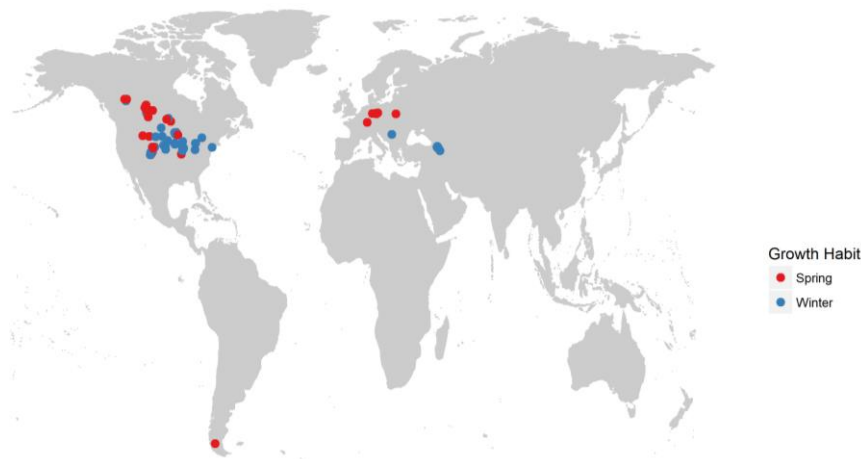


Figure 1. Map of pennycress collection sites. Each dot represents one pennycress collection. Red dots represent spring type pennycress lines that do not require a cold period to flower, while blue represents winter type lines that require cold to flower.

Using genetic markers and cluster analysis, we tested if the pennycress collections could be grouped into separate populations. We identified four populations (Figure 2).

Populations P1 and P3 consist of collections made in Armenia, while populations P2 and P4 consist of a mix of collections from North America, Europe, and the single collection from South America. Following cluster analysis, we used principal components analysis (PCA) to evaluate the geographic origins of these populations and how much genetic variation is explained the shared genetic markers of these groups (Figure 3). When including all pennycress collections in PCA, we found that the Armenian collections form a separate group and the division between Armenian and all other collections explains 17.5% of the genetic variation (Figure 3A). However, the non-Armenian collections could not be clearly evaluated, so a second PCA analysis was completed by removing the Armenian lines (Figure 3B). In this analysis the division between populations

P2 and P4 from the cluster analysis explains 13.3% of the remaining genetic variation. Population P2 (indicated by the red circle) consists of European collections and collections from the U.S. Midwest and Rocky Mountains. Population P4 (blue circle) includes collections from Canada, Minnesota, and other cold climates.

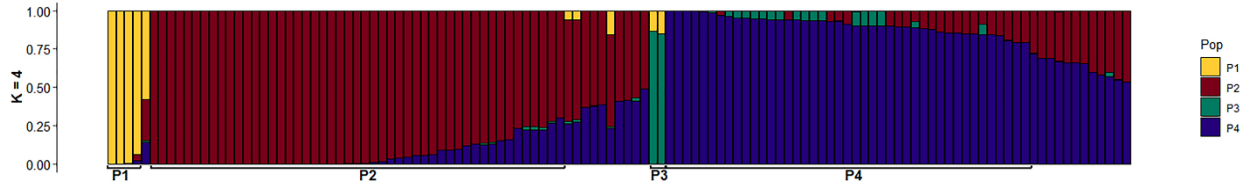


Figure 2. Pennycress collections grouped using genetic markers and cluster analysis. Each vertical bar represents a single pennycress collection, while colors represent the proportion of genetic markers that belong to a population. Pennycress collections with greater than 70% membership in a specific population are considered to belong to that population. If membership is less than 70% in any population, the pennycress collection is considered genetically mixed.

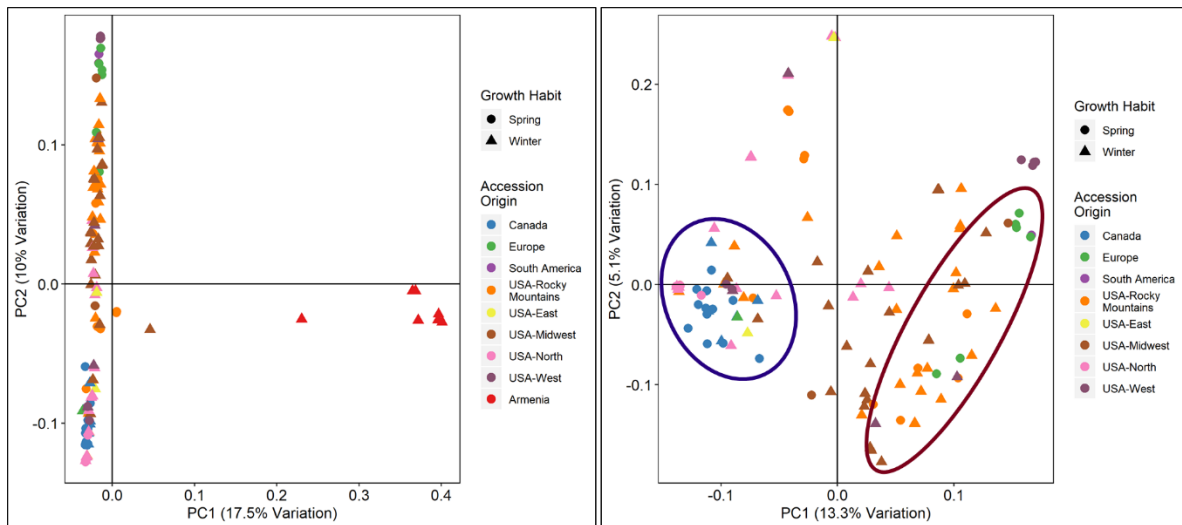


Figure 3. Principal component analysis of pennycress collections. Collections are colored by geographic region. Analysis was completed on A) all pennycress collections and B) non-Armenian pennycress accessions. Circles delineate non-Armenian populations P2 (red) and P4 (blue) determined by K=4 STRUCTURE analysis.

Our analysis shows that additional genetic diversity would benefit pennycress breeding. As a new crop, pennycress may face unforeseen biotic and abiotic challenges, and new collections of wild pennycress germplasm could increase the diversity available for breeding. However, based on the present analysis, the search for diverse pennycress accessions for use in breeding should focus on areas outside of the U.S. and Western Europe. Opportunities for genetically diverse accessions can be found in the Caucasus region of Western Asia or the Fertile Crescent region where pennycress likely originated. This research was recently published in Frels et al. 2019.

Reference: Frels, K., R. Chopra, K.M. Dorn, D.L. Wyse, M.D. Marks, and J.A. Anderson. 2019. *Genetic diversity of field pennycress (Thlaspi arvense) reveals untapped variability and paths toward selection for domestication*. *Agronomy* 9:302. <https://doi.org/10.3390/agronomy9060302>