

196. Using mutation-based breeding approaches to domesticate pennycress into a new oilseed crop

Evan Johnson, Erin Daniels, Kevin Dorn, and M. David Marks*

University of Minnesota, St. Paul

<http://pennycress.umn.edu>

Project Goals: Develop pennycress into a new oilseed crop that can be intercropped between corn and soybeans in the Upper Midwest.

Thlaspi arvense (field pennycress; pennycress herein) is being targeted as a new winter-grown oilseed cover crop and biodiesel feedstock [1]. Pennycress is a member of the Brassicaceae family and is related to model species *Arabidopsis thaliana* and current oilseed crop species *Brassica napus* and *rapa* [2]. Unlike these latter two species, pennycress can be grown in the interval between the corn/soybean rotation in the Midwestern United States. It can be seeded into standing corn, allowed to overwinter and then harvested in the spring, allowing for a summer crop of short-season soybeans [3]. Thus, it has potential to provide a new source of biofuel without requiring new land or greatly changing current farming practices. Additionally, it provides a winter cover on land that is traditionally left barren, which will reduce nutrient leaching and soil erosion.

Pennycress was chosen as a potential new crop species because it already harbors a number of desirable traits. These include a high oilseed yield (1100 to 2250 kg/ha), a high seed oil content (30-40% by seed weight), extreme cold tolerance, fast seed maturation in the spring, good plant stature (1>meter), and seed pods that exhibit less shattering compared to those of related species. However, many improvements need to be made to make pennycress a successful new crop species. In a recent review, Sedbrook et al. described strategies to rapidly improve and domesticate pennycress, particularly mutation breeding [1]. We will use both forward mutant screens, and reverse genetic approaches that will rely on our recently developed genomic resources for pennycress, which include both transcriptome and genome assemblies [4, 5]. We know from work with *Arabidopsis* that mutations can confer what can be considered agronomically desirable phenotypes. For example, various mutations in *Arabidopsis* have been shown to increase seed size, decrease seed dormancy, improve oil quality, speed up flowering and reduce seed shattering.

To begin our mutation-based breeding strategy, seeds were treated with three types of mutagens: EMS, fast neutrons, and gamma rays. These were planted in the fall of 2013 and M2 seeds were collected in the spring of 2014. That fall 1,000 rows were sowed, each containing seeds derived from pools of 10 M1 plants. To date, we are in the process of phenotypically screening M2 plants derived from 10,000 M1 plants. Already, over 100 mutants having phenotypes of interest have been identified. These include mutants with agronomically important traits such as early maturation, larger seeds, and light-colored seed coats, which we know from *Arabidopsis* are likely to produce seeds with higher oil content and reduced dormancy [6]. In the spring of 2015, we will screen the 1000 rows of plants in the field for additional traits of interest. We anticipate finding many more mutants with desirable traits. In addition, we are banking seeds and tissues that will be used for TILLING, with the ultimate goal of directly identifying mutations in genes that are known to produce desirable traits when mutated in *Arabidopsis* [7].

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