

Winter Oilseed Quarterly Update #9: Advancements in field pennycress (*Thalpi arvense*) domestication

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Pennycress has great potential to be a useful oilseed that also functions as a cover crop. However, wild pennycress has weedy traits that detract from its utility as an oilseed crop. Wild pennycress produces seed pods that easily break open (shatter) resulting in pre-harvest seed loss (Figure 1a), and the seed oil contains high levels of erucic acid, which while suitable for bio-jet fuel production, is considered inedible and reduces the value of the oil and meal. Wild pennycress also produces high levels of the bitter-tasting glucosinolate, sinigrin, which reduces seed meal palatability and nutritional value. The main goal of this research was to identify pennycress lines lacking these wild and weedy traits.



Figure 1: (a) Field grown wild-type plant compared to a reduced shatter plant (b) – Adopted from Chopra et al. (2019)

Historically, domesticating a crop by removing weedy traits has taken hundreds to thousands of years. We have demonstrated that pennycress is easy to genetically characterize due to its small diploid genome and the similarity of its genes to the well-studied plant *Arabidopsis*¹. Using traditional mutation-based breeding methods, cost-effective DNA sequencing, and the application of knowledge from *Arabidopsis*, we have rapidly identified and validated mutations that reduce weedy traits in less than five years. For example, we identified three independent mutations of the *ind1* gene. Plants carrying this mutation have reduced pod shatter (Figure 1, Figure 2a). The edible oil trait was identified in two lines with mutations in the *fae1* gene. These two lines were identified as having a similar level of erucic acid as canola varieties with the “zero erucic” seed oil trait (Figure 2b). In addition, a reduced glucosinolate

pennycress mutant with edible protein meal was identified (Figure 2c). The causative mutation was identified and confirmed as a change in the *AOP2* gene. Each of these breeding lines has undergone several rounds of characterization and confirmation in field and laboratory trials. We have begun to stack these mutations into our top breeding lines using marker-assisted selection technologies. The breeding lines with up to three stacked mutations will undergo seed increase and multiple location field testing beginning in Fall 2019.

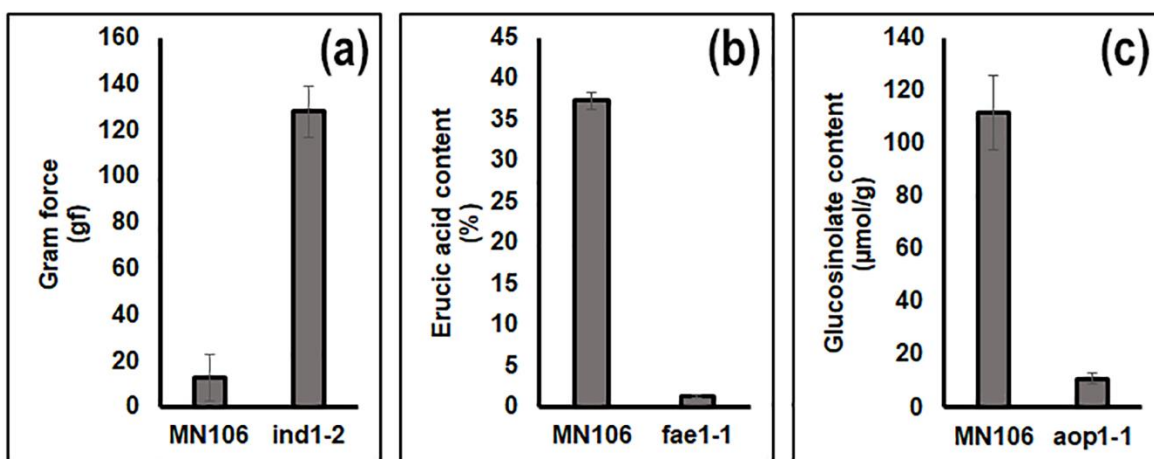


Figure 2. Mutant traits for introduction into top breeding lines. a) Force required to break seed pods at maturity, b) Seed oil erucic acid content, and c) Seed glucosinolate content. **MN106**: wild-type line with undesirable phenotypes, **ind-2**: reduced shatter line, **fae1-1**: reduced erucic acid line, **aop2-1**: reduced glucosinolate line.

We have made a detailed characterization on each of these traits available as a scientific report titled “Progress toward the identification and stacking of crucial domestication traits in pennycress” at <https://www.biorxiv.org/content/10.1101/609990v1.article-info>².

References

1. Chopra, R.; Johnson, E.B.; Daniels, E.; McGinn, M.; Dorn, K.M.; Esfahanian, M.; Folstad, N.; Amundson, K.; Altendorf, K.; Betts, K.; et al. Translational genomics using Arabidopsis as a model enables the characterization of pennycress genes through forward and reverse genetics. *Plant J.* 2018, *96*, 1093–1105.
2. Chopra, R.; Johnson, E.B.; Emenecker, R.; Cahoon, E.B.; Lyons, J.; Kliebenstein, D.J.; Daniels, E.; Dorn, K.M.; Esfahanian, M.; Folstad, N.; et al. Progress toward the identification and stacking of crucial domestication traits in pennycress. *bioRxiv* 2019, 609990