

use of NTF, the two 4-year rotation sequences hold promise as stable, profitable, and ecologically-friendly crop rotations for the low-precipitation zone.

Study 2 was initiated in September 2015 following the completion of the 6-year safflower experiment (see article on page 28). The previous 3-year WW-safflower-UTF rotation was replaced by a 3-year WC-spring wheat-UTF system. Individual plot size in this study is 30 x 500 feet. The study site contains 56 plots covering 20 acres and has been the focus of cropping systems research for the past 20 years. As seed-zone moisture is generally greater in UTF (Study 2) compared to NTF (Study 1), WC will be planted in late August, if possible. If planting of WC is not possible, spring canola will be planted in late March. Excellent WC stands were achieved during this first year from an August 25, 2015 planting into UTF (Fig. 1). Due to widespread cold damage to *Brassica napus* WC varieties in recent years we, collectively, decided to use a *Brassica rapa* WC variety in this study due to improved cold tolerance and despite reduced seed yield potential compared to *Brassica napus* types. Long time Ritzville area WC grower Curtis Hennings suggested and provided the variety "Largo" for this study (Fig. 1).



Figure 1. Stand of 'Largo' *Brassica rapa* winter canola on the Ron Jirava farm near Ritzville, WA. This crop was planted with a deep-furrow drill on August 25, 2015. Photos were taken on April 5, 2016. Note the flowers are already well initiated on this date.

Based on experience of regional WC growers, only phosphorus is applied at time of planting WC in both Study 1 and Study 2. Nitrogen and sulfur is stream jetted in a Solution 32 formulation with a sprayer in a split application during the fall and again in early spring.

## Rotational Effects of Winter Canola on Subsequent Spring Wheat as Related to the Soil Microbial Community



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Inclusion of canola as a rotational crop in the inland Pacific Northwest has expanded in recent years with the increased demand for canola-based products. Wheat grown after canola is generally reported to have greater grain yield compared to wheat grown after wheat. In a 7-year on-farm winter canola (WC) rotation study conducted near Reardan, WA, yields of spring wheat (SW) following WC were reduced compared to yields following winter wheat (WW). The objective of this research is to determine the differences and similarities in the soil microbial communities associated with WC and WW. If a shift in the microbial community between crops exists, we want to determine if the changes are connected to SW yield response.  $\beta$ -Glucosidase (BG) enzyme activity in WW was significantly greater compared to WC (Fig. 1A) in the first year (CS1), with the effect carrying over to the subsequent SW (CS2) in 3 of 5 crops years (CY). The BG enzymes are widely distributed among soil fungi and involved in the degradation of cellulose providing energy for soil microorganisms. Differences in BG activity could suggest alterations in the soil fungal community. Results of phospholipid fatty acid (PLFA)

analysis indicate that fungal groups of the soil microbial community in WC were suppressed. In particular, mycorrhizal fungi (MF) were significantly suppressed in WC compared to WW in 4 of the 5 CY for CS1 and CS2 demonstrating carry over to the subsequent SW crop (Fig. 1B). Preliminary data from this work suggest the preceding canola crop may have suppressed MF associations with the subsequent SW crop, which could explain the reduction in the observed SW yields. This study will provide research-based information of the influence brassica crops have on soil microbial health and crop yields to growers, scientists, and industry personnel.

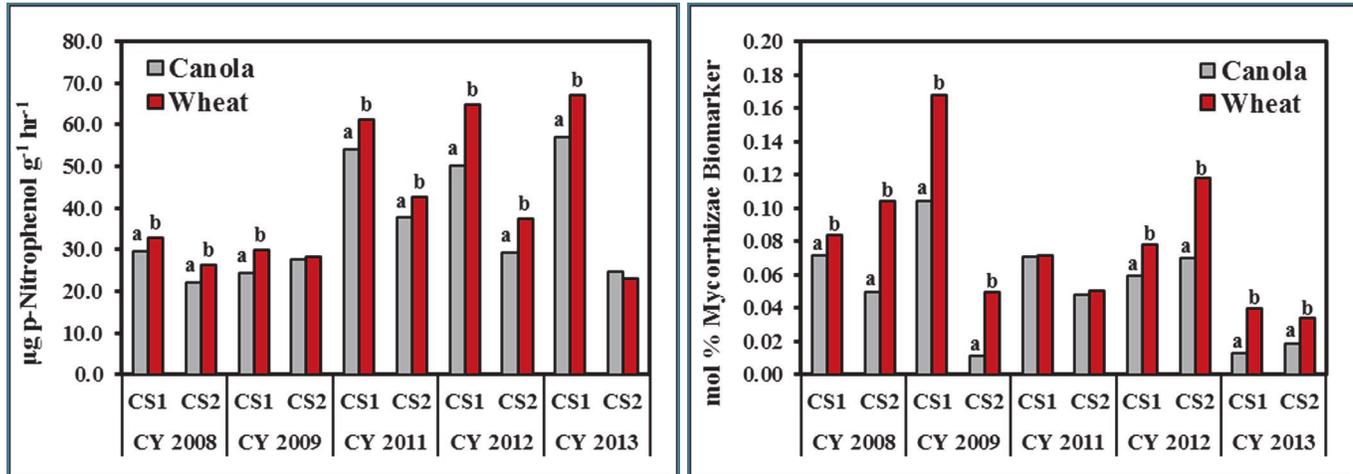


Figure 1. A) Difference in soil microbial enzyme activity in WC and WW treatments as determined by  $\beta$ -Glucosidase. B) Difference in biomarker indicators for soil mycorrhizal fungi in WC and WW treatments as determined by PLFA. Cropping sequence (CS) 1 represents data from the initial canola and wheat plots in the first year. CS2 represents data from the SW treatment following the WC and WW treatments. Different letters indicate significance @ $p < 0.05$ .

## Manipulating the *AT-hook Motif Nuclear Localized (AHL) Gene* Family for Bigger Seeds with Improved Stand Establishment



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In low rainfall dryland-cropping areas of eastern Washington, stand establishment can have a major impact on yields of camelina and canola. During dry years these seeds need to be planted in deep furrows so that the developing seedling has access to water in the soil. One approach to facilitate stand establishment is to develop varieties with larger seeds and longer hypocotyls as seedlings while maintaining normal stature as adults. Few mechanisms, however, have been identified that uncouple adult stature from seedling height. The Neff lab has identified an approach to improve stand establishment by uncoupling seedling and adult phenotypes through the manipulation of members of the *AHL* family. When these genes are over-expressed, the result is seedlings with shorter hypocotyls. When the activity of multiple genes is disrupted, the result is seedlings with taller hypocotyls, demonstrating that these genes control seedling height in a redundant manner. In the Brassica *Arabidopsis thaliana*, we have identified a unique allele (*sob3-θ*) for one of these genes, *SOB3/AHL29*, that over-expresses a protein with a disrupted DNA-binding domain and a normal protein/protein interaction domain. In *Arabidopsis*, this mutation confers normal adult plants that produce larger seeds and seedlings with hypocotyl stems that can be more than twice as long as the wild type. The goal of this project is to enhance camelina and canola seedling emergence when they are planted deeply in low-rainfall dryland-cropping regions (generally less than 12"/year) or in wheat stubble. This can be achieved by manipulating *AHL* gene family members to develop varieties that have long hypocotyls as seedlings yet maintain normal growth characteristics as adult. The current aims for this project are: 1) Analyze seed size of *AHL* mutations in *Arabidopsis*; 2) Identify, clone and characterize *AHL* gene family members from camelina and canola; 3) Generate transgenic camelina and canola expressing *AHL* genes; 4) Use CRISPR/Cas9-based genome editing to modify *AHL* genes; 5) Characterize seedling morphology in canola varieties previously