

Figure 1. Soil microbial lipid abundance. Biomarker groups and total PLFA concentrations (nmol/g) of soil at 0-5 (A), and 5-10 (B) cm depths from crop years 2009 to 2014 (6 replicates each year). Values are least square means (n=120). Error bars indicate standard error. Values within each biomarker group with different letters are significantly different ($p \leq 0.05$)

In a 6-year on-farm canola-wheat rotation study conducted on the Hal Johnson farm east of Davenport, WA, grain yields of spring wheat (SW) following winter canola (WC) were reduced an average of 17% compared to yields following winter wheat (WW) (see related article on page 40). With soil samples collected and archived from that study, the objective of this research was to determine the differences and similarities in the soil microbial communities associated with WC and WW, and if those differences were correlated to SW yield response. Microbial biomass and community composition were determined using phospholipid fatty acid analysis (PLFA).

Results showed that WC generally led to decreased microbial biomass compared to WW. Notably, fungi, and AM fungi were more prone than bacteria to the apparent canola rotation effect. The reduction in fungi and AM fungi were also observed in SW following WC, indicating a residual affect (Fig. 1). However, the longer-term effects (i.e., after one year) were negligible. These results demonstrate the relationship between soil microbial community composition and crop productivity. Our data suggest that WC can have significant effects on microbially-mediated soil processes such as nutrient cycling that could potentially produce short-term yield declines in subsequent crops. Data from this study will help enable regional farmers to adjust their sequence of planting canola in wheat-based rotations to allow for continued crop diversification and to maintain optimum crop yield potential.

SOB3/AHL29 Regulates Seed Size and Hypocotyl Elongation in Plants



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Seed shape and size are important agronomic traits because they can affect yield, ease of harvesting, and seedling establishment especially under adverse conditions (e.g. drought, weed and pest pressure). The development of crop varieties that have large seeds and long hypocotyls as seedlings yet maintain normal growth characteristics as adults is challenging for traditional breeding because the regulation of seed/seedling size is a complex and can also be linked to other agronomic traits such as heading date or flowering time.

Based on our previous findings, some of the *AHL* (ΔT -Hook Containing, Nuclear Localized) genes play crucial roles in determining seed size and hypocotyl length in *Arabidopsis thaliana*, a model brassica plant. When we express particular

mutant forms in two of the *AHL* genes *AHL29/SOB3* (*Suppressor of Phytochrome B-4 #3*) and *AHL27/ESC* (*ESCAROLA*) the resulting transgenic *Arabidopsis thaliana* plants have normal adult growth that give rise to larger seeds and seedlings with longer hypocotyls than the wild type. *Arabidopsis thaliana* and *Camelina sativa* are from same family (Brassicaceae) and both have similar genomes. *Camelina sativa* is an emerging oilseed crop in dryland cropping systems. We have also seen

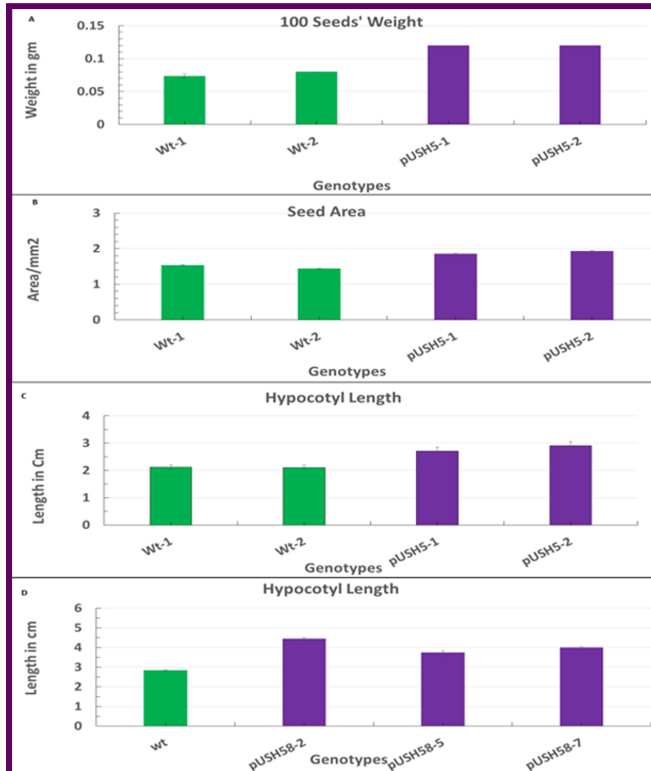


Figure 1. Graphic representation of transgenic *Camelina sativa* expressing the *Arabidopsis thaliana* *SOB3-6* mutation (pUSH5) based on (A) seed weight, (B) seed area and, (C) hypocotyl length.

similar results when generating transgenic *Camelina sativa* overexpressing the same mutant forms of *AHL29/SOB3* and *AHL27/ESC*. Based on our preliminary results, we proposed: (1) to compare seed size of different mutations of *Arabidopsis thaliana* *AHL29/SOB3* and *AHL27/ESC* to identify the specific mutations that confer bigger seeds and longer hypocotyls than the wild type and; (2) translate the finding from *Arabidopsis thaliana* to the oil seed crop *Camelina sativa*. In this study we have generated transgenic lines of *Arabidopsis thaliana* overexpressing different *AHL* mutations. We have then generated transgenic *Camelina sativa* plants overexpressing similar mutated *Arabidopsis thaliana* genes as well as similar genes from *Camelina sativa* (*SOB3-6-like*). Seedlings hypocotyl length, seed size and seed weight were then measured and analyzed using the appropriate software. Our results show that transgenic plants expressing a particular mutation in *SOB3* (*SOB3-6*), as well as a similar mutation in *ESC* (*ESC-11*), confer bigger seeds and taller seedlings than non-transgenic lines in *Arabidopsis thaliana*. The *SOB3-6* mutation can make seeds that are 50% bigger and seedlings that are twice as tall as non-transgenic plants. In addition, the *ESC-11* mutation can make seeds that are ~25% bigger and seedling that are 50% taller than non-transgenic plants. Other mutations we have created in *SOB3* can make seedlings slightly taller but cannot make seeds any bigger than wild type. When we overexpressed the *Arabidopsis thaliana* *SOB3-6* mutation in *Camelina sativa*, seeds can be 50% bigger and seedlings can be 50% taller than non-transgenic plants. When we overexpressed the *Camelina sativa* *SOB3-6-like* mutation in *Camelina sativa*, seeds can be 50% bigger and seedlings can be ~65% taller than non-transgenic plants. Taken together, *SOB3* modulates seed size and hypocotyl length in *Arabidopsis thaliana* and *Camelina sativa* which, may lead to better seedling establishment and increased yield in dryland cropping system.

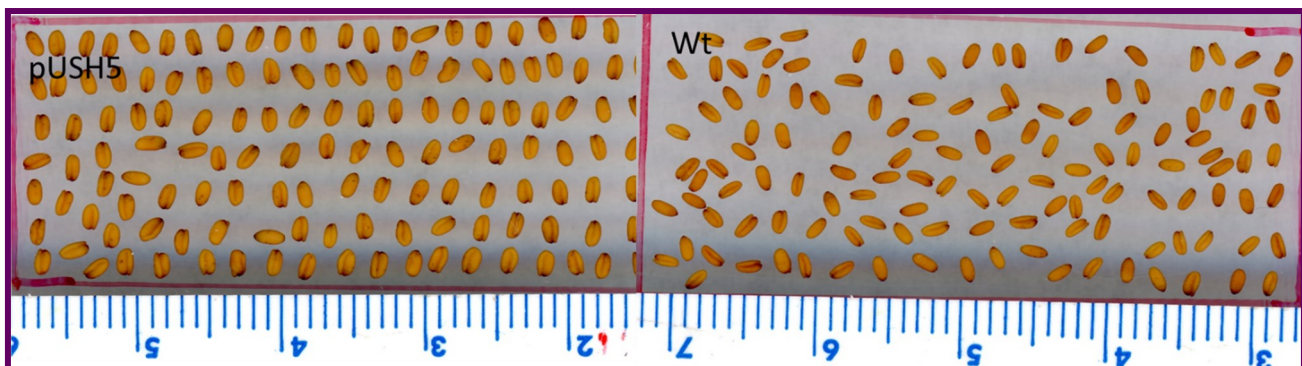


Figure 2. Picture is of transgenic *Camelina sativa* seeds expressing the *Arabidopsis thaliana* *SOB3-6* mutation compared to non-transgenic wildtype plants (Wt).