Nitrogen cycling in root associated soils at bolting, flowering and seed pod filling across eight diverse *Brassica napus* (canola) genotypes

Shanay Williams[1], Sally Vail[2], Bobbi Helgason[1], Steven D. Siciliano[1], and Melissa Arcand[1]

[1]Department of Soil Science, University of Saskatchewan; [2]Saskatoon Research Centre, Agriculture and Agri-Food Canada

Introduction

In 2018, Canada produced over 20 million metric tonnes of *Brassica napus* L. (canola)[1]. However, canola requires relatively large inputs of nitrogen (N) to produce high yields[2]. Consequently, producers must use N fertilizers to alleviate N constrains in the soil. Nitrogen use efficiency (NUE) has become an important goal in sustainable agriculture. To improve NUE and advance breeding efforts in this area, we must examine plant-soil interactions that enhance N uptake. For example, root structure affects the extent of soil nutrient exploration and soil microorganisms influence N cycling processes, including the release of plant available forms of N like nitrate-N (NO_3^--N) and ammonium-N (NH_4^+-N).

Objectives

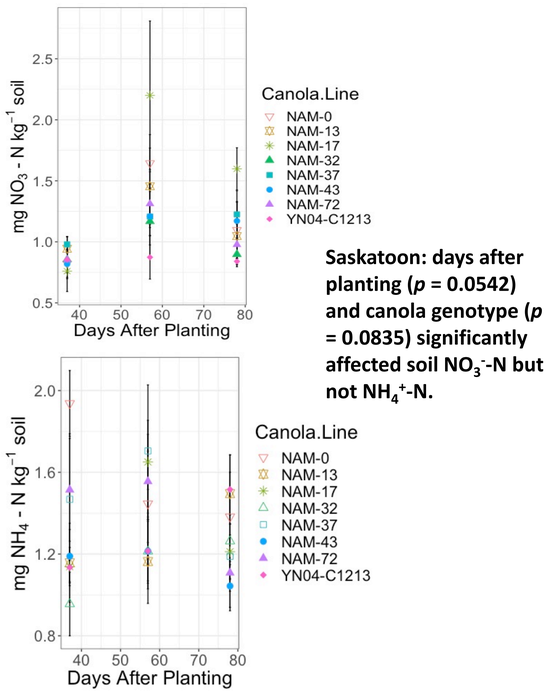
To determine whether soil N processes and root structure differ among diverse canola genotypes, and whether these patterns are affected on a temporal scale.

Methods

Figure 1. Saskatoon canola field before bolting, at flowering, and at seed-pod filling.

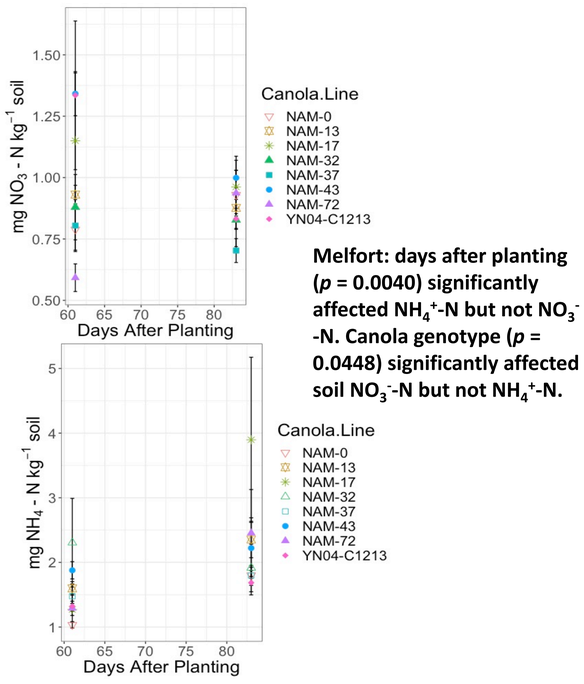
Eight canola genotypes were grown in a random complete block design with 3 replicates, at Saskatoon, SK (Dark Brown Chernozem) and Melfort, SK (Black Chernozem). Roots and root associated soils were collected using a soil corer (length = 10 cm and diameter = 5 cm). Samples were collected before bolting, at flowering and at seed pod filling. Soil NO_3^--N and NH_4^+-N, and potential mineralization-N, were determined using KCl extractions[3]. Root structure was analyzed using WinRHIZO 2013. Analyses of variance using mixed effects were used to analyze the data; genotypes and days after planting were fixed effects and blocking was a random effect. Statistical tests were declared significant at $P < 0.05$.

Preliminary Results



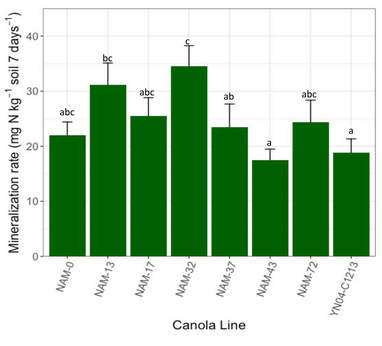
Saskatoon: days after planting (p = 0.0542) and canola genotype (p = 0.0835) significantly affected soil NO_3^--N but not NH_4^+-N.

Figure 2. Saskatoon: Soil NO_3^--N (top) and NH_4^+-N (bottom) mg kg^{-1} from 30-80 days after planting across 8 canola genotypes, error bars represent standard error of the mean.



Melfort: days after planting (p = 0.0040) significantly affected NH_4^+-N but not NO_3^--N. Canola genotype (p = 0.0448) significantly affected soil NO_3^--N but not NH_4^+-N.

Figure 3. Melfort: Soil NO_3^--N (top) and NH_4^+-N (bottom) mg kg^{-1} from 30-80 days after planting across 8 canola genotypes, error bars represent standard error of the mean.



Saskatoon: days after planting (p = 0.0049) and canola genotype (p = 0.0006) significantly affected soil potential mineralization-N.

Figure 4. Mean mineralization rate across eight diverse genotypes at Saskatoon. Canola genotypes explained a significant source of variation in potential mineralization. Error bars represent standard error of the mean.

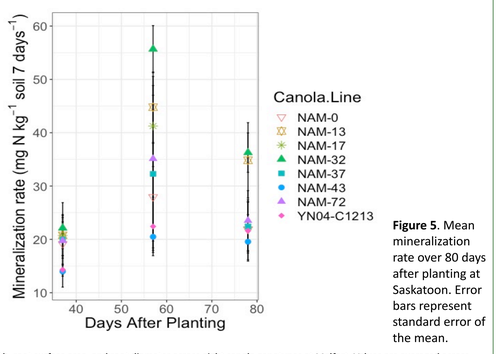


Figure 5. Mean mineralization rate over 80 days after planting at Saskatoon. Error bars represent standard error of the mean.

Table 1. Mean root length, root surface area, and root diameter across eight canola genotypes at Saskatoon. Values are averaged across three time points, with sample number = 9 per genotype. Highlighted values with unique letters are significantly different using Tukey-HSD test. Error represents standard error of the mean.

Genotype	Mean root length (cm)	Mean root surface area (cm^2)	Mean root diameter (mm)
NAM-0	355.56 ± 29.0 ^{ab}	75.5 ± 5.3 ^{a}	0.69 ± 0.03 ^{ab}
NAM-13	326.7 ± 40.9 ^{a}	76.4 ± 6.7 ^{a}	0.79 ± 0.07 ^{abc}
NAM-17	294.7 ± 33.7 ^{a}	74.1 ± 7.9 ^{a}	0.80 ± 0.02 ^{bc}
NAM-32	292.2 ± 32.0 ^{a}	89.0 ± 10.5 ^{a}	0.98 ± 0.05 ^{c}
NAM-37	480.0 ± 54.4 ^{b}	88.8 ± 10.1 ^{a}	0.60 ± 0.03 ^{a}
NAM-43	335.3 ± 72.4 ^{a}	70.7 ± 4.3 ^{a}	0.69 ± 0.05 ^{ab}
NAM-72	325.2 ± 39.3 ^{a}	76.4 ± 9.2 ^{a}	0.78 ± 0.07 ^{abc}
YN04-C1213	357.3 ± 46.3 ^{ab}	81.5 ± 6.7 ^{a}	0.77 ± 0.06 ^{abc}

Table 2. Mean root length, root surface area, and root diameter across eight canola genotypes at Melfort. Values are averaged across three time points, with sample size = 9 per genotype. Highlighted values with unique letters are significantly different using Tukey-HSD test. Error represents standard error of the mean.

Genotype	Mean root length (cm)	Mean root surface area (cm^2)	Mean root diameter (mm)
NAM-0	480.4 ± 77.0 ^{ab}	76.7 ± 10.6 ^{ab}	0.52 ± 0.04 ^{a}
NAM-13	523.2 ± 54.9 ^{ab}	85.3 ± 8.6 ^{ab}	0.54 ± 0.05 ^{a}
NAM-17	336.8 ± 38.2 ^{a}	60.2 ± 7.6 ^{a}	0.59 ± 0.06 ^{a}
NAM-32	444.7 ± 52.4 ^{ab}	71.0 ± 7.7 ^{ab}	0.52 ± 0.03 ^{a}
NAM-37	560.4 ± 64.7 ^{b}	85.0 ± 6.8 ^{ab}	0.53 ± 0.05 ^{a}
NAM-43	382.6 ± 24.9 ^{ab}	76.4 ± 2.6 ^{ab}	0.64 ± 0.03 ^{ab}
NAM-72	323.7 ± 25.5 ^{ab}	94.7 ± 9.8 ^{b}	0.94 ± 0.10 ^{b}
YN04-C1213	489.4 ± 61.7 ^{ab}	81.0 ± 8.7 ^{ab}	0.58 ± 0.09 ^{a}

Discussion

The differences in NO_3^--N among genotypes (Figures 1 & 2) may be due to 1) genotype differences in soil microbiomes influencing soil N cycling[4]; 2) differences in the structure of the plant roots enabling exploration and access to soil N[5]; 3) rates of transpiration, which can affect mass flow of NO_3^--N and subsequent uptake from the soil[6].

Soil NO_3^--N was highest at flowering at Saskatoon and Melfort (Figures 1 & 2) potentially because of increased mineralization (Figure 4) and subsequent nitrification. Soil NH_4^+-N decreased over time at Saskatoon, and increased at Melfort from flowering to seed-pod filling (Figures 1 & 2).

At Saskatoon, canola genotype NAM-32 had the highest mineralization rate and NAM-43 and YN04-C1213 had the lowest (Figure 3), indicating that plant-specific factors are influencing soil N cycling. Interestingly, NAM-32 had significantly lower root length, but significantly larger root diameter and numerical highest root surface area (Table 1), suggesting potential for high root-soil interactions that could influence N mineralization (Figure 3). Also, NAM-37 had significantly longer root length and significantly smaller root diameter at both sites (Tables 1 & 2). This genotype potentially has great ability to explore the soil to find nutrients when compared to other genotypes.

Conclusion

Canola genotypes significantly affected soil N processes and root dimensions for both sites. The differences in soil N processes may be due to factors influencing microbial N cycling and the rate of plant N uptake. Further analysis and subsequent studies will examine the mechanisms driving differences in soil inorganic N and N uptake between these diverse genotypes; as well as the rhizosphere and root microbiomes associated with these genotypes.

References:

[1]Statistics Canada. 2018. Table 32-10-0359-01 Estimated areas, yield, production, average farm price and total farm value of principal field crops, in metric and imperial units. [2]Grant, C.A.; Bailey, L.D. Fertility Management in Canola Production. Can. J. Plant Sci. 1993 , 73 , 651–670. [3]Maynard, D.G., Karla, Y.P., Crumbaugh, J.A., 2008. Nitrate and exchangeable ammonium nitrogen. In: Carter, M., Gregorich, E. (Eds.), Soil Sampling andMethods of Analysis, second ed. CRC Press, Boca Raton, Fl, pp. 71e75. [4]Marschner, H. 1995 Mineral nutrition of higher plants, 2nd edn. Academic, London. [5]Hodge, A., Berta, G., Doussan, C., et al. 2009. Plant root growth, architecture and function. Plant Soil 321: 153–187. [3]Cahill, J.F., and G.G. McNickle. 2011. The behavioral ecology of nutrient foraging by plants. Annu Rev Ecol Evol Syst 42:289-311. [6]Lu, M., Yang, Y., Luo, Y., et al. 2011. Responses ecosystem nitrogen cycle to nitrogen addition: a meta-analysis. New Phytol 189:1040–1050.