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

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Introduction

In 2018, Canada produced over 20 million metric tonnes of Brassica napus (canola). However, canola requires relatively large inputs of nitrogen (N) to produce high yields. 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 (NO₃-N) and ammonium-N (NH₄-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

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 NO₃-N and NH₄-N, and potential mineralization-N, were determined using KCl extractions. 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

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Mean root length (cm)</th>
<th>Mean root surface area (cm²)</th>
<th>Mean root diameter (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>NAM-0</td>
<td>23.5 ± 6.21</td>
<td>74.9 ± 6.21</td>
<td>0.89 ± 0.03</td>
</tr>
<tr>
<td>NAM-13</td>
<td>22.3 ± 6.21</td>
<td>74.9 ± 6.21</td>
<td>0.89 ± 0.03</td>
</tr>
<tr>
<td>NAM-17</td>
<td>22.3 ± 6.21</td>
<td>74.9 ± 6.21</td>
<td>0.89 ± 0.03</td>
</tr>
<tr>
<td>NAM-32</td>
<td>22.3 ± 6.21</td>
<td>74.9 ± 6.21</td>
<td>0.89 ± 0.03</td>
</tr>
<tr>
<td>NAM-35</td>
<td>22.3 ± 6.21</td>
<td>74.9 ± 6.21</td>
<td>0.89 ± 0.03</td>
</tr>
<tr>
<td>NAM-57</td>
<td>22.3 ± 6.21</td>
<td>74.9 ± 6.21</td>
<td>0.89 ± 0.03</td>
</tr>
</tbody>
</table>

Discussion

The differences in NO₃-N among genotypes (Figures 1 & 2) may be due to 1) genotype differences in soil microbiomes influencing soil N cycling; 2) differences in the structure of the plant roots enabling exploration and access to soil N; 3) rates of transpiration, which can affect mass flow of NO₃-N and subsequent uptake from the soil.

Soil NO₃-N was highest at flowering at Saskatoon and Melfort (Figures 1 & 2) potentially because of increased mineralization (Figure 4) and subsequent nitrification. Soil NH₄-N increased 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 higher 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

Tables

Table 1: Mean root length, root surface area, and root diameter across eight genotypes at Saskatoon. Values are averaged across two time points, with same number of days per genotype. Highlighted values in columns are significantly different using Tukey HSD test given at P = 0.05.

Table 2: Mean root length, root surface area, and root diameter across eight genotypes at Saskatoon. Values are averaged across two time points, with same number of days per genotype. Highlighted values in columns are significantly different using Tukey HSD test given at P = 0.05.

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

Figure 2: Soil NO₃-N (top) and NH₄-N (bottom) ng kg⁻¹ from 30-40 days after planting across 8 canola genotypes, error bars represent ± standard error of the mean.

Figure 3: Mean mineralization rates across eight genotypes at Saskatoon. Canola genotypes explored a significant range of variation in potential mineralization. Error bars represent ± standard error of the mean.

Figure 4: Mean mineralization rates across eight genotypes at Saskatoon. Canola genotypes explored a significant range of variation in potential mineralization. Error bars represent ± standard error of the mean.

Figure 5: Melfort: days after planting (p = 0.0049) and canola genotype (p = 0.0066) significantly affected soil potential mineralization-N.