Trails Identification to Improve Yield Potential and Nitrogen Use Efficiency in Wheat

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Introduction
Nitrogen (N) is critical to but expensive for growth and development of wheat. The ability to take advantage of existing and applied N determines nitrogen use efficiency (NUE), the capacity by which plant uptake and transport N into biomass and grains (Todeschini et al. 2015). This capacity can be dissected into the impact of N on grain number (GN) and kernel weight (KW), which together, make the ultimate sink-size in wheat. In this study, we evaluate these yield deterministic traits (GN and KW) through field-based phenotyping of representative Purdue-bred experimental lines.

Objectives
- Understand the responsiveness of GN and KW to N input.
- Identify interacting and non-interacting wheat germplasm to N input.

Methods
We grew 30 representative Purdue-bred experimental lines in split plot design (N as main plots and lines as sub-plots) under two contrasting N availability environments i.e., low N (< 45 lbs/acre) and high N (100 lbs/acre).

Results
- Grain number showed a greater response (27.90%) than kernel weight (no change) to decreases in N input, meaning that deficiency in N causes the plant to produce grains (sink) with proportional size.
- KW was highly heritable (0.92 and 0.91) in both N environments with GN having heritability of 0.58 and 0.44, respectively per treatment.
- Under both high and low N environments, GN was correlated significantly with biomass (0.77, 0.90) and spikes per unit area (0.59, 0.69).

Table 1. N effects on yield and component traits over 30 representative lines of SRWW at low N (< 45 lbs/acre) and high N (100 lbs/acre).

<table>
<thead>
<tr>
<th>Traits</th>
<th>High N</th>
<th>Low N</th>
<th>Change</th>
<th>High N</th>
<th>Low N</th>
</tr>
</thead>
<tbody>
<tr>
<td>Grain yield (GY)</td>
<td>91*</td>
<td>76*</td>
<td>-13.0%</td>
<td>0.78</td>
<td>0.87</td>
</tr>
<tr>
<td>Biomass (BIO)</td>
<td>123</td>
<td>105</td>
<td>-14.6%</td>
<td>0.14</td>
<td>0.32</td>
</tr>
<tr>
<td>Spikes per unit area (SPUA)</td>
<td>55</td>
<td>56</td>
<td>-9.30%</td>
<td>0.63</td>
<td>0.78</td>
</tr>
<tr>
<td>Kernels per spike (KPS)</td>
<td>32**</td>
<td>27**</td>
<td>-15.60%</td>
<td>0.73</td>
<td>0.72</td>
</tr>
<tr>
<td>Grain number (GN)/unit area</td>
<td>1.3K**</td>
<td>1.0K*</td>
<td>-27.90%</td>
<td>0.58</td>
<td>0.44</td>
</tr>
<tr>
<td>Kernel weight (KW)</td>
<td>39**</td>
<td>39*</td>
<td>No change</td>
<td>0.92</td>
<td>0.91</td>
</tr>
</tbody>
</table>

Table 2. Correlations among YLD, BIO, KPS, SPUA, thousand kernel weight (TKW), and GN at high N (100 lbs/acre - upper right) and low N (< 45 lbs/acre - lower left). Significant levels of 0.05*, 0.01**, and 0.001***.

- GN is highly significant under both environments, having an impact on yield with response to N availability.
- KW is relatively “fixed” across these experimental lines when source (N) is limiting.

Figure 2. Multiple regression GY_i = β_0 + β_1GN_i + β_2KW_i + ε_i analysis evaluating GY in response to variation in GN and KW under two contrasting N environments. Signif. codes: ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05.

Figure 3. Yield of 30 breeding lines under low N and high N environments. All except three lines showed non-interacting patterns. The three N interacting lines were 10565C1-1, 04719A1-16-1-47-4, and 10222A1-09-2, acknowledging that not all lines respond similarly to changes in N.

References

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