EVALUATION OF GENOTYPE BY ENVIRONMENT INTERACTION FOR GRAIN YIELD IN DURUM WHEAT USING NON-PARAMETRIC STABILITY STATISTICS

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ABSTRACT

If genotype (G) ranks change from one environment (E) to another, genotype by environment interactions (GEI) reflects the need for testing Gs in numerous Es in order to obtain reliable results. The aim of this study was to compare 16 non-parametric stability statistics (NPSSs) for GEI on grain yields of 15 durum wheat genotypes, consisting of 11 advanced lines selected from Turkish National Durum Wheat Breeding Program (TNDWBP) and four checks, tested in 12 rain-fed environments during the 2 cropping seasons (2009–2010 and 2010-2011) in Turkey. The combined ANOVA indicated that G, E and GEI effects were significant for grain yield. According to analyses of NPSSs, the highest in ranking (TOP), percentage of adaptability (PA), rank mean (RM) and yield-stability (YS) statistics were positively associated with grain yield and therefore characterized under the dynamic concept of stability. In addition, spearman rank correlation analysis revealed that only TOP, PA, RM and YS statistics would be useful for simultaneous selection for high grain yield and stability. Based on the 16 NPSSs used in this study, Dumlupinar cultivar (G15) was both the most stable and one of the highest yielding ones. On the other hand, G5 and G7 were the most stable ones among the advanced lines tested, but their yield performances were lower. As a result, this study showed that the crossing block of TNDWBP should be enriched by germplasm being capable of dynamic stability, wide adaptation and higher yielding.

Key words: Durum Wheat (T. durum L.), Grain Yield, Genotype by Environment Interaction, Non-parametric Stability Statistics

INTRODUCTION

Durum wheat landraces were formed around 7000 BC in Anatolia, Turkey (Nesbitt and Samuel, 1996). Turkey is blessed with agro-climatic regions suitable for the cultivation of durum wheat and among the top 3 durum wheat producing countries in the world with 3 Mt of production during 2009 (Yildirim et al., 2013). In Mediterranean Basin, durum wheat is mainly grown under rain-fed conditions, characterized by unpredictable rainfall and a large incidence of abiotic and biotic stresses. Drought and heat during the grain filling period, nutrient deficiencies, soil problems, diseases, and pests are the main yield constraints (Royo et al., 2009). Prevailing abiotic and biotic stresses cause GEIs in MEYTs (Kang, 2002). GEI is one of the overwhelming challenges against adoption and promotion of new cultivars released by durum wheat breeding programs in Mediterranean countries (Habash et al., 2009).

There are two major approaches to studying GEI and determining adaptation of genotypes (Huehn, 1996). The first and most common approach is parametric, which relies on distributional assumptions about genotypic, environmental and GEI effects. The second major approach is the nonparametric or analytical clustering approach, which relates environments and phenotypes relative to biotic and abiotic environmental factors without making specific modeling assumptions. For practical applications, however, most breeding programs incorporate some elements of both approaches (Becker and Leon, 1988).

The parametric stability methods have good properties under certain statistical assumptions, like normal distribution of errors and interaction effects; however, they may not perform well if these assumptions are violated (Huehn, 1990). That means parametric tests for significance of variances and variance-related measures could be very sensitive to the underlying assumptions. Thus, it is wise to search for alternative approaches that are more robust to departures from common assumptions, such as nonparametric measures (Nassar and Huehn, 1987). Thus, the level of association between the estimates of stability and adaptability from different models is the indicative if one or more statistics could be used for reliable prediction of responses in different
environments. This association can also help breeders to choose statistics that better obey the concept of stability (Duarte and Zimmermann, 1995).

There are several NPSSs commonly used. They can be simply estimated and interpreted. Nonparametric procedures proposed by St Pierre et al. (1967), Langer et al. (1979), Huehn (1979; 1996), Ketata (1988), Fox et al. (1990), Kang and Magari (1995), and Thennarasu (1995) are based on the ranks of genotypes in each environment and genotypes with similar ranking across environments are classified as stable.

The objectives of this study were to (i) identify durum genotypes that have both high mean yield and stable yield performance across different environments for rain-fed areas of Turkey, and (ii) study the relationships among NPSSs.

MATERIALS AND METHODS

Field Trials

Fifteen durum wheat genotypes (Table 1) were grown in 12 rain-fed environments (Table 2) from the Central Anatolian Region and Aegean Transitional Zone of Turkey during the two consecutive cropping seasons (2009-2010 and 2010-2011). The genotypes comprised 4 checks (registered cultivars) and 11 advanced lines from TNDWB. The experimental layout was a randomized complete block design with 4 replications. Sowing was done with an experimental drill in 1.2 m by 7 m plots, consisting of 6 rows spaced 20 cm apart. The seeding rate was 550 seeds m⁻². Fertilizer application was 27 kg N ha⁻¹ and 69 kg P₂O₅ ha⁻¹ at the planting and 50 kg N ha⁻¹ at the stem elongation stage. Harvesting was done with an experimental combine in 1.2 m by 5 m plots. Grain yield was obtained by expressing plot grain yields on a hectare basis (t ha⁻¹). Details of the 15 genotypes and 12 environments are given in Tables 1 and 2, respectively.

Statistical Analyses

ANOVA, Spearman’s rank correlation and comparison of the means with LSD test (P<0.05) were performed using SAS© 9.1. SAS codes proposed by Hussein et al. (2000) for NPSSs S⁽¹⁾ and S⁽⁶⁾ (Huehn, 1996) and TOP (Fox et al., 1990) and by Lu (1995) for S⁽¹⁾ and S⁽³⁾ (Nassar and Huehn, 1987) were used in the analyses. The other NPSSs RM, RSD and YSD (Ketata, 1988), PA (St Pierre et al., 1967), R₁ and R₂ (Langer et al., 1979), YS (Kang and Magari, 1995), NP⁽¹⁾, NP⁽²⁾, NP⁽³⁾ and NP⁽⁴⁾ (Thennarasu, 1995) were estimated using Excel©. Principal components analysis (PCA) was performed using Biplot and Singular Value Decomposition Macros for Excel© (Lipkovich and Smith, 2002).

Table 1. Codes, advanced line parentages and cultivar names of the 15 durum wheat genotypes

<table>
<thead>
<tr>
<th>Code</th>
<th>Cultivar</th>
<th>Yield (t ha⁻¹)</th>
</tr>
</thead>
<tbody>
<tr>
<td>G2</td>
<td>KIZLTAN</td>
<td>3.11 df</td>
</tr>
<tr>
<td>G6</td>
<td>KUNDURU</td>
<td>2.60 h</td>
</tr>
<tr>
<td>G11</td>
<td>ALTINTAS</td>
<td>3.04 ef</td>
</tr>
<tr>
<td>G15</td>
<td>DULMULIPINAR</td>
<td>3.28 bd</td>
</tr>
</tbody>
</table>

Advanced line

<table>
<thead>
<tr>
<th>Code</th>
<th>Cultivar</th>
<th>Yield (t ha⁻¹)</th>
</tr>
</thead>
<tbody>
<tr>
<td>G1</td>
<td>KRISTAL//AKBASAK/BOTNO</td>
<td>3.33 bc¹</td>
</tr>
<tr>
<td>G5</td>
<td>YERLI//AKBUG&quot;S&quot;/HEVIDIK/3/B52/4/C1252</td>
<td>2.98 fg</td>
</tr>
<tr>
<td>G8</td>
<td>BERK/G75T181/BAGACAK&quot;S&quot;/3/KIZLTAN</td>
<td>3.27 bd</td>
</tr>
<tr>
<td>G10</td>
<td>HARA456/4/61-130/414-44//68111/WARD/3/69T02/69T11//ZF7113</td>
<td>3.83 a</td>
</tr>
<tr>
<td>G12</td>
<td>16-61-130/UVY162/64140/WARD</td>
<td>3.12 df</td>
</tr>
<tr>
<td>G14</td>
<td>MENCEKI&quot;S&quot;/DWIRNAZ99-6//KUMBET</td>
<td>2.82 g</td>
</tr>
</tbody>
</table>

Mean: 3.13; LSD (0.05) = 0.17

¹Lower case letters stand for genotype rankings based on LSD (0.05)
RESULTS

ANOVA and Genotype by Environment Interaction

The ANOVA revealed that E and G main effects and GEI were significant at P<0.001 (Table 3). The Es accounted for the 73.8 % of total variation for grain yield, followed by GEI which captured 20.6 %, while G accounted for only 5.6 %.

The GEI effect was greater by about four times than the G effect, indicating the presence of remarkable GEI. It was confirmed by the fact that the GEI mean grain-yield varied from 1.05 t ha⁻¹ for environment E5 to 4.72 t ha⁻¹ for E10 (Table 2).

Genotypic mean grain yields ranged from 2.60 t ha⁻¹ for G6 to 3.82 t ha⁻¹ for G10 with a mean of 3.13 t ha⁻¹ (Table 1). Among the registered cultivars (G2, G6, G11 and G15), merely G15 had higher grain yield than the grand mean, whereas 5 (G10, G4, G1, G8 and G9) out of 11 advanced lines were higher yielding ones.

Table 2. Codes, cropping seasons, mean grain yields and precipitation amounts for 12 environments

<table>
<thead>
<tr>
<th>Environment Code</th>
<th>Cropping Season</th>
<th>Location</th>
<th>Mean Yield (t ha⁻¹)</th>
<th>Precipitation (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>E1</td>
<td>2009-2010</td>
<td>Konya</td>
<td>2.80 g</td>
<td>320</td>
</tr>
<tr>
<td>E2</td>
<td>2009-2010</td>
<td>Cumra</td>
<td>2.60 h</td>
<td>281</td>
</tr>
<tr>
<td>E3</td>
<td>2009-2010</td>
<td>Gozlu</td>
<td>3.21 e</td>
<td>325</td>
</tr>
<tr>
<td>E4</td>
<td>2009-2010</td>
<td>Kutahya</td>
<td>1.47 j</td>
<td>289</td>
</tr>
<tr>
<td>E5</td>
<td>2009-2010</td>
<td>Usak</td>
<td>1.61 j</td>
<td>278</td>
</tr>
<tr>
<td>E6</td>
<td>2010-2011</td>
<td>Konya</td>
<td>2.30 l</td>
<td>342</td>
</tr>
<tr>
<td>E7</td>
<td>2010-2011</td>
<td>Cumra</td>
<td>4.56 b</td>
<td>311</td>
</tr>
<tr>
<td>E8</td>
<td>2010-2011</td>
<td>Karaman</td>
<td>3.81 c</td>
<td>326</td>
</tr>
<tr>
<td>E9</td>
<td>2010-2011</td>
<td>Nigde</td>
<td>3.85 c</td>
<td>368</td>
</tr>
<tr>
<td>E10</td>
<td>2010-2011</td>
<td>Aksaray</td>
<td>4.72 a</td>
<td>354</td>
</tr>
<tr>
<td>E11</td>
<td>2010-2011</td>
<td>Ankara</td>
<td>3.61 d</td>
<td>398</td>
</tr>
<tr>
<td>E12</td>
<td>2010-2011</td>
<td>Eskisehir</td>
<td>2.98 f</td>
<td>345</td>
</tr>
</tbody>
</table>

LSD (0.05) 0.157

Lower case letters stand for environmental rankings based on LSD (0.05)

Table 3. Combined analysis of variance for grain yield data of 15 durum wheat genotypes grown at 12 environments

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>SS</th>
<th>MS</th>
<th>F</th>
<th>Model</th>
<th>Explained (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Environment (E)</td>
<td>11</td>
<td>716.11</td>
<td>65.10</td>
<td>127.58***</td>
<td>Random</td>
<td>73.8</td>
</tr>
<tr>
<td>Replication (E)</td>
<td>36</td>
<td>18.37</td>
<td>0.51</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Genotype (G)</td>
<td>14</td>
<td>54.37</td>
<td>3.88</td>
<td>2.98***</td>
<td>Fix</td>
<td>5.6</td>
</tr>
<tr>
<td>G x E Interaction (GEI)</td>
<td>154</td>
<td>200.50</td>
<td>1.30</td>
<td>6.74***</td>
<td>Random</td>
<td>20.6</td>
</tr>
<tr>
<td>Error</td>
<td>504</td>
<td>97.37</td>
<td>0.19</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>719</td>
<td>1086.72</td>
<td>1.00</td>
<td></td>
<td></td>
<td>100.0</td>
</tr>
</tbody>
</table>

CV (%) = 14.04  R² = 0.91  Mean = 3.13 t ha⁻¹

Non-parametric Stability Statistics

Estimated values and ranks of 16 NPSSs and grain yield means (Y) for 15 durum wheat genotypes tested in 12 environments during the two cropping seasons are presented in Tables 4 and 5, respectively.

Ketata (1988) proposed four NPSSs: rank’s mean (RM) and its standard deviation (RSD) and yield mean (Y) and its standard deviation (YSD). According to RM and Y, genotypes G10 and G4 were the most desirable ones, while genotypes G5 and G6 based on YSD and genotypes G7 and G3 based on RSD were identified as the most stable ones (Tables 4 and 5). However G3, G5, G6 and G7 were lower yielding genotypes.

The NPSS of Fox et al. (1990) consists of scoring the percentage of environments in which each genotype ranked in the TOP, MIDDLE and BOTTOM third of trial entries. A genotype usually found in the TOP third of entries across environments can be considered relatively well adapted and stable. Thus, G4 and G10 were adapted genotypes, because they ranked in the TOP third of genotypes in a high percentage of environments (high TOP value, 67 %), and was followed by G15 (50 %) (Tables 4 and 5). The undesirable genotypes identified by this method were G3, G6 and G7.

Kang and Magari (1995) proposed a NPSS, YS, uses both yield (Y) and Shukla’s stability (S) variance (Shukla, 1972). The genotypes with the highest YS values are the most favorable ones. According to the YS statistic, G1 and G15 had the highest values and therefore were stable genotypes with high yield, followed by G9 and G10 (Tables 4 and 5).
A genotype can be evaluated for its adaptation using the percentage of adaptability (PA) (St Pierre et al., 1967). This method measures proportion of environments in which a given genotype outperforms the average of all genotypes included in the trial (Duarte, Zimmermann, 1995). The genotypes G4, G10 and G15 had the highest PA value (75 %), which indicates that the yields of these genotypes were superior to the overall yield of the 15 genotypes in the trials, while G7 had lowest PA value (8.33 %) (Tables 4 and 5).

Langer et al. (1979) suggested two indexes (R1 and R2) related to the ranges in productivity of genotypes as crude measures of production response. The first, denoted R1, equals the difference between the minimum and maximum yields of a genotype in a series of environments, and the second, denoted R2, is the difference between the yields of a variety in the lowest and best production environments. Based on statistic R1, the most stable genotypes were G6, G5 and G11 with lower yields, whereas G10, G8 and G2 were unstable ones with higher yields (Tables 4 and 5). As for R2, G14, G6 and G5 were the most stable and lower yielding genotypes. However, the unstable were G10, G9 and G1 whose yields were higher than the average.

NPSSs S(1), S(2), S(3) and S(6) were developed by Huehn (1979; 1996). The S(1) and S(2) statistics are based on ranks of genotypes across environments and they give equal weight to each environment. Genotypes with fewer changes in rank are considered to be more stable (Becker and Leon, 1988). These two statistics ranked genotypes similarity for stability. The significance tests for S(1) and S(2) were also developed by Nassar and Huehn (1987). According to significance levels of X2 tests for S(1) and S(2), there were significant differences in rank stability among the 15 genotypes grown in 12 environments. Genotypes G15 and G7 had the lowest values of S(1) (P<0.01) while G2 had the highest in S(1) (P<0.05). In

### Table 4. Mean grain yield (Y) and estimates of 16 non-parametric stability statistics for 15 durum wheat genotypes tested in 12 environments

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Y</th>
<th>YSD</th>
<th>RM</th>
<th>RSD</th>
<th>TOP</th>
<th>YS</th>
<th>PA</th>
<th>R1</th>
<th>R2</th>
</tr>
</thead>
<tbody>
<tr>
<td>G1</td>
<td>3.33</td>
<td>1.29</td>
<td>6.75</td>
<td>4.03</td>
<td>41.66</td>
<td>15</td>
<td>50.00</td>
<td>4.04</td>
<td>4.04</td>
</tr>
<tr>
<td>G2</td>
<td>3.11</td>
<td>1.33</td>
<td>8.58</td>
<td>5.58</td>
<td>41.66</td>
<td>7</td>
<td>50.00</td>
<td>4.18</td>
<td>2.69</td>
</tr>
<tr>
<td>G3</td>
<td>2.94</td>
<td>1.05</td>
<td>8.92</td>
<td>3.09</td>
<td>8.33</td>
<td>1</td>
<td>33.33</td>
<td>3.58</td>
<td>3.58</td>
</tr>
<tr>
<td>G4</td>
<td>3.43</td>
<td>1.38</td>
<td>5.33</td>
<td>4.62</td>
<td>66.66</td>
<td>9</td>
<td>75.00</td>
<td>3.87</td>
<td>3.87</td>
</tr>
<tr>
<td>G5</td>
<td>2.98</td>
<td>0.96</td>
<td>8.75</td>
<td>3.36</td>
<td>25.00</td>
<td>4</td>
<td>33.33</td>
<td>2.75</td>
<td>2.55</td>
</tr>
<tr>
<td>G6</td>
<td>2.60</td>
<td>0.79</td>
<td>12.08</td>
<td>3.34</td>
<td>8.33</td>
<td>-3</td>
<td>16.67</td>
<td>2.33</td>
<td>1.90</td>
</tr>
<tr>
<td>G7</td>
<td>2.95</td>
<td>1.02</td>
<td>10.00</td>
<td>1.65</td>
<td>0.00</td>
<td>-6</td>
<td>8.33</td>
<td>3.31</td>
<td>3.31</td>
</tr>
<tr>
<td>G8</td>
<td>3.27</td>
<td>1.47</td>
<td>7.58</td>
<td>5.00</td>
<td>41.66</td>
<td>4</td>
<td>50.00</td>
<td>4.40</td>
<td>3.62</td>
</tr>
<tr>
<td>G9</td>
<td>3.21</td>
<td>1.17</td>
<td>8.25</td>
<td>4.47</td>
<td>41.66</td>
<td>11</td>
<td>41.67</td>
<td>4.08</td>
<td>4.08</td>
</tr>
<tr>
<td>G10</td>
<td>3.83</td>
<td>1.61</td>
<td>4.25</td>
<td>4.56</td>
<td>66.66</td>
<td>11</td>
<td>75.00</td>
<td>5.76</td>
<td>5.76</td>
</tr>
<tr>
<td>G11</td>
<td>3.04</td>
<td>1.01</td>
<td>9.08</td>
<td>4.27</td>
<td>25.00</td>
<td>5</td>
<td>41.67</td>
<td>2.83</td>
<td>2.63</td>
</tr>
<tr>
<td>G12</td>
<td>3.12</td>
<td>1.07</td>
<td>8.42</td>
<td>4.10</td>
<td>16.66</td>
<td>8</td>
<td>41.67</td>
<td>3.16</td>
<td>2.84</td>
</tr>
<tr>
<td>G13</td>
<td>3.06</td>
<td>0.97</td>
<td>7.58</td>
<td>3.96</td>
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<td>6</td>
<td>50.00</td>
<td>3.00</td>
<td>2.84</td>
</tr>
<tr>
<td>G14</td>
<td>2.82</td>
<td>1.11</td>
<td>8.08</td>
<td>4.56</td>
<td>33.33</td>
<td>-8</td>
<td>66.67</td>
<td>3.61</td>
<td>3.12</td>
</tr>
<tr>
<td>G15</td>
<td>3.28</td>
<td>1.19</td>
<td>6.33</td>
<td>3.23</td>
<td>50.00</td>
<td>13</td>
<td>75.00</td>
<td>3.77</td>
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</tr>
<tr>
<td>Mean</td>
<td>3.13</td>
<td>1.16</td>
<td>8.00</td>
<td>3.99</td>
<td>33.33</td>
<td>5.13</td>
<td>47.22</td>
<td>3.64</td>
<td>3.25</td>
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</table>

<table>
<thead>
<tr>
<th>Genotype</th>
<th>S(1)</th>
<th>S(2)</th>
<th>S(3)</th>
<th>S(6)</th>
<th>NP(1)</th>
<th>NP(2)</th>
<th>NP(3)</th>
<th>NP(4)</th>
</tr>
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<tbody>
<tr>
<td>G1</td>
<td>5.68</td>
<td>25.53</td>
<td>26.36</td>
<td>5.75</td>
<td>4.08</td>
<td>0.58</td>
<td>0.72</td>
<td>0.63</td>
</tr>
<tr>
<td>G2</td>
<td>6.57*</td>
<td>30.87*</td>
<td>38.90</td>
<td>7.01</td>
<td>4.83</td>
<td>0.51</td>
<td>0.62</td>
<td>0.80</td>
</tr>
<tr>
<td>G3</td>
<td>4.27</td>
<td>13.36</td>
<td>11.07</td>
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<td>2.83</td>
<td>0.31</td>
<td>0.39</td>
<td>0.57</td>
</tr>
<tr>
<td>G4</td>
<td>5.81</td>
<td>24.69</td>
<td>46.31</td>
<td>8.51</td>
<td>4.50</td>
<td>1.13</td>
<td>0.89</td>
<td>0.74</td>
</tr>
<tr>
<td>G5</td>
<td>3.93</td>
<td>10.96</td>
<td>14.20</td>
<td>3.88</td>
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<td>0.27</td>
<td>0.36</td>
<td>0.51</td>
</tr>
<tr>
<td>G6</td>
<td>6.00</td>
<td>25.60</td>
<td>10.04</td>
<td>2.45</td>
<td>4.33</td>
<td>0.32</td>
<td>0.40</td>
<td>0.84</td>
</tr>
<tr>
<td>G7</td>
<td>2.07**</td>
<td>3.29**</td>
<td>3.00</td>
<td>1.40</td>
<td>1.42</td>
<td>0.14</td>
<td>0.17</td>
<td>0.27</td>
</tr>
<tr>
<td>G8</td>
<td>5.87</td>
<td>25.15</td>
<td>36.27</td>
<td>6.49</td>
<td>4.33</td>
<td>0.58</td>
<td>0.63</td>
<td>0.70</td>
</tr>
<tr>
<td>G9</td>
<td>5.96</td>
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<td>4.33</td>
<td>0.51</td>
<td>0.59</td>
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</tr>
<tr>
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*P<0.05, **P<0.01  *Symbols: Y-Mean yield (t ha⁻¹), YSD-Yield standard deviation, RM-Rank mean, RSD-Rank’s standard deviation (Ketata, 1988), YS-Yield stability statistic (Kang and Magari, 1995), PA-Percentage of adaptability (St Pierre et al., 1967), R1 and R2-Range indexers (Langer et al., 1979), TOP-Proportion of environments in which a genotype ranked in the top three (Fox et al., 1990), S(1), S(2), S(3) and S(6)-Ranks of adjusted yield means of genotypes (Huehn, 1979), NP(1), NP(2), NP(3) and NP(4)-Ranks of adjusted yield means of genotypes (Thennarasu, 1995).
case of $S^{(2)}$, G7 and G15 also the lowest values (P<0.01 and 0.05, respectively), whereas G2 and G10 had highest values of $S^{(2)}$ (p<0.05). If $S^{(1)}$ and $S^{(2)} = 0$, it refers a stable genotype (Huehn, 1990). For both statistics, G7 and G15 were stable, but the former was lower yielding and the latter was higher yielding (Tables 4 and 5).

The statistics $S^{(1)}$ and $S^{(6)}$ combine yield and stability based on yield ranks of genotypes in each environment. These parameters measure stability in units of the mean rank of each genotype (Huehn, 1979). The lowest value for each of these statistics indicates maximum stability for a certain genotype. As for $S^{(1)}$ and $S^{(2)}$, G7 was the most stable according to the $S^{(3)}$ and $S^{(6)}$ parameters. The mean yield of G7 followed by G6 and G3 were the lowest genotypes tested. The highest mean yield was for G10 followed by G4, but they were unstable (Tables 4 and 5).

### Table 5. Rank order of 15 durum wheat genotypes based on 16 non-parametric stability statistics

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Mean: 8.00 8.00 7.33 7.73 4.13 6.87 3.47 8.00 8.00

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Mean: 8.00 8.00 8.00 8.00 6.73 6.80 6.00 7.20

Symbols: Y-Mean yield (t ha⁻¹), YSD-Yield standard deviation, RM-Rank mean, RSD-Rank’s standard deviation (Ketata, 1988), YS-Yield stability statistic (Kang and Magari, 1995), PA-Percentage of adaptability (St-Pierre et al., 1967), R₁ and R₂-Range indexes (Langer et al., 1979), TOP-Proportion of environments in which a genotype ranked in the top third (Fox et al., 1990), $S^{(1)}, S^{(2)}, S^{(3)}$ and $S^{(6)}$-Ranks of adjusted yield means of genotypes (Huehn, 1979), $NP^{(1)}, NP^{(2)}, NP^{(3)}$ and $NP^{(4)}$-Ranks of adjusted yield means of genotypes (Thennarasu, 1995).

Results of Thennarasu’s (1995) NPSSs, which are calculated from ranks of adjusted yield means and the ranks of genotypes considering these NPSSs, are shown in Tables 4 and 5. According to the first method ($NP^{(1)}$), genotypes G7, G15 and G5 were stable in comparison with the other genotypes. Genotype G7 had the lowest value of $NP^{(2)}$ and was stable, followed by G5 and G11. Because of the high values for $NP^{(2)}$, the stabilities of G10 followed by G4 were low, although they had the highest mean yield (Table 4). $NP^{(3)}$, like $NP^{(2)}$, identified G7 as the most stable genotype, although it was one of the lowest yielding genotypes. The next most stable genotypes were G5 and G15 which the former had low mean yield performance but the latter did not. The unstable genotypes based on $NP^{(3)}$ were G10 followed by G4 and G1, which had the highest mean yields. Stability parameter $NP^{(3)}$ identified G7 as a stable genotype, followed by G15 and G11; but like $NP^{(2)}$ and $NP^{(3)}$, identified G14, G6 and G2 as unstable. The results of three NPs ($NP^{(1)}, NP^{(2)}$ and $NP^{(3)}$) were very similar to
each other and identified G10 and G4 as unstable, although they had the highest mean yield performances. According to all of Thennarasu’s (1995) NPSSs, G7 was the most stable genotype, although it was one of the lowest mean yielding ones.

Relationships among the Non-parametric Stability Statistics

The Spearman’s rank correlations between each pair of NPSSs (Table 6) demonstrated positive significant rank correlations between mean yield (Y), RM (r = 0.83**), TOP (r = 0.83**), YS (r = 0.87) and PA (r = 0.71**), but negative significant with YSD (r = -0.80**), R1 (r = -0.70**), R2 (r = -0.82**), S3 (r = -0.65**), S6 (r = -0.71**), NP1 (r = -0.70**) and NP3 (r = 0.67). Mean yield showed negative but non-significant correlation coefficients with RSD, S1, S2 and NP3, while it exhibited independence in relation to NP4. Standard deviation of mean yield (YSD) was significantly positively associated with RSD, R1, R2, S1, S3, S6, NP1, NP2 and NP3, while had negative significant relations with RM, TOP, YS and PA.

Table 6. Spearman’s rank correlation coefficients between yield means (Y) and 16 non-parametric stability statistics of 15 durum wheat genotypes tested in 12 environments

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<td>PA</td>
<td>0.77**</td>
<td>0.77**</td>
<td>0.90**</td>
<td>0.92**</td>
<td>0.85**</td>
<td>0.96**</td>
<td>1.00</td>
<td></td>
</tr>
<tr>
<td>R1</td>
<td>0.83**</td>
<td>0.82**</td>
<td>0.57*</td>
<td>0.53*</td>
<td>0.84**</td>
<td>0.68**</td>
<td>0.66**</td>
<td>1.00</td>
</tr>
<tr>
<td>R2</td>
<td></td>
<td></td>
<td></td>
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</tr>
</tbody>
</table>

*P< 0.05, **P<0.01  *Symbols: Y-Mean yield (t ha⁻¹), YSD-Yield standard deviation, RM-Rank mean, RSD-Rank’s standard deviation (Ketata, 1988), YS-Yield stability statistic (Kang and Magari, 1995), PA-Percentage of adaptability (St-Pierre et al., 1967), R1 and R2-Range indexes (Langer et al., 1979), TOP-Proportion of environments in which a genotype ranked in the top third (Fox et al., 1990), S1, S2, S3, S6 and S16-Ranks of adjusted yield means of genotypes (Huehn, 1979), NP1, NP2, NP3 and NP4-Ranks of adjusted yield means of genotypes (Thennarasu, 1995).

Rank’s mean (RM) was significantly positively correlated with TOP, YS and PA. Conversely, it possessed significantly negatively correlations to R2, S3, S6, NP2 and NP3. As for standard deviation (RSD), it showed negative significant correlations with TOP and PA. On the other hand, RSD had positive significant associations with R1, S1, S2, S3, S6, NP1, NP2, NP3 and NP4.

The percentage of environments in which it ranked in the top third of genotypes (TOP) exhibited positive significant relationships with YS and PA. In contrast, it was negative significant relations with R1, R2, S3, S6, NP1, NP2 and NP3.

Yield-stability statistic (YS) had negative significant correlations with R1, R2, S6 and NP2, but merely a positive significant relation with PA. In case of the percentage of adaptability (PA), it had negative significant correlations with R1, S1, S6, NP2 and NP3.

From the genotype yield mean ranges or indices in differential responses to test environments, the first range or index, R1, exhibited positive significant associations with R2, S1, S2, S3, S6, NP1, NP2 and NP3.
Meanwhile, the second range, $R_2$, was significantly positively correlated with $NP_i^{(2)}$ and $NP_i^{(3)}$.

The all pair-wise correlation coefficients among the NPSSs $S_i^{(1)}$, $S_i^{(2)}$, $S_i^{(3)}$, $S_i^{(4)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$ were positively significant at $P<0.01$.

Principal Components Analysis

To better understand the relationships among the NPSSs, a principal components analysis (PCA) was performed. According to the PCA, the two first principal components (PCs) explained 84% (66 and 18% by PC1 and PC2, respectively) of the total variance of the original variables. The relationships among the 16 NPSSs with yield mean are graphically displayed in a biplot, depicted by PC1 vs. PC2 scores (Figure 1). In this biplot, the first PC1 axis visually distinguished the all NPSSs into three groups. Group 1 consisted of $Y$, $TOP$, $YS$, $RM$ and $PA$, where were grouped at the negative side of PC1 axis. Group 2 comprised $NP_i^{(4)}$, $S_i^{(2)}$, $S_i^{(1)}$, $NP_i^{(4)}$ and $RSD$ while Group 3 had $NP_i^{(3)}$, $NP_i^{(2)}$, $S_i^{(3)}$, $S_i^{(6)}$, $R_1$, $YS$ and $R_2$, where both were located at the positive side of PC1 axis. NPSSs from Group 2 were insignificantly but negatively correlated with the NPSSs from Group 1. In contrast, NPSSs from Group 3 were significantly negatively correlated with the NPSSs from Group 1 (Table 6).

![Figure 1. Biplot, which was depicted by PC1 vs. PC2 scores, obtained from principal component analysis conducted based on ranks of 15 durum wheat genotypes for 16 non-parametric stability statistics.](image)

Symbols: $Y$-Mean yield (t ha$^{-1}$), $YS$-Yield standard deviation, $RM$-Rank mean, $RSD$-Rank’s standard deviation (Ketata, 1988), $YS$-Yield stability statistic (Kang and Magari, 1995), PA-Percentage of adaptability (St-Pierre et al., 1967), $R_1$ and $R_2$-Range indexes (Langer et al., 1979), TOP-Proportion of environments in which a genotype ranked in the top third (Fox et al., 1990), $S_i^{(1)}$, $S_i^{(2)}$, $S_i^{(3)}$ and $S_i^{(6)}$-Ranks of adjusted yield means of genotypes (Huehn, 1979), $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$-Ranks of adjusted yield means of genotypes (Thennarasu, 1995).

**DISCUSSION**

GEI is a universal phenomenon existing in MEYTs and complicates the selection of superior genotypes (Ebdon and Gauch, 2002; Yan and Kang, 2003). Various methods are used for reducing GEI effects and facilitating genotype characterization, as selection criteria together with the mean yield of the genotypes. Accordingly, genotypes with minimal variance for yield across environments are considered stable. This idea of stability may be considered as a biological or static concept of stability (Becker and Leon, 1988). This concept of stability is not acceptable to most breeders and agronomists, who prefer genotypes with high mean yields and the potential to respond to agronomic inputs or better environmental conditions (Becker, 1981). The high yield performance of released cultivars is one of the most important targets of breeders; therefore, they prefer a dynamic concept of stability (Becker and Leon, 1988).

In our study, the PC1 separated mean yield ($Y$), $TOP$, $YS$, $PA$ and $RM$ (Group 1) from the other NPSSs (Groups 2 and 3) (Figure 1). Based on the concepts of stability, namely the static (biological) and dynamic (agronomical) ones, PC1 distinguished NPSSs that the statistics $Y$, $TOP$, $YS$, $PA$ and $RM$ were related with dynamic stability
(Group 1) and other remaining methods (Groups 2 and 3) were associated with static stability (Mohammadi et al., 2012). Meanwhile, the highly positive significant correlation between TOP, YS, PA, RM and mean yield (Y) indicated that they were possibly the best NPSSs to be used for identifying higher yielding genotypes. Consequently, any one of these NPSSs would be preferred to select stable and higher yielding genotypes in a breeding program.

Flores et al. (1998) pointed out that the TOP, YS and RM procedures were associated with mean yield (Y) and the dynamic concept of stability. Kang and Magari (1995) found that the YS method was related with high yield performance, and therefore this stability statistic defined stability with dynamic concept. Sabaghnia et al. (2006), Mohammadi et al. (2007), Segherloo et al. (2008) and Yong-Jian et al. (2010) found positive significant correlations between TOP, YS and Y in lentil (L. culinaris L.), durum wheat (T. durum L.), chickpea (C. arietinum L.) and maize (Z. mays L.), respectively. Moreover, significant associations between Y, TOP, YS and PA were indicated by Mohammadi and Amri (2013) in durum wheat (T. durum L.).

The high yield performance of released cultivars is one of the most important breeding objectives; therefore, breeders prefer a dynamic concept of stability (Becker and Leon, 1988). In this research, G10, G4, G15, G9 and G8 had a stable yield performance based on the TOP, YS, PA and RM statistics. We found that the NPSSs of Huehn (1996) (S(1), S(2), S(3) and S(6)) and the NP(1), NP(2), NP(3) and NP(4) of Themaramsu (1995), Ketata’s (1988) RSD and YSD and R1 and R2 proposed by Langer et al. (1979) grouped together (Groups 2 and 3 in Figure 1), since these NPSSs classified genotypes as stable or unstable in a similar fashion. Sabaghnia et al. (2006) found positive significant correlations among these NPSSs in lentil (L. culinaris L.). Scapim et al. (2000) also reported positive significant correlations between S(1) and S(2) in maize (Z. mays L.). Flores et al. (1998) revealed high rank correlations between S(1) and S(2) in faba bean (V. faba L.) and pea (P. sativum L.). Nassar and Huehn (1987) reported that S(1) and S(2) were associated with the static (biological) concept of stability, as they define stability in the sense of homeostasis. The stability statistics of NP(1), S(1), S(2), NP(3) and RSD represent static concepts of stability, and are not correlated with mean yield (Y). Therefore, these stability statistics could be used as compromise methods to select genotypes with moderate yield and high stability (Akcura et al., 2009).

Like the Group 2, the NPSSs (NP(3), NP(2), S(3), S(6), R1, YSD and R2) from Group 3 identified genotypes that were stable based on the static or biological concept of stability, but unlike Group 2, they were also strongly negatively correlated with high mean yield (Y). This concept of stability is not acceptable to most breeders and agronomists, who prefer genotypes with high mean yields and the potential to respond to agronomic inputs or better environmental conditions (Becker, 1981). For example, genotypes G5, G7 and G11 had stable yield performance but had low mean yield based on the NPSSs from Group 3 in our study. Therefore, we do not recommend use of these NPSSs for genotype selection. Mohammadi et al. (2007) and Yong-Jian et al. (2010) reported that the NPSSs S(3), S(6), NP(2), NP(3) and NP(4) were not suitable for detecting stable and high yielding genotypes.

**CONCLUSION**

Our study indicated that group 1 (TOP, YS, PA and RM with yield mean) NPSSs can be used as selection criteria in a breeding program for detecting higher yielding and stable genotypes tested in MEYTs. With respect to 16 NPSSs used in the current study, G15 was the most stable and third highest yielding genotype. However, it was an officially registered cultivar. G5 and G7 were the most stable ones among the all advanced lines tested, but their yield performances were lower. As a consequence, this study underlined that the crossing block of TNDWBP should be enhanced by germplasm carrying genes determining wide adaptation and higher yielding ability.

**ACKNOWLEDGMENTS**

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**LITERATURE CITED**


