Combining superior agronomic performance and terminal heat tolerance with resistance to spot blotch (*Bipolaris sorokiniana*) of wheat in the warm humid Gangetic Plains of South Asia

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Abstract

Seven hundred twenty-nine lines of diverse wheat germplasm lines were evaluated in eight locations of three countries (India, Nepal and Bangladesh) of South Asia for 5 years (1999–2000 to 2003–2004) through Eastern Gangetic Plains Screening Nursery (EGPSN) organized by CIMMYT South Asia, Nepal, for agronomic performance and tolerance to spot blotch of wheat. Each year, the number of lines represented a new set of 150 lines that included six common checks and a different local check at each of the eight locations. One hundred and five lines, 21 in each year, advanced from EGPSN were also tested for 5 years (2000–2001 to 2004–2005) in five locations of South Asia through Eastern Gangetic Plains Yield Trials (EGPYT) to verify spot blotch tolerance and superior yield performance of the selected germplasm. Many lines yielded significantly more than the best check and possessed high levels of spot blotch resistance under warm humid environments of South Asia. The most promising 25 lines have been listed as sources of strong resistance, with 9 lines better yielding than the best resistant check PBW 343 in fewer days to maturity. Most of these superior lines represented elite CIMMYT germplasm and around half were derived from Kauz and Veery. The line EGPYT 67, Kauz//Kauz/Star/3/Prinia/4/Milan/Kauz, was the best for spot blotch resistance, yield, days to maturity, and 1000 grain weight (TKW). The next two lines in the order of merit were EGPYT 84 (Mrg/Buc//Blo/Pvn/3/Pjb 81) and EGPYT 69 (Chirya3/Pastor). The results demonstrate that additional spot blotch resistant wheat genotypes with high grain yield and TKW, and early maturity, have become available as a result of the regional and international collaboration in South Asia.

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Keywords: Spot blotch; *Bipolaris sorokiniana*; *Cochliobolus sativus*; wheat; *Triticum aestivum*; Germplasm; Yield; Resistance; Heat tolerance

1. Introduction

The importance of wheat as a staple food of South Asia is well known. Its enhanced productivity in the post Green Revolution period played a key role in ensuring food security in this thickly populated part of the world, which mainly comprises of India, Pakistan, Nepal and Bangladesh (Evenson et al., 1999; Joshi et al., 2007a). However, in the past decade there was only marginal increase in the productivity of wheat in South Asia, while the population continued to grow faster than in most other parts of the world. In particular, the eastern parts of South Asian nations, including India, Nepal and Bangladesh, are lagging behind their western counterparts (Joshi et al., 2007a). The two major characteristics of the eastern part of South Asia are high temperatures and humidity (Joshi et al., 2007c). This leads to two important stresses: heat and spot blotch disease caused by *B. sorokiniana* (Sacc.) shoem. *Drechslera sorokiniana* (Sacc.)
Subram and Jain (syn. Helminthosporium sativum, teleomorph 
Cochliobolus sativus) (Dubin and van Ginkel, 1991; Joshi et al., 
2004a,b; Sharma and Duveiller, 2004; Pandey et al., 2005). Saari 
(1998) reported that the average yield losses due to leaf blight in 
the Indian subcontinent were as much as 17.5%.

It is generally believed that the level of resistance in high-
yielding wheat genotypes is still unsatisfactory and needs to be 
improved significantly in warmer humid regions of South Asia 
(Sharma et al., 2004a; Sharma and Duveiller, 2006; Joshi et al., 
2007a,b,c). Consequently, an integrated approach, with host 
resistance as a major component, is generally considered best 
for controlling the disease (Hetzel et al., 1991; Mehta et al., 
1992; Joshi and Chand, 2002). For a long time, breeders 
avocated selecting tall and late genotypes for resistance (Dubin 
et al., 1998). Recently, it has been established that plant 
height and earliness are not associated with resistance and it is 
possible to obtain resistant lines that are dwarf and early 
maturing (Joshi et al., 2002). Another report showed that the 
erect leaf present in some of CIMMYT’s best-yielding durum 
and bread wheat lines (Fischer, 1996) tends to reduce spot 
blotch severity (Joshi and Chand, 2002). Leaf tip necrosis of 
wheat, which is known to be due to the presence of gene 
Lin and is reported to be linked with genes Lr34 and Yr18, has 
been suggested as a morphological marker for spot blotch resistance 
(Joshi et al., 2004a).

Another major problem faced by the wheat-growing areas of 
South Asia is high temperature, mainly terminal heat stress 
(Joshi et al., 2007a) as defined by Fischer and Byerlee (1991) 
due to mean daily temperatures above 17.5 °C in the coolest 
month. Both the proximity to the equator and the popular 
cropping systems, which involve late sowing of wheat, are the 
major causes of exposure of wheat in India and other 
neighboring countries to high temperatures during grain filling 
(Tandon, 1994; Rane et al., 2000). Therefore, breeding for high 
temperature tolerance in wheat is another major objective of 
wheat improvement programs in South Asian countries, 
including India, Nepal and Bangladesh. This need is expected to 
grow further in light of growing global warming (Lillemo 
et al., 2005; Joshi et al., 2007a). According to an estimate, there 
are currently around 9 million ha of wheat in tropical or 
subtropical areas (Lillemo et al., 2005) that experience yield 
losses due to high temperature stress in many countries, 
including Bangladesh, India, Nigeria, Uganda, Sudan and 
Egypt, that have long traditions of cultivating wheat. However, 
the current estimates indicate that in India alone, around 13.5 
million ha area is heat stressed (Joshi et al., 2007a). This area 
is likely to become much larger if current trends and future 
predictions about global warming continue. Furthermore, 
current recommendations for crop management practices to 
reduce heat stress rely heavily on additional inputs, especially 
irrigation water (Badaruddin et al., 1999). Because water 
resources around the globe are shrinking (WMO, 1997), there is 
a need for more sustainable and environmentally friendly 
approaches for increasing productivity. In light of the above, 
efforts are being made to identify and disseminate appropriate 
germplasm, especially for small-scale and marginal farmers in 
South Asia (Ortiz Ferrara et al., 2001; Joshi et al., 2005). Recent 
reports suggest that wheat production is not meeting demand in 
India, a major wheat producer of South Asia (Nagarajan, 2005; 
Anon., 2006). One reason is terminal heat stress caused by 
increasing temperatures (Joshi et al., 2007a).

In view of the continued threat of spot blotch disease and 
increasing heat stress to the wheat crop, there is an urgent need 
to identify and develop genetically improved germplasm 
incorporating tolerance to these two stresses and superior 
agromonic features suited to South Asia. To achieve this, a 
regional nursery and a trial called the Eastern Gangetic Plains 
Screening Nursery (EGPSN) and the Eastern Gangetic Plains 
Yield Trial (EGPYT) were distributed to different centers of 
India, Nepal and Bangladesh, by CIMMYT from 2000–2001 to 
2004–2005. The objective of the nursery was to assemble elite 
wheat lines provided by National Agricultural Research 
Programs from India, Bangladesh, Nepal, and CIMMYT and 
to distribute and test them in a range of environments in the 
Eastern Gangetic Plains. The primary goal was to identify, 
select and share improved wheat germplasm regionally, with 
combined resistance/tolerance to B. sorokiniana and heat 
tolerance, along with leaf rust resistance and superior 
agromonic traits (fewer days to maturity, to fit different 
cropping systems; white bold seeds; high-yield potential; good 
adaptation).

2. Materials and methods

2.1. Experimental data

We drew upon 5 years of data from two regional, multi-
environment trials targeting India, Nepal and Bangladesh: the 
EGPSN and the EGPYT. The trials were developed jointly by 
the National Wheat Research Program (NWRP) of Nepal and 
the CIMMYT office in Kathmandu, Nepal, as a regional effort 
of CIMMYT to strengthen the identification and dissemination 
of adapted genotypes for South Asia.

2.2. The EGPSN multi-environment trial

In each of the years, the EGPSN comprised 143 entries and 7 
checks: Bhrikuti (an improved check from Nepal), Sonalika or 
RR-21 (a long-term check from India, spot blotch susceptible), 
Kanchan (an improved check from Bangladesh), Chriya-3 (a 
spot blotch resistant check from CIMMYT, Mexico), PBW 343 
(an improved check from India), Achyut (an improved check 
from Nepal), and a local check of each location. Local checks 
varied for each of the eight locations. This way each year we 
tested 150 lines (143 lines, 6 common checks and 1 local check) 
at each of the locations. The checks were same in all the 5 years 
but 143 lines changed. Thus, at 8 locations over 5 years there 
were 715 lines, 6 common checks and 8 local checks, making 
total number of lines 729. The lines used in the EGPSN 
were derived using diverse genetic backgrounds, keeping in 
view their suitability to the warm humid locations of South 
Asia. Breeding programs from Bangladesh, Nepal and India 
contributed elite wheat lines developed and/or identified by 
their own programs.
The EGPSN was grown at eight locations in India, Nepal and Bangladesh, during 1999–2004. Out of the eight locations, four (Varanasi, Karnal, Shillongani, Sabour) were in India, two (Dinajpur and Jessore) in Bangladesh, and two (Rampur and Bhairahawa) in Nepal (Table 1). All locations are known to be favorable for spot blotch development and (except Karnal, India) are characterized by high temperatures and humidity. For spot blotch development and (except Karnal, India) are characterized by high temperatures and humidity. For example, if a score of 59 is recorded, 5 would represent the height of plants on which the disease is developed and 9 represents the average severity up to that level, assessed as the percent of the leaf area infected, i.e., 90% spot blotch lesions appeared on the leaves. For each score, percentage disease severity was based on the following formula:

\[
\text{Severity} (\%) = \left( \frac{D_1}{9} \times \left( \frac{D_2}{3} \right) \right) \times 100
\]

2.4. Area Under the Disease Progress Curve (AUDPC) and agronomic traits

Observations were recorded for spot blotch severity on three different dates and area under the disease progress curve was determined. For recording spot blotch disease, the double-digit (DD, 00-99) system was used, which is a modification of Saari and Prescott’s severity scale to assess foliar diseases in wheat (Saari and Prescott, 1975; Eyal et al., 1987). The first digit (D1) indicates vertical disease progress on the plant and the second digit (D2) indicates severity measured on the diseased leaf area. For example, if a score of 59 is recorded, 5 would represent the height of plants on which the disease is developed and 9 represents the average severity up to that level, assessed as the percent of the leaf area infected, i.e., 90% spot blotch lesions appeared on the leaves. For each score, percentage disease severity was based on the following formula:

\[
\text{Severity} (\%) = \left( \frac{D_1}{9} \times \left( \frac{D_2}{3} \right) \right) \times 100
\]

AUDPC (van der Plank, 1963; Roelfs et al., 1992) was calculated using the following formula:

\[
\text{AUDPC} = \sum_{i=1}^{n} \left[ \left( \frac{Y_i + Y_{(i+1)}}{2} \right) \times (t_{(i+1)} - t_i) \right]
\]

where \( Y_i \) is the disease level at time \( t_i \), \( t_{(i+1)} - t_i \) the time (days) between two disease scores and \( n \) is the number of dates on which spot blotch was recorded.

For proper comparison, AUDPC values were standardized by maturity recorded for each genotype at each location to make it AUDPC percent days (Reynolds and Neher, 1997). Observations were also recorded for days to maturity, grain yield, 1000 grain weight (TKW), and spot blotch severity. For days to maturity, an entry was considered to have matured when at least 50% of the peduncles were mature. The 1000 kernel weight was measured as the weight of 1000 grains in grams at

<table>
<thead>
<tr>
<th>Country/location</th>
<th>Latitude</th>
<th>Longitude</th>
<th>Altitude (m)</th>
<th>Rainfall (mm)</th>
<th>Mean temperature (°C)</th>
</tr>
</thead>
<tbody>
<tr>
<td>India</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Varanasi</td>
<td>25°18'N</td>
<td>83°03'E</td>
<td>128.9</td>
<td>1000</td>
<td>12.4</td>
</tr>
<tr>
<td>Karnal</td>
<td>29°43'N</td>
<td>75°57'E</td>
<td>252.0</td>
<td>850</td>
<td>10.1</td>
</tr>
<tr>
<td>Sabour</td>
<td>25°15'N</td>
<td>84°4'E</td>
<td>29.0</td>
<td>1350</td>
<td>14.7</td>
</tr>
<tr>
<td>Shillongani</td>
<td>26°N</td>
<td>90°45'E</td>
<td>50.2</td>
<td>1650</td>
<td>13.6</td>
</tr>
<tr>
<td>Bangladesh</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Dinajpur</td>
<td>25°38'N</td>
<td>88°41'E</td>
<td>38.2</td>
<td>1600</td>
<td>13.2</td>
</tr>
<tr>
<td>Jessore</td>
<td>23°11'N</td>
<td>89°11'E</td>
<td>6.7</td>
<td>1900</td>
<td>14.8</td>
</tr>
<tr>
<td>Nepal</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Bhairahawa</td>
<td>25°30'N</td>
<td>83°25'E</td>
<td>107.0</td>
<td>1000</td>
<td>11.6</td>
</tr>
<tr>
<td>Rampur</td>
<td>27°40'N</td>
<td>80°19'E</td>
<td>228.0</td>
<td>1050</td>
<td>10.9</td>
</tr>
</tbody>
</table>

* Mean annual rainfall is based on last 20 years.
* Mean temperature of 3 months (January–March) for last 10 years.
12% moisture content. The grain yield was taken as kilograms per hectare adjusted at 12% moisture content.

2.5. Statistical analyses

All analyses were done using SAS software (SAS Institute, 2003). For the EGPSN, the analysis of variance for all four traits was done separately for each of the 5 years using data of 8 locations for 143 lines and 14 checks (6 common and 1 different in each of the 8 locations). The GLM procedure was used for ANOVA since the local check was different in each of the locations, whereas 143 lines changed in each of the years.

For the EGPYT, ANOVA was performed using combined data for 109 lines (105 lines and 4 checks) at 5 locations over 5 years. Since the 21 varieties changed across years, year was considered a bigger blocking factor, with replications of square matrices within years. To identify superior lines across locations, we performed stability analysis using the SREG model (Crossa et al., 2002) for the response of the 109 EGPYT genotypes (105 lines and 4 common checks) on the combination of the 5 sites and 5 years for AUDPC percent days, grain yield, days to maturity and 1000 grain weight.

The sites regression model (SREG) was

\[ \tilde{y}_{ij} = \mu_j + \sum_{k=1}^{r} \lambda_k \alpha_k \gamma_{jk} + \epsilon_{ij} \]

where \( \tilde{y}_{ij} \) is the mean of the \( i \)th cultivar in the \( j \)th environment for \( g \) cultivars and \( e \) sites (\( i = 1, 2, \ldots, g \) and \( j = 1, 2, \ldots, e \); \( \mu_j \) is the site mean; \( \lambda_k (\lambda_1 \geq \lambda_2 \geq \ldots \geq \lambda_r) \) are scaling constants (singular values) that allow the imposition of orthonormality constraints on the singular vectors for cultivars, \( \alpha_k = (\alpha_{1k}, \ldots, \alpha_{gk})' \) and sites, \( \gamma_k = (\gamma_{1k}, \ldots, \gamma_{ek})' \), such that \( \sum \alpha_{ik}^2 = \sum \gamma_{jk}^2 = 1 \) and \( \sum \alpha_{ik} \gamma_{jk} = \sum \gamma_{jk} \gamma_{jk} = 0 \) for \( k \neq k' \); \( \alpha_{ik} \) and \( \gamma_{jk} \), for \( k = 1, 2, 3, \ldots \), are called “primary,” “secondary,” “tertiary,” \( \ldots \), effects of \( i \)th cultivar and the \( j \)th site, respectively; \( \epsilon_{ij} \) is the residual error assumed to be normally and independent distributed with 0 means and variance \( \sigma^2 r \) (where \( \sigma^2 \) is the pooled error variance and \( r \) is the number of replications). The number of bilinear terms is \( t \leq \min (g, e) \). Estimates of the multiplicative parameters in the \( k \)th bilinear term are obtained as the \( k \)th component of the deviations from the additive part of the model. In the SREG model, only the main effects of cultivars plus the \( G \times E \) are absorbed into the bilinear terms.

3. Results

The analysis of variance of 729 germplasm lines tested over 5 years at 8 locations indicated significant differences among genotypes for AUDPC percent days, grain yield, days to maturity, and 1000 grain weight in each of the years (Table 2). Likewise, the combined analysis of 109 genotypes of the EGPYT showed significant differences for the three traits (AUDPC percent days, grain yield and days to maturity) but not for 1000 grain weight (TKW) among selected lines advanced from the EGPSN (Table 3).

The adjusted means of AUDPC percent days of 109 genotypes from the EGPYT (data of all lines not shown) varied from 261 (line 75; TRACHA-2/CMH76-252/PVN’S) to 1043 (Sonalka-susceptible check) whereas the range of best 25 lines was 261–440. The top 25 lines (Table 4) showed mean AUDPC percent day values of less than 500; 12 were significantly superior to the best check PBW 343 (AUDPC percent days = 369). Mean values over environments (data not shown) displayed substantial variability for genotype performance across environments. Lines 75, 67, 74, 63, 62, 84, 64, 82, 57 and 53 were the 10 best performers across 25 environments (Table 4).

<table>
<thead>
<tr>
<th>Source and traits</th>
<th>d.f.</th>
<th>Mean sum of squares of 5 years</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>AUDPC percent days</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Location</td>
<td>7</td>
<td>2539362.00(^{**})</td>
</tr>
<tr>
<td>Line</td>
<td>156</td>
<td>40528.94(^{**})</td>
</tr>
<tr>
<td>Error</td>
<td>1036</td>
<td>14909.38</td>
</tr>
<tr>
<td><strong>Grain yield</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Location</td>
<td>7</td>
<td>2279027.61(^{**})</td>
</tr>
<tr>
<td>Line</td>
<td>156</td>
<td>16174.68(^{**})</td>
</tr>
<tr>
<td>Error</td>
<td>1036</td>
<td>8610.31</td>
</tr>
<tr>
<td><strong>Days to maturity</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Location</td>
<td>7</td>
<td>12211.88(^{**})</td>
</tr>
<tr>
<td>Line</td>
<td>156</td>
<td>30.56(^{**})</td>
</tr>
<tr>
<td>Error</td>
<td>1036</td>
<td>7.82</td>
</tr>
<tr>
<td><strong>1000 grain weight</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Location</td>
<td>7</td>
<td>2308.97(^{**})</td>
</tr>
<tr>
<td>Line</td>
<td>156</td>
<td>83.93(^{**})</td>
</tr>
</tbody>
</table>

\(^{**}\) Significant at \( P = 0.01 \).
Grain yield of 109 germplasm lines displayed a range of 3348–4719 kg ha\(^{-1}\), whereas, the best 25 lines for spot blotch tolerance showed a range of 3390–4719 kg ha\(^{-1}\) (Table 4). The mean values of grain yield (Table 4) showed that nine lines viz., 67, 84, 57, 39, 92, 69, 45, 40 and 20 that displayed significantly lower AUDPC percent days than the best check (PBW 343 for AUDPC) also yielded significantly superior to the best check (Bhrikuti) for grain yield.

Although days to maturity in germplasm lines showed a range of 104.6–118.8 days, the best 25 lines for AUDPC were in the range of 112.4–118.7 days and thus none of them (best 25 lines) were significantly earlier than the best check Sonalika (111.8 days) (Table 4). In comparison, the four checks showed mean days to maturity in the range of 111.8–118.7 days. Thousand grain weights showed a wide range (21.5–47.1 g), whereas the best 25 performer for AUDPC showed a range of 29.0–46.2 g. Only one line (No. 62; GAA/KEA/GAA) was significantly superior to the best check (PBW 343) for 1000 grain weight. However, two other lines (No. 67 and 84) that were significantly superior to best checks for spot blotch resistance and grain yield, showed 1000 grain weight of more than 40 g.

Fig. 1 displays the main effects of genotypes (G) plus the G/E effects for the 109 EGPYT wheat lines in 25 environments (combination of 5 years and 5 locations) for

### Table 3
Mean sum of squares of spot blotch AUDPC percent days, yield and yield traits tested in the EGPYTs in five locations of South Asia for 5 years

<table>
<thead>
<tr>
<th>Source</th>
<th>d.f.</th>
<th>Mean sum of squares of 5 years</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>AUDPC percent days</td>
</tr>
<tr>
<td>Location</td>
<td>4</td>
<td>4973.799.7 **</td>
</tr>
<tr>
<td>Year (location)</td>
<td>20</td>
<td>4503.475.5 **</td>
</tr>
<tr>
<td>Rep (loc × year)</td>
<td>25</td>
<td>5780.7.5 **</td>
</tr>
<tr>
<td>Block (loc × year × rep)</td>
<td>200</td>
<td>2444.6 **</td>
</tr>
<tr>
<td>Line</td>
<td>108</td>
<td>2153.771.1 **</td>
</tr>
<tr>
<td>Line × location</td>
<td>432</td>
<td>4006.4.4 **</td>
</tr>
<tr>
<td>Error</td>
<td>460</td>
<td>2214.1.7</td>
</tr>
</tbody>
</table>

** Significantly different at \(P = 0.01\).

### Table 4
List of best performing twenty five germplasm lines for AUDPC percent days, yield and yield traits tested over 5 years in 5 locations of South Asia

<table>
<thead>
<tr>
<th>No.</th>
<th>Lines</th>
<th>Pedigree</th>
<th>AUDPC percent days</th>
<th>Yield (kg ha(^{-1}))</th>
<th>DM (days)</th>
<th>1000 grain weight (g)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.</td>
<td>EGPYT 75</td>
<td>TRACHA-2/CH176-252/PVN'S'</td>
<td>261.70 **</td>
<td>3586.64</td>
<td>115.72</td>
<td>36.06</td>
</tr>
<tr>
<td>2.</td>
<td>EGPYT 67</td>
<td>KAUZ/KAUZ/STAR/3/PRINIA/4/MILAN/KAUZ</td>
<td>294.95 **</td>
<td>4371.78 **</td>
<td>114.21</td>
<td>42.08</td>
</tr>
<tr>
<td>3.</td>
<td>EGPYT 74</td>
<td>KAUZ 2/K134(60)/VEE</td>
<td>307.99 **</td>
<td>3390.40</td>
<td>116.73</td>
<td>34.96</td>
</tr>
<tr>
<td>4.</td>
<td>EGPYT 63</td>
<td>MRNG/BUC/BLO/PVN/PJB</td>
<td>310.56</td>
<td>3599.04</td>
<td>115.60</td>
<td>39.20</td>
</tr>
<tr>
<td>5.</td>
<td>EGPYT 62</td>
<td>GAA/KEA/GAA</td>
<td>310.79 **</td>
<td>3613.20</td>
<td>114.08</td>
<td>46.20 *</td>
</tr>
<tr>
<td>6.</td>
<td>EGPYT 64</td>
<td>MRNG/BUC/BLO/PVN/PJB</td>
<td>313.80</td>
<td>4719.89 **</td>
<td>115.63</td>
<td>41.21</td>
</tr>
<tr>
<td>7.</td>
<td>EGPYT 68</td>
<td>NL 251/SHI 22</td>
<td>372.92 **</td>
<td>3479.80</td>
<td>115.54</td>
<td>37.49</td>
</tr>
<tr>
<td>8.</td>
<td>EGPYT 65</td>
<td>CRK/HD 2172/8/AIS 58/6/KAL/B/5/ALD/4/OLN/TRM/7/CA/7/MAYA/PVN</td>
<td>334.78 **</td>
<td>3505.89</td>
<td>115.17</td>
<td>34.96</td>
</tr>
</tbody>
</table>

** Significant superior to the best check (\(P = 0.01\)) in pair wise comparisons performed using pdiff option in LSMEANS statement.
AUDPC percent days. The environments that contributed most to the G and G × E variability are located further apart in the biplot and these were S2 (Bhairahawa) and S5 (Varanasi), whereas the other environments that were closer to the center of the biplot (S1, S3 and S4) contributed less to the total G × E and therefore can be considered more stable locations that discriminated genotypes more similarly. The environments S1 (Jessore) and S3 (Dinajpur) did not appear to be highly correlated with the other two unstable environments (S2 and S5). Their angles are quite large, indicating that they discriminated genotypes very differently. Considering that the first component of the SREG analysis accounted for the non-crossover G × E interaction variability and that the second component is due to the crossover G × E variance, the ideal genotype is the one with the highest values for the first component and a value close to zero for the second component. Genotype 75 and 84 seems to be nearest to the definition of an ideal genotype (Fig. 1) and they were good performers for AUDPC percent days in most of the 25 environments. Other genotypes that appeared superior were lines 67, 82, 64, 62, 74, 63, 57 and 53. On the other hand, genotypes located on the opposite quadrant, such as genotypes 24, 18 and 59 were the worst performers for AUDPC percent days in most environments (Fig. 1).

In the stability analysis for grain yield over 25 environments (Fig. 2), the S4 (Rampur) displayed the highest instability for grain yield followed by S5 (Varanasi). The three other locations (Jessore, S1; Bhairahawa, S2; Dinajpur, S3) were relatively more stable. In the biplot analysis in 25 environments, the most stable genotypes for grain yield were lines 37, 84, 30, 45 and 35. The most unstable genotypes were 76, 77, 74 and 73 (Fig. 2).

When stability analysis was done for days to maturity (Fig. 3), it was found that S5 (Varanasi) was the most unstable environment followed by S3 (Dinajpur), whereas Jessore (S1) was the most stable environment. The location Varanasi (S5) was observed to be very different from the two other unstable environments (S4 = Rampur and S2 = Bhairahawa). Since the genotypes were promoted from the EGPSN to the EGPYT based on early maturity requirements of South Asia, most of the genotypes fit a narrow maturity range, and the biplot thus showed clustering of most of the genotypes near the center. The genotypes most stable for earlier days to maturity were 6, 1, 11, 8 and 90, whereas genotypes 20, 17, 10 and 82 were not stable (Fig. 3). Genotype 14 was very early, but was relatively less stable (Fig. 3). Similarly, for 1000 grain weight, Fig. 4 displays the main effects of genotypes (G) plus the G × E effects of the 109 wheat lines in 25 environments (combinations of 5 sites and 5 years). For this trait, lines showed relatively lesser variability and location than other three traits. The location S1 (Jessore) appeared stable but very different from the other four locations (Fig. 4). The genotype 22 appeared the most stable for grain
weight, while genotypes 18, 20, 17, 14, 9, 3, 8 and 10 were the most unstable.

4. Discussion

Leaf blight of wheat caused by B. sorokiniana was not regarded as an important pathogen in South Asia before the Green Revolution (Saari, 1998; Chaurasia et al., 1999). However, the pathogen grew in importance after the Green Revolution and is currently considered as the No. 1 pathogen in the eastern parts of South Asia (Saari, 1998). Since the eastern part of the Gangetic plains of South Asia (especially India) is considered crucial for meeting future food demands, elite germplasm lines having superior agronomic performance and high standards of spot blotch resistance are being sought with the utmost priority (Joshi et al., 2007a). The same is considered true for the eastern parts of Nepal and for Bangladesh, where population growth is not slowing and almost the entire wheat area is affected by spot blotch and terminal heat stress (Sharma et al., 2004a). In the last few decades, many studies were conducted in South Asia to find suitable sources of germplasm for this disease (Chaurasia et al., 1999; Joshi et al., 2002, 2004a, 2007b; Joshi and Chand, 2002; Sharma et al., 2004b). However, high resistance to disease in the background of robust yield potential lines still continues to elude NARS programs (Joshi et al., 2007a).

Although elite wheat lines obtained from different sources were used for initial testing in the EGPSN, germplasm lines showed significant differences for spot blotch AUDPC percent days and agronomic traits (Table 2). This suggested that variation for spot blotch resistance is present in the advanced lines of South Asian countries. This fact was also substantiated by the presence of significant variation for spot blotch AUDPC percent days in the EGPYT (Table 3), which consisted of a select group of lines promoted from the EGPSN based on their overall performance. Of the best 25 lines for spot blotch AUDPC percent days (Table 4), 21 were derived from CIMMYT elite germplasm, whereas only 4 lines came from NARS (all 4 were from Nepal). A previous study (Chaurasia et al., 1999) also showed that compared to Indian germplasm, CIMMYT lines possessed better resistance against leaf blight of wheat. Although these best 25 lines represented different genetic backgrounds, many possessed Veery and Kauz followed by Buc and Seri in their pedigree. The successful Veery lines produced in the early 1980s (Rajaram et al., 1990) resulted from a cross with a winter wheat parent containing a 1RS chromosome (1B/1R translocation from cereal rye). Among useful traits, Veery lines possess healthy stay-green, recently shown to be associated with resistance to spot blotch of wheat (Joshi et al., 2007b). Two of the best lines (69 and 70) were derived from Chirya 3. This line also has good stay-green and carries strong resistance to spot blotch (Joshi et al., 2007b). The other line in the pedigrees of most superior lines is Kauz, also a Veery derivative. In the study by Chaurasia et al. (1999), most leaf-blight-resistant lines were derived from ‘Kauz’ and ‘Seri’, both developed by CIMMYT. Other studies (Joshi et al., 2002, 2004a; Joshi and Chand, 2002) report similar findings, suggesting that resistance to spot blotch in many of the advanced lines of South Asia is being contributed by a limited number of CIMMYT ‘hallmark’ varieties and that such germplasm is paramount to increasing yield potential (Rasmusson, 1996). This has been demonstrated by cultivars such as Kauz and Baviacora, derived from parents of a narrow genetic base (Rajaram et al., 2002). On the other hand, use of a wider genetic base in crossing programs is also important (Kronstad, 1996). In the present investigation, around half of the best 25 lines belonged to genetic backgrounds different from Veery or Kauz. These lines can be used to sustain yield potential in South Asia breeding programs.

It was interesting to note that many spot blotch resistant lines also had significantly higher grain yields than the best check, Kanchan (Table 4; Figs. 1–4). Nine lines that performed significantly superior to best checks with regards to both spot blotch AUDPC and grain yield were lines 67 (Kauz/Kauz/Star/3/Prinia/4/Milan/Kauz), 84 (Mrng/Buc/Blo/Pvn/3/Pjb 81), 57 (Weaver//Vee/Pj/3/Milan), 39 (Bow/Buc/Bul), 92 (NC2668-11B-020B-2B-0B), 69 (Chirya3/Pastor), 45 (Cmh 84.3631/Munia/Milan/Kauz), and 40 (Seri 82/Vee’s/Snb’s) and 20 (Fch/3/Sn/1/Nk 1) (Table 4). Among these, the Kauz-derived line (line 67; Kauz//Kauz/Star/3/Prinia/4/Milan/Kauz) possessed early maturity (114 days) and substantially high 1000 grain weight (42.08 g). The other two lines (line 69, Chirya3/ Pastor and line 84, Mrng/Buc/Blo/Pvn/3/Pjb 81) also had early maturity (113 and 114 days) and high (42.26 and 41.21 g) 1000 grain weight. The remaining seven lines having significantly higher resistance and yield compared to the best check, showed 114–117 days to maturity and acceptable 1000 grain weight (37.8–41.5 g) with the exception of line 40 (Seri 82/Vee’s/ Snb’s) and 20 (Fch/3/Sn/1/Nk 1) which showed low (32.06 and 29.05 g, respectively) 1000 grain weight. The biplots also displayed the stable performance of these lines across 25 environments for resistance and yield. Recently, some of the Veery and Kauz derived lines have also shown superior performance under zero or reduced tillage, practices quickly gaining popularity in South Asia (Joshi et al., 2007d).
Although eastern parts of South Asia require earlier-maturing lines, due to shorter winter (Aggarwal, 1991; Rane et al., 2000), a maturity of up to 120 days is considered acceptable (Joshi et al., 2007a). Early maturity should be combined with good disease resistance, high yield, and good grain weight. The presence of significantly higher yield in resistant lines obtained in this study also indicates the presence of tolerance to terminal heat stress, another major cause of low yields in South Asia (Nagarajan, 2005; Joshi et al., 2007a).

South Asia is different from many other hot locations in the world due its high humidity (Joshi et al., 2007a). For breeding purposes, CIMMYT defined two distinct sub-mega-environments within its mega-environment (ME) 5 (Braun et al., 1992), ME5A, with high relative humidity, and ME5B with low relative humidity. Results of CIMMYT international yield trials over 40 environments confirmed that the main factor determining $G \times E$ in hot climates was relative humidity (Reynolds et al., 1998), whereas more subtle effects explain $G \times E$ in the hot but drier environments (Vargas et al., 1998).

The results here suggest that numerous genotypes possessing good spot blotch resistance also carry high-yield potential under the hot, humid conditions of South Asia. These genotypes could be used in wheat improvement programs aimed at developing superior genotypes for yield and spot blotch resistance in India, Bangladesh and Nepal, thereby contributing to food security in the region.

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References


