FIELD RESISTANCE TO SPOT BLOTCH IS NOT ASSOCIATED WITH UNDESIRABLE PHYSIO-MORPHOLOGICAL TRAITS IN THREE SPRING WHEAT POPULATIONS

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SUMMARY

Spot blotch, caused by Coelobolus sativus (Ito and Kurbayzshi) Drechsler ex Dastur is a serious constraint to production of wheat (Triticum aestivum L.) in tropical and sub-tropical environments. Previous efforts to develop genotypes with high levels of resistance combined with other desirable agronomic features have been unsuccessful. This failure was assumed to be largely due to the association of undesirable characters with heightened resistance but information on the existence of such associations is limited. Recently, high levels of resistance have been reported in CIMMYT synthetic wheat genotypes. Our study was done on three populations derived from the spot blotch resistant genotypes ‘Milan/Shanghai #7’, ‘Chirya. 3’ and ‘NL 971’ crossed with the susceptible commercial cultivar ‘BL1473’. Fifteen different physio-morphological traits and areas under disease progress curves (AUDPC) were evaluated in F2 and F1 generations during 2005-2006 at Rampur (Chitwan, Nepal). The majority of traits showed weak negative significant or non-significant genetic and phenotypic correlation with AUDPC except Area Under SPAD (soil plant analysis development) decline curve (AUSDC) and flag leaf duration. Results showed no undesirable genetic association of resistance with physi-morphological characters, and thus independent selection for individual traits is possible. In addition, AUSDC and flag leaf duration have potential application as complementary traits in selecting for high resistance.

Key words: Bipolaris sorokinina, Coelobolus sativus, plant ideotype, trait association, physiological traits.

INTRODUCTION

In the last two decades spot blotch of wheat (Triticum aestivum L.), caused by Coelobolus sativus (Ito and Kurbayzshi) Drechsler ex Dastur, also called Helminthosporium leaf blight (HLB) or foliar blight, has been an important disease in warmer wheat-growing regions, affecting livelihood of millions of small farmers (Alam et al., 1994; Dubin and van Ginkel, 1991; Duveiller and Gilchrist, 1994; Duveiller et al., 1998; Lapis, 1985; Sharma et al., 2003). Spot blotch causes substantial yield loss (20-100%) by blighting the leaves and inducing premature senescence (Duveiller and Gilchrist, 1994; Meheta, 1998). Development of resistant wheat cultivars has been identified as the best option to help millions of subsistence farmers residing in the South Asian Gangetic plains, where the cost of fungicides is prohibitive. Currently grown cultivars in this region have low level of resistance (Sharma and Duveiller, 2006).

The best leaf blight-resistant wheats in South Asia were reported to be late and tall, two less desirable agronomic characters (Dubin et al., 1998) and breeders doubted the possibility to develop early maturing resistant genotypes. During the last decade, breeders’ efforts to develop genotypes with high levels of resistance and desirable agronomic traits were largely unsuccessful. Studies were made to elucidate relationships of disease severity with different agronomic features. Studies reported less spot blotch resistance in short plants with early maturity (Dubin et al., 1998; Sharma et al., 1997a, 1997b). Negative correlations were also observed between spot blotch resistance and different agronomic traits such as grain yield (Gilchrist and Pfeiffer, 1991; Sharma et al., 1997a), thousand kernel weight (Sharma et al., 1997a), biomass yield (Sharma et al., 1997a), harvest index (Sharma et al., 1997a) and grain fill duration (Gilchrist and Pfeiffer, 1991). However, some recent studies show no or weak association between these agronomic traits (Sharma et al., 2006; Joshi et al., 2002).

Recently new synthetic hexaploid wheats resistant to the disease have been identified in South Asian breeding programs (Duveiller and Sharma, 2005; Duveiller et al., 2005; Siddique et al., 2006). These synthetic wheats are obtained by crossing tetraploid wheat with Aegilops tauschii Coss. and are known for their high physiological profile, although performance during the process of introgression is largely unknown (Del Blanco et al., 2000). Unfortunately, promising spot blotch resistant genotypes identified so far have some undesirable agro-
nomic features (Sharma and Duveiller, 2007). Although the introgression of the resistance genes into local commercial cultivars is underway, consequences could be positive and negative. For instance, positive consequences could be an increase of physiological efficiency (contributing to increased abiotic stress tolerance), in addition to improved spot blotch resistance. Negative consequences could include failure to develop desirable genotypes due to undesirable associations and residual effects of “wild” genes. Therefore, the interrelationship of different physio-morphological traits and spot blotch resistance in such populations needs to be studied.

Physiological traits have caught the attention of breeders due to limitations of conventional yield-based selections, particularly for stressed environments (Reynolds et al., 2001). Application of such traits in addition to conventionally measured traits such as grain yield and disease resistance might be useful to develop high performing genotypes. Thus, evaluation of such traits might help in the better understanding of physiological processes, the development of suitable selection strategies, and the identification of traits for an indirect selection process.

Association of different physio-morphological traits with spot blotch resistance is not well elucidated. Erect leaf posture was shown to reduce spot blotch incidence in wheat (Joshi and Chand, 2002). Differences among resistant and susceptible genotypes for chlorophyll decline measurements as well as flag leaf anatomy have been observed (Rosyara et al., 2007). A positive correlation between the stay-green trait and HLB severity has been observed (Rosyara et al., 2007). Our study examines the genetic association of different physio-morphological traits and spot blotch resistance in populations derived from new CIMMYT resistant genotypes.

MATERIALS AND METHODS

Three resistant genotypes; ‘Milan/Shanghai #7’ (pedigree: VS73.600/MIRLO/3/BOW//YE/TRF/4/Shanghai #7), ‘Chirya.3’ (pedigree: CS/Thcu//Nee3/Ald/Pvn/4//Ningmai No.4/Oleson//Ald/Yangmai No.4) and ‘NL 971’ (pedigree: Mrng/Buc//Blo/Pvn/3/PJb 81) were crossed with the susceptible genotype ‘BL1473’ (pedigree: Nepal 297/NL531). BL 1473 is an early-maturing, spot-blotch-susceptible commercial cultivar from Nepal (Duveiller and Sharma, 2005; Sharma and Duveiller, 2007; Sharma et al., 2004, 2007). These three genotypes are known for their stable and high levels of resistance.

Crossoes were made in the 2003 wheat-growing main season (November to March) at Rampur (Chitwan, Nepal, 27°40’N and 84°19’E at 228 metres above sea level). The F1 plants were grown in an off-season, high-altitude field nursery in 2004 (June to October) at Marpha, (Nepal, 28°43’N and 83°15’E, at 2,900 meters in the Himalaya) to produce the F2 seed. F2 and F3 generations were evaluated at Rampur during 2005-2006 (Table 1). Relative humidity in Rampur is usually higher than elsewhere in the lowlands of Nepal, known as the Tarai. This favors early onset of spot blotch epidemics, with the first lesions (1 to 4 mm) already visible about 4-5 weeks after sowing. During the past several years, spot blotch has been severe on wheat at this site.

The F2 seeds were planted (seed to seed distance of 0.20 m and row to row distance of 0.25 m) in rows 4 m long. The parents of particular crosses were planted at regular intervals after every 40 progeny plants. One spike per plant was harvested from all F2 plants. The seeds of each spike were planted in a separate of 1 m length (known as head row). The spacing between two head rows was 0.25 m. The parents of the particular populations were planted after every 20 progeny rows. Both F2 and F3 generations were grown in three replicated randomized complete block designs. Sonalika (most susceptible genotype for spot blotch) was grown as spreader rows around and in between the blocks to give uniform natural inoculum pressure. The F2 generation was sown on 26 November 2005, and the F3 on 27 November 2006.

Fertilizers were applied at 120 Kg N, 60 Kg P2O5, and 40 Kg K2O per hectare. Split application of nitrogen was done. Hundred kilograms of nitrogen was broadcasted as basal dose whereas the remaining 20 Kg was top-dressed at active tillering stage. Plots were weeded by hand. The trials were managed under natural disease infection; no supplementary artificial inoculation was required due to high and uniform natural inoculum pressure. The experimental field had no residue from the previous wheat crop. The field remained submerged in floodwater for several weeks in August and September in both years, which is a typical situation in the rice growing lowlands of Nepal.

Disease progress and physio-morphological traits were measured in F2 individual plants or five randomly select-
ed plants per F3 head rows. Main tillers of five plants (randomly selected) were tagged and measurements were done on these. Spot blotch disease scoring was started when the flag leaf of susceptible genotypes had more than 25% diseased leaf area. Three disease readings (percentage of diseased leaf area on flag leaf) were made at 5 to 7 day intervals. The disease readings were used to calculate the Area Under Disease Progress Curve (AUDPC) using the following formula (Das et al., 1992).

\[
\text{AUDPC} = \sum_{i=1}^{n-1} \frac{[X(i+1) + X(i)]}{2} (T(i+1) - T_i)
\]

Where

- \(X_i\) = Disease severity on the \(i^{th}\) date
- \(T_i\) = Date on which the disease was scored
- \(n\) = number of dates on which disease was recorded

A Minolta Chlorophyll Meter (Model: SPAD-502) was used for non-destructive measurement of flag leaf chlorophyll content (Rosyara et al., 2007). The chlorophyll content was recorded in Minolta company-defined SPAD values. Single F2 individual plants or the five plants (same tiller) was recorded in Minolta company-defined SPAD content (Rosyara et al., 2007). The chlorophyll content was averaged (Rosyara et al., 2007). The chlorophyll content measurements were repeated three times following disease observations (within 1-2 days of these) and the readings were used to calculate the AUSDC using the following formula (Rosyara et al., 2007).

\[
\text{AUSDC} = \sum_{i=1}^{n-1} \frac{[S(i+1) + S_i]}{2} (T(i+1) - T_i)
\]

Where

- \(S_i\) = SPAD value on the \(i^{th}\) date
- \(T_i\) = \(i^{th}\) day
- \(n\) = number of dates of recording SPAD value

Days to flag leaf emergence were recorded when more than 90% of the plant tillers in each entry (F2 individual plants or F3 head rows) had a flag leaf completely emerged i.e. completely opened or unfolded. Similarly flag leaf death was scored when 90% of the tillers in each entry were completely dead. Flag leaf duration was calculated as number of days from emergence to death. Each entry was considered headed when 90% of the shoots had the entire spike emerged from the flag leaf. Days to anthesis was recorded when 90% of the shoots had the entire spike going to anthesis. Days to peduncle drying was recorded when 90% tillers had peduncles dried. Days to maturity (DM) was recorded when 90% of tillers had matured glumes (green colour completely lost).

Flag leaf angle was measured with a protractor just after ear emergence. Flag leaf length (from ligule to leaf tip) was measured after five weeks of heading. Flag leaf width was measured at tip (2 cm from heading), centre (exact centre), and base (2 cm from base) and averaged. Plant height (from ground level to the tip of the spikes) was measured at physiological maturity. Peduncle length (from flag leaf ligule to spike base) and last internode length (from flag leaf ligule to penultimate leaf ligule) were measured five weeks after heading. Spike length (from spike base to tip, excluding awns) was measured at maturity. Spikes were threshed individually and grains were counted to calculate number of grains per spike. One hundred kernels were randomly selected, counted and weighed to record the hundred-kernel weight (HKW).

Frequency distribution and phenotypic correlation were calculated using the SAS (1990) software. Similarly, genetic correlation was calculated using parent and offspring covariances as outlined by Sexton (2004) using the SAS (1990) software. Transgressive segregates were defined as those progeny lines having mean disease severities greater than one standard deviation below or above individual parental means.

**RESULTS**

Leaf blight severity was very high during the study period, as shown by AUDPC of susceptible genotype BL 1473 (Table 2). Spot blotch was observed as early as the third week of February, after the heading stage. Disease symptoms (oval to elongated light brown to dark brown blotches) were uniformly visible on all plants. Toward maturity, disease severity on the susceptible parent reached 100% but was below 25% on the resistant parents. Isolates from representative diseased leaf samples showed conidia of C. sativus on the lesions. No other diseases than spot blotch were evident during the study period. Weather conditions were optimal for wheat cultivation in 2005 but rainfall was inadequate during 2006. The effect of the dry spell was minimized by increased irrigation.

In all populations, the frequency distribution of AUDPC values showed a negative skew indicating the dominance of resistance over susceptibility (Fig. 1). NL971 had slightly higher AUDPC compared to other resistant parents. Transgressive segregates were observed for AUDPC (Fig. 1). There were contrasting differences among resistant and susceptible parents for physio-morphological traits (Table 2). Means and standard deviations for physio-morphological traits are presented in Table 3.
The majority of ‘plant architecture’-related traits showed very low (positive or negative), non-significant (p>0.05) genotypic and phenotypic correlation with spot blotch severity (Table 4). Peduncle length, last internode length, flag leaf angle, flag leaf width, spike length, and grain per spike showed non-significant
(p>0.05) genetic and phenotypic correlation with AUDPC (Table 4). Phenotypic correlation between plant height and AUDPC was moderately negative and significant (p<0.05). The genetic correlation between these two traits was mostly non-significant (p>0.05).

Phenotypic and genetic correlation between chlorophyll content at anthesis and AUDPC was low and negative. In contrast, AUSDC (a measure of chlorophyll decline after anthesis) showed strong phenotypic and genetic negative correlation with AUDPC (Table 5, Fig. 2). Flag leaf duration was negatively correlated with AUDPC and showed that resistant genotypes have longer flag leaf life than susceptible genotypes (Table 5, Fig. 2). The AUDPC showed weakly significant (p<0.05) negative correlation with maturity-related traits including days to heading, anthesis, maturity, and peduncle dryness. Also, hundred-kernel weight showed a weak negative correlation with AUDPC (Table 4, Fig. 2). The genetic correlation between HKW and AUDPC was higher than phenotypic correlation. Transgressive segregants were observed for all traits studied and showed possibility to find desirable variants.

Fig. 1. Frequency distribution for Area Under Disease Progress Curve (AUDPC) in spring wheat populations evaluated at Rampur, Chitwan, Nepal during 2005-2006. Abbreviations: RP, resistant parent; SP, susceptible parent.
DISCUSSION

The study confirms that genotypes ‘Milan/Shanghai #7’, ‘Chirya.3’ and ‘NL 971’ are highly resistant to spot blotch. Previously ‘Milan/Shanghai #7’ and ‘Chirya.3’ were reported to have two non-allelic dominant resistant genes (Neupane et al., 2007). Although none of these genotypes were reported as immune, they have low disease progress when compared to susceptible genotypes. These genotypes have both desirable (for example: high chlorophyll content at anthesis, high AUSDC and low AUDPC) and undesirable traits (for example: late maturity and tall plant height) for breeding purpose (Table 2).

In recent years, synthetic hexaploid wheats [derived from so-called “wide” crosses between a Triticum turgidum var. durum (Desf.) Husnot and Triticum tauschii (Coss.) Schmal] are identified as important resistance source to spot blotch resistance (Sharma and Duveiller, 2007; Sharma et al., 2004). Such synthetic hexaploids have proven to be a useful source for resistance or tolerance to other biotic and abiotic stresses (Gorham, 1990; Limin and Fowler, 1993). Synthetic hexaploids are routinely crossed and backcrossed with common hexaploid wheat to achieve desirable agromonic traits. Wild ancestors of common wheat

Table 4. Phenotypic and genetic correlation between AUDPC and plant architecture related traits in spring wheat populations evaluated Rampur, Chitwan, Nepal during 2005-2006.

<table>
<thead>
<tr>
<th>Cross</th>
<th>Gen</th>
<th>PHT (cm)</th>
<th>PDL (cm)</th>
<th>LIL (cm)</th>
<th>FLL (cm)</th>
<th>FLA (°)</th>
<th>FLW (cm)</th>
<th>SPL (cm)</th>
<th>GPS</th>
<th>HKW (g)</th>
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<tr>
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<tr>
<td>BL 1473 x MS 7</td>
<td>F₂</td>
<td>-.42 a</td>
<td>ns b</td>
<td>-.22</td>
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<td>-.21</td>
<td>-.19</td>
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<td>ns</td>
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<td>ns</td>
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<td>-.41</td>
<td>-.24</td>
<td>-.37</td>
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<tr>
<td>BL 1473 x Chirya.3</td>
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<td>-.37</td>
<td>ns</td>
<td>-.35</td>
<td>-.20</td>
<td>-.23</td>
<td>ns</td>
<td>ns</td>
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<td>-.32</td>
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<tr>
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<td>-.30</td>
<td>ns</td>
<td>-.17</td>
<td>-.50</td>
<td>ns</td>
<td>-.41</td>
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<td>-.23</td>
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<tr>
<td>BL 1473 x NL 971</td>
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<td>-.29</td>
<td>ns</td>
<td>ns</td>
<td>-.39</td>
<td>ns</td>
<td>-.28</td>
<td>-.27</td>
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<td>-.28</td>
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<td>-.22</td>
<td>-.23</td>
<td>ns</td>
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<td>-.45</td>
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</table>

Abbreviations: Gen- generations, PHT - plant height, PDL - peduncle length, LIL - last internode length, FLL - flag leaf length, FLA - flag leaf angle, FLW - flag leaf width, SPL - spike length, GPS - grains per spike, HKW - hundred kernel weight, AUDPC - area under disease progress curve, MS 7 - Milan/Shanghai #7

a Only significant (p < 0.05) have been shown.
b ns = p > 0.05

Table 5. Phenotypic and genetic correlation between AUDPC and physiological traits in spring wheat populations evaluated at Rampur, Chitwan, Nepal during 2005-2006.

<table>
<thead>
<tr>
<th>Trait</th>
<th>Gen</th>
<th>CCA (SPAD value)</th>
<th>AUSDC</th>
<th>FLD (days)</th>
<th>DH</th>
<th>DA</th>
<th>DM</th>
<th>DPD</th>
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<td>-.30</td>
<td>-.41</td>
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<tr>
<td></td>
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<td>-.38</td>
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<tr>
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<td>-.71</td>
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<td>-.56</td>
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<td>ns</td>
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<td>-.24</td>
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</table>

Abbreviations: Gen, generation; CCA, chlorophyll content at anthesis; AUSDC, area under SPAD decline curve; FLD, flag leaf duration; DH, days to heading; DA, days to anthesis; DM, days to maturity; DPD, days to peduncle dryness; AUDPC, area under disease progress curve; MS 7, Milan/Shanghai #7

a Only significant (p < 0.05) are shown.
b ns = p > 0.05.
(Triticum aestivum L.) and synthetic wheats are reported to have higher photosynthetic rates compared to modern wheat cultivars (Austin et al., 1989; Carver and Nevo, 1990; del Blanco et al., 2000). Nevertheless, using an alien source in a breeding program can have uninvited consequences by co-transfer of undesirable traits (Knott and Dvorak, 1976). Fortunately, the resistant genotypes showed no undesirable associations with the physio-morphological traits examined.

Plant type traits showed weak correlation with leaf blight resistance in all populations and generations studied (Table 4). Among the plant type traits, plant height is one of the most important traits to wheat breeders. The results showed weak negative association between spot blotch resistance and plant height, consistent with Sharma et al. (2006). Studies in the past reported a negative association between these two traits (Gilchrist et al., 1992; Sharma et al., 1997b; Dubin et al., 1998). Such differences could be due to the difference in resistance source and parents involved. This study supports the view that it is possible to develop dwarf and resistant genotypes. In contrast to Joshi and
Chand (2002), flag leaf angle measurements were weakly correlated with AUDPC in all populations studied. There study showed weak negative correlation between AUDPC and maturity-related traits (Sharma et al., 2006; Sharma and Bhatta, 1999). Previously, a negative correlation had been observed between these two traits (Dubin et al., 1998; Mahto, 2001). Such association between spot blotch severity and maturity is most likely due to high temperatures and occasional hot winds during the late grain filling period. At temperatures above 28°C late re-

temperatures and occasional hot winds during the late blotch severity and maturity is most likely due to high, 1998; Mahto, 2001). Such association between spot et al. association had been observed between these two traits (Dubin Sharma and Bhatta, 1999). Previously, a negative correlation between AUDPC and maturity-related traits (Sharma et al., 2007; Sharma and Duveiller, 2004). The senescence of flag leaves is ly correlated with AUDPC in all populations studied. The resistant genotypes often develop severe disease symptoms (Nema and Joshi, 1973; da Luz and Bergstrom, 1986). In fact, the effect of heat stress can not be separated from spot blotch disease at this stage. In this study, both early maturing resistant genotypes and late maturing susceptible genotypes (recombinant genotypes) were observed. The results further support possibility to develop early maturing resistant genotype(s).

The phenotypic correlation between HKW and AU- DPC was low to moderate, in contrast to the results of Sharma et al. (1997b). Moreover, the genetic correlation was higher than the phenotypic correlation for HKW. A lower correlation between HKW and AUDPC could be due to the tolerance of some genotypes. The susceptible parent, ‘BL 1473’ is a potential donor for such tolerance as the genotype was found tolerant to spot blotch in previous studies (Rosyara et al., 2007; Sharma and Duveiller, 2007). Also, the genotype can tolerate complete removal of both flag and penultimate leaves at anthesis (Rosyara et al., 2005). This indicates that there should be some type of compensatory mechanism (for example higher remobilization of stem reserves during grain filling or increased spike photosynthesis) responsible for the tolerance of this genotype. Interestingly, ‘BL1473’ has long and robust peduncle (Table 2). Theoretically, the most ideal plant genotypes can be developed by combining both tolerance and resistance properties together.

Post-anthesis chlorophyll decline showed high genetic correlation with spot blotch resistance. A high pheno-
typic correlation between these two traits was observed by Rosyara et al. (2007). Leaf chlorophyll content has been a trait of interest particularly in stressed environments (Yang et al., 2002; Al Hakimi et al., 1998). Previous studies have shown that total chlorophyll content per unit area is a good indicator of the strength of photosynthetic tissue (Nageswara Rao and Wright, 1994), high photosynthetic rate and maximum photosynthetic activity (Fischer et al., 1998). Also, chlorophyll content has been correlated with heat tolerance (Yang et al., 2002) and drought tolerance (Al Hakimi et al., 1998).

A low rate of chlorophyll decline has been reported to be associated with tolerance to other biotic and abiotic stresses (Gorham, 1990; Limin and Fowler, 1993). Transfer of resistance will increase AUSDC values in spot blotch stressed environments. Abiotic stresses have been reported to increase spot blotch severity (Sharma and Duveiller, 2004). The senescence of flag leaves is one important consequence of spot blotch severity in susceptible genotypes (Rosyara et al., 2007). For optimum grain filling, flag leaves should remain photosynthetically active until physiological maturity. Spot blotch significantly reduced flag leaf duration but not grain fill-
duration (Fig. 2). This indicates complete death of flag leaves before attainment of crop maturity.

The majority of traits studied showed weak genetic association with spot blotch severity, indicating absence of undesirable associations based on traits evaluated. Such weak associations could be due to one or more mechanisms that reduce genetic correlation between traits of interest (such as independent assortment, low linkage and absence of pleotropic gene action). Such independent inheritance reduces the burden to breeders by providing opportunity to combine any desired traits with spot blotch resistance. A few traits showed high positive genetic correlation with spot blotch resistance (for example, high AUSDC lines had higher disease re-
sistence or low AUDPC). Such traits, potentially, can be used as complementary traits for development of geno-
types for spot blotch stressed environments. Our results therefore apply in the development of breeding strategy for such environments.

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