

Progress of researches done to understand host-pathogen relationship for spot blotch pathogen of wheat

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Abstract

The importance of spot blotch disease for wheat production in our country and south Asia is well known. It is extremely important in north-eastern wheat growing region which grows wheat in around 9 mha. This disease did not get due attention before 1990s. However, in last decade a number of researches were conducted to understand various issues concerning host-pathogen relationship of this disease. Our understanding on various issues is much improved compared to a decade ago. For instance, now researchers have established the epidemiology, there is better knowledge about pathogen survival and variability, there are better sources of resistance, inheritance and association with morpho-physiological traits is clearer and molecular markers are also available. Many of recent cultivars and advanced lines carry significantly superior resistance to varieties grown in 70s to 90s. However, there is need to carry on good basic and applied research to develop even more resistant lines in high yield potential background.

Keywords: Spot blotch, molecular markers, disease resistance

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Introduction

Spot blotch is a major disease of wheat in the warmer and humid growing regions of the world (Kumar *et al.*, 2002) and has special significance in the eastern Gangetic Plains (EGP) of south Asia that includes India, Nepal and Bangladesh (Sharma and Duveiller, 2004; Joshi *et al.*, 2007a). This disease is caused by *Bipolaris sorokiniana* (Sacc.) Shoemaker and was reported as early as 1914 by Mohy (Joshi *et al.*, 1973). Spot blotch was not so important before Green Revolution but became a major disease as the area of wheat under rice-wheat cropping system expanded in to hot humid areas of EGP (Saari, 1998). At present, leaf blight is regarded as the most serious disease of wheat in the North Eastern Plains Zone (NEPZ) of India. The average yield losses due to spot blotch in India were reported to be 15.5% (Dubin and van Ginkel, 1991) and 17% (Saari, 1998). Spot blotch is highly influenced by environmental conditions, especially temperature and humidity (Chaurasia *et al.*, 2000; Duveiller *et al.*, 2005; Pandey *et al.*, 2005), therefore the pathogen is predicted to spread to cooler wheat producing areas *i.e.* Punjab, Haryana and Western Uttar Pradesh, due to global warming (Joshi *et al.*, 2007a). Owing to its growing importance, a number of studies were conducted in the last decades with an impressive progress (Table 1)

Variability in the pathogen

Morphological and cultural variability in *B. sorokiniana* has been reported by various workers (Maraite *et al.*, 1998; Chand *et al.*, 2003; Pandey *et al.*, 2005; Jaiswal *et al.*, 2007). Chand *et al.* (2003) reported various morphological groups of pathogen at different stages of disease development with dark green to black (Fig. 1) population as the main constituent of the epidemic since they displayed faster growth and higher sporulation under field conditions.

Maraite *et al.* (1998) observed the difference in the pathogenicity among the isolates and found selection for aggressiveness over years. Many wheat cultivars that were resistant at the time of their release became susceptible after a few years of cultivation, most likely due to the development of new pathogenic strains. This may be due to the selection of variants in the population, as variation for aggressiveness in the pathogen population has been reported (Pandey *et al.* 2005). Jaiswal *et al.*, (2007) found a high level of polymorphism but it displayed nine groups instead of five, as shown by morpho-pathological classification. Hence, they suggested that morpho-pathological classification does not reflect total variability that is present in the DNA and, therefore, molecular characterization would be more reliable (Jaiswal *et al.*, 2007).

B. sorokiniana initially behaves as a biotroph and later shifts to a necrotroph by producing a number of hydrolytic enzymes that play an important role in the pathogenesis and aggressiveness (Kumar *et al.*, 2001). In a recent report, a negative correlation was reported between aggressiveness and melanin content in the cell wall of *B. sorokiniana* (Bashyal *et al.*, 2010). *B. sorokiniana* produces a distinct dark brown or black pigment, melanin, by polyketide biosynthesis; the last step being the polymerization of 1, 8-dihydroxynaphthalene (DHN) (Eliahu *et al.*, 2007). Genes involved in melanin biosynthesis have been isolated in *B. oryzae*, a rice pathogen closely related to *Cochliobolus heterostrophus*, and in *C. agenarium* (Goldberg, 1994; Goossen *et al.*, 1994; Maeda and Fukuda, 1996).

Survival of *B. sorokiniana* in nature

Several theories were proposed for the survival and reappearance of the spot blotch pathogen which is very much required for integrated management of this pathogen. While some workers (Shaner, 1981) proposed seed as the main source of inoculum, others (Chinn *et al.*, 1962; Reis and Santos, 1987) reported surviving free dormant conidia

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in soil as a major source. Presence of green bridge through alternate grass hosts were also suggested to help in survival of this pathogen (Nelson and Kline, 1962; Misra, 1973; Duveiller and Gilchrist, 1994).

Chand *et al.* (2002) reported that dormant conidia surviving on wheat straw could be an important source of survival of *B. sorokiniana*. The saprophytic survival of the pathogen occurs on plant debris after the harvest of the crop. When humidity increased and reached close to the saturation, pathogenic conidia present on the crop residue germinated and then produced saprophytic conidia (Chand *et al.*, 2002). In an earlier study (Reis and Santos, 1987) found that free conidia were viable in the soil even after 37 months. Pandey *et al.* (2005) reported that probably green-bridge does not exist and seeds are the most important source of inoculum for the reappearance of spot blotch of wheat in rice-wheat cropping systems in eastern India. Of 22 species (weeds and grasses) normally found to be associated with rice-wheat fields were tested for the presence of *B. sorokiniana*, only three (*Setaria glauca*, *Echinochloa colonum* and *Pennisetum typhoides*) carried *B. sorokiniana*. However, isolates from these hosts were not found to infect wheat.

Sources of resistance

Till 1990s the available resistance sources could be broadly grouped in to three categories i.e. Latin American, Chinese and wild relative of wheat and alien species (Ginkel and Rajaram, 1988). Latin American sources are derived from Brazil while Chinese from the Yangtze River basin. Some of these resistant sources are Yangmai, Ning, Longmai and Shanghai with different accession numbers. Alien sources include *Thynosporium curvifolium* and *Aegilops squarrosa*. Transfer of resistance from alien species (*Thynopyrum curvifolium*, *Elymus curvifolius* and *T. tauschii*) to common bread wheat was also reported (Mujeeb-Kazi *et al.*, 1996). One of promising genotype developed by these alien sources was Chirya which has been widely studied for conventional and molecular studies.

The evaluation of germplasm over the years has proved that durum wheat (AB genome) is more susceptible than *aestivum* (ABD) (Chand *et al.*, 2000), indicating the presence of resistance genes in D genome. Several useful germplasm having good resistance to spot blotch has been reported by different workers (Chaurasia *et al.*, 1999; Sharma *et al.*, 2004; Joshi *et al.*, 2007b, c, d). Wheat somaclonal variants showing better resistance are also reported (Arun *et al.*, 2003).

Genetics of resistance

Inheritance studies on resistance to spot blotch are quite limited but general consensus is that many genes control resistance to this disease. Early studies (Srivastava *et al.*, 1971, Srivastava, 1982; Adlakha *et al.*, 1984) indicated monogenic control, but later on polygenic inheritance was established (Velazquez Cruz, 1994; Joshi *et al.*, 2004b). The experience of wheat workers to achieve partial resistance in breeding

populations (Dubin and van Ginkel, 1991, Duveiller and Gilchrist, 1994, Dubin and Rajaram, 1996) also suggested polygenic control. Recently, molecular markers (Kumar *et al.*, 2009, 2010) proved that several genes are responsible for resistance to this disease.

Association with traits

Resistance to spot blotch has been demonstrated to be associated with leaf angle (Joshi *et al.*, 2002) and stay green trait (Joshi *et al.*, 2007d). Earlier, resistance was considered to be associated with the late growth stage of the plant. However, when large number of lines was evaluated for resistance at fixed intervals ignoring growth stages (Zadoks *et al.*, 1974), the frequency distribution of genotypes differed from the distribution in which disease score was assessed on similar growth stages (Joshi *et al.*, 2002). The evaluation of homozygous resistant lines in the F₃, F₄ and F₅ generations of 'tall resistant x dwarf susceptible' and 'late resistant x early susceptible' also suggested that a genetic association between resistance and taller plant height or longer days to maturity is not always true.

In many spot blotch screening nurseries, early maturing genotypes (Ciano 67 and Sonalika) are used as susceptible check (Maraita *et al.*, 1998; Dubin *et al.*, 1998; Minh *et al.*, 1998) and disease scoring is compared to the susceptible check when it reaches a maximum level. Thus, late maturing genotypes appear resistant due to disease escape. This might have led to selection of late heading lines for spot blotch resistance (Dubin *et al.*, 1998). The absence of genetic association of resistance to spot blotch with plant height and days to maturity as observed in the present study suggested that breeding populations should have susceptible checks in different maturity and height groups for proper comparison of resistance. It also suggested that if scoring for disease severity is combined with growth stage, selection for resistance in the segregating generations will be more effective.

Another important trait that displayed strong association with resistance to spot blotch was leaf tip necrosis (*Ltn*) (Joshi *et al.*, 2004a). The results confirmed that leaf tip necrosis is strongly associated with moderate resistance to spot blotch and can be used as a morphological marker to facilitate selection for resistance (Fig. 2) (Joshi *et al.*, 2004a). Interestingly, this trait can also be used as a marker for selecting *Lr34/Yr18* genes known to be present in chromosome 7DS (Dyck, 1987). *Lr34/Yr18* also confers resistance to powdery mildew (*Blumeria graminis*) (Spielmeyer *et al.*, 2005), stem rust (*Puccinia graminis tritici*) (Dyck, 1987), and barley yellow dwarf virus (Singh, 1993).

Molecular markers for resistance

In last few years, molecular markers for spot blotch have also been identified in some of the resistant genotypes (Table 2). Kumar *et al.* (2009) investigated 'a cross of Yangmai 6' (a Chinese source of resistance) and Sonalika and reported four quantitative trait loci (QTL) on the chromosome 2AL, 2BS, 5BL and 6DL. These QTLs explained around 60%

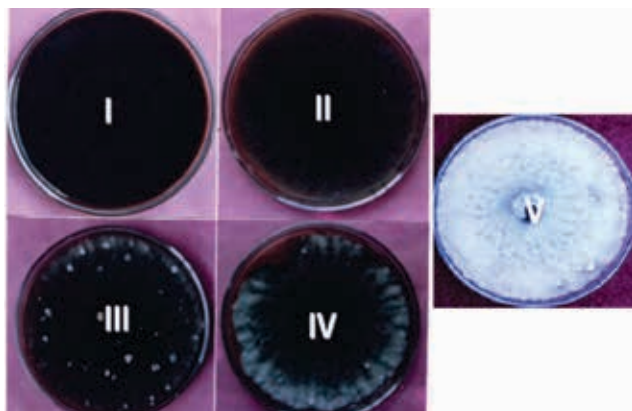


Fig. 1 Variability in the isolates of spot blotch pathogen *B. sorokiniana* of wheat (Chand *et al.*, 2003; Pandey *et al.*, 2005; Jaiswal *et al.*, 2007)



Fig. 2 Leaf tip necrosis (*Ltn*) a reliable morphological maker for resistance to spot blotch disease in wheat (Joshi *et al.*, 2004a)

of phenotypic variation. In addition, RILs developed by using two other genotypes (Ning 8201 and Chirya 3) with susceptible Sonalika were also investigated. Four other QTLs present on 2AS, 2BS, 5BL and 7DS were detected that explained 62% of the phenotypic variation (Kumar *et al.*, 2010). Among these, two appear robust: *Xgwm148* (chromosome 2B) and *Xgwm111* (chromosome 7D).

Progress in identifying and breeding resistant wheat varieties

Till 1990s it used to be generally accepted that spot blotch resistance of high yielding genotypes was not satisfactory. The slow progress in breeding for resistance to spot blotch (Rajaram 1988) was suggested to be due to several reasons including the lack of understanding of resistance, the variability of the pathogen and the aggressiveness of *B. sorokiniana* which seems to increase over time (Hetzler 1992). However, over years a number of resistant sources and cultivars were developed due to greater awareness about the significance of this disease. Kumar *et al.* (2007) developed a new technique for monoconidial culture of the most aggressive isolate in a given population of *B. sorokiniana* of

wheat and barley which can be effectively used for screening of germplasm.

Proper characterization and association of locations is very important for screening superior breeding lines capable of reducing harvest losses to the disease. The importance of using suitable sites to evaluate germplasm for particular traits is well recognized. In a hierarchical cluster analysis that was used to group locations on the basis of genotype x location (G x L) interaction effects for spot blotch AUDPC, the diverse south Asia was divided into two broad regions and four sub-regions (Joshi *et al.*, 2007b). The locations Varanasi (India) and Bhairahawa (Nepal) were identified as the most suitable sites for evaluation of spot blotch, followed by Rampur (Nepal). The major determinant for the clustering was mean temperature. The results suggest that the major wheat region of South Asia can be divided into sub-regions, which may reduce the cost of resistance evaluation and aid in developing wheat with resistance to this disease. In this study, the best three locations were in India (Varanasi) and Nepal (Rampur and Bhairahwa), which is useful knowledge because until the late 1990s, wheat cultivars grown in Nepal were the primary cultivars released for eastern Gangetic

Table 1 The progress of research on host-pathogen interaction with respect to spot blotch of wheat in last 10 years

Seven questions 10 years ago	Current solutions
Pathogen is a complex in EGP	The main pathogen is <i>B. sorokiniana</i>
Epidemic population unknown	Now known
Survival of pathogen and epidemiology not known	Survival and epidemiology established
Resistance sources scanty	Substantial resistance sources available
Inheritance debatable	Established that few genes (polygenes) control resistance
Association with traits questionable	Association with different traits established
No markers for resistance	Both morphological (<i>Ltn</i>) and molecular markers (SSR) available

EGP = Eastern Gangetic Plains

Table 2 SSR markers and QTLs position for resistance to spot blotch in three crosses of spring wheat (Kumar *et al.*, 2009; 2010)

QTLs	Spring wheat crosses		
	Yangmai 6 × Sonalika	Ning 8201 × Sonalika	Chirya 3 × Sonalika
<i>Qsb.bhu-2A</i>	C-2AL1-0.78 (<i>Xgwm445</i> – 192 bp)	C-2AS5-0.78 (<i>Xgwm425</i> – 136 bp)	-
<i>Qsb.bhu-2B</i>	C-2BS1-0.53-0.75 (<i>Xgwm148</i> – 163 bp)	2BS1-0.53-0.75 (<i>Xgwm148</i> – 163 bp)	2BS1-0.53-0.75 (<i>Xgwm148</i> – 163 bp)
<i>Qsb.bhu-5B</i>	C-5BL6-0.29 (<i>Xgwm067</i> – 78 bp)	C-5BL6-0.29 (<i>Xgwm067</i> – 81 bp)	-
<i>Qsb.bhu-7D</i>	-	7DS5-0.36-0.61 (<i>Xgwm111</i> – 137 bp)	7DS5-0.36-0.61 (<i>Xgwm111</i> – 137 bp)

Table 3 Pedigree of some agronomically superior lines with high resistance to spot blotch compared to susceptible check Sonalika

No	Pedigree	AUDPC % days*
1	TRACHA-2//CMH76-252/PVN'S'	260
2	KAUZ//KAUZ/STAR/3/PRINIA/4/MILAN/KAUZ	295
3	KAUZ*2//K134(60)/VEE	310
4	MRNG/BUC//BLO/PVN/3/PJB 81	310
5	GAA/KEA//GAA	315
6	MRNG/BUC//BLO/PVN/3/PJB 81	315
7	NL 251/ZSH 22	330
8	CKR/HD2172/8/IAS58/6/KAL//BB/5/ALD/4/OLN/TRM//7C/ ALD/ 7 /MAYA/ PVN	335
9	WEAVER//VEE/PJN/3/MILAN	340
10	KAUZ*2//K134(60)/VEE	345
11	Baz (ATTILA*2/STAR/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ)	
12	Francolin (WAXWING*2/VIVITSI)	
	Sonalika (Check)	1750
	LSD	98.3

*Average of three years of testing under field conditions at Varanasi

plains of India and, presently, about half of the advanced lines adapted in Bangladesh come from Nepal (Joshi *et al.*, 2007b).

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 level 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. 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., 2004). Current studies suggest that variation for spot blotch resistance is present in the advanced lines of South Asian countries most of which includes CIMMYT derived lines (Joshi *et al.*, 2007c). A previous study (Chaurasia *et al.*, 1999) showed that when compared to Indian germplasm, CIMMYT lines possessed better resistance against leaf blight of wheat. The successful Veery lines produced in the early 1980s (Rajaram *et al.*, 1990) possessed healthy stay-green, recently shown to be associated with resistance to spot blotch of wheat (Joshi *et al.*, 2007d). Many of the superior lines are derived from Chirya and 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. The results (Table 3) so far here suggest that numerous genotypes possessing good spot blotch resistance and high yield potential under the hot, humid conditions of

South Asia are either established or under advanced state of testing (Joshi *et al.*, 2011).

Future thrust

Spot blotch of wheat has assumed high interest due to losses caused by this disease in the 2nd largest wheat growing zone (NEPZ) of our country. Although substantial progress has been made in last few years in understanding host-pathogen relationship of this disease, much more research is required. The two major issues that need special attention are development of near-immune lines and robust molecular markers. Presently, immune lines for this disease are not available. Therefore, attempt should be made to develop such lines. Molecular markers are reported but there is scope for fine mapping to obtain much more robust markers. In addition, pre-breeding efforts are also needed to obtain good donors of resistance. All these efforts would be highly useful for breeders to enhance the level of resistance in agronomically superior backgrounds that fit well under climate change.

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