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Review Article

Spot blotch disease of wheat – a new thrust area for sustaining productivity

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Abstract

Spot blotch caused by *Bipolaris sorokiniana* is a major disease of wheat in warm and humid regions of the world including South East Asian countries such as India, Nepal and Bangladesh. The fungus has a worldwide distribution but as a pathogen it is the most aggressive under the conditions of high relative humidity and temperature associated with the low fertility of soils in South Asia, South America, Africa, and Australia. The yield loss due to the disease is very significant especially in North Eastern Plains Zone (NEPZ) of India, Nepal Terai and North Western Bangladesh. Early symptoms are characterized by small, dark brown lesions ranging 1 to 2 millimeter long without chlorotic margin. In susceptible genotypes, these lesions extend very quickly in oval to elongated blotches, light brown to dark brown in colour. They may reach several centimeters before coalescing and inducing the death of the leaf. The pathogen has morphological and molecular variations among the isolates. Ideal conditions for spot blotch development on the leaves are relative humidity of near 95 per cent with an average temperature in the coolest month above 17°C and long periods (more than 12 to 18 hours) of leafs wetness caused by rainfall, irrigation, fog or dew. Recently a number of genotypes have been identified as donors for improving host resistance. The best way to control spot blotch is through an integrated approach including varietal replacement, agronomic management and need based application of fungicides. The use of molecular tools in identifying QTLs for spot blotch resistance, pathogenic variability and exercising marker assisted selection has good scope for effective management of this pathogen for ensuring food security in the world.

Keywords: Spot blotch, pathogenicity, host resistance, QTLs, disease management

Introduction

Wheat is the most important cereal crop after rice in India and major staple food of South Asian region countries. The world's population is increasing by one billion in every 11 years and at present rate, it is expected to be 8.4 billion by the year 2025. Its importance in household food security is well recognized. Green revolution played a key role in ensuring food security in this population dense region of the world, which mainly comprises of India, Pakistan, Nepal and Bangladesh (Joshi *et al.*, 2007). Yield trials conducted by different breeding centers around the world have shown that the production of bread wheat is constrained by several biotic and abiotic stresses (Duveiller, 2004). The warmer parts of the world are mainly affected by many diseases and among these diseases, spot blotch or foliar blight caused by *Bipolaris sorokiniana* (Sacc. in Sorok). Shoem is one of the most concerning disease in warm and humid regions of India and other South Asian countries due to its wide spread prevalence and increasing severity (Joshi *et al.*, 2002). It is an important disease in that mega environment which is characterized by high humid conditions around and after heading stage. The occurrence of *Bipolaris sorokiniana* as wheat pathogen in the North-western part of the Russian Federation (Smurova, 2008) suggests that this fungus has the potential to become a serious wheat pathogen in Europe. *B. sorokiniana* under European conditions causes yield losses mostly due to root rot (Rossi *et al.* 1995) and seed black point, which negatively affects seed germination and causes root rots in seedlings (Hudec and Muchova, 2008). Further, the wide spread use of conservation tillage practices may also be favorable for spot blotch incidence in the South East Asia (Duveiller and Sharma, 2009). It is the major biotic constraint in wheat in the Gangetic plains, especially in the rice-wheat cropping system and is the main limiting factor to growing wheat in South-East Asia (Duveiller *et al.*, 1998). At present spot blotch of wheat is a major pathogen at national level in India and its frequency is highest in north eastern plains zone amongst six agro climatic zones due to prevalence of hot and humid weather conditions.

Symptoms

The dark brown necrotic spots (boat shaped) occur on the coleoptiles, leaves, crowns, stems, and roots with or without yellow halo around these. Darkening of the sub crown internode is a characteristic symptom. Lesions on the leaves start as a few mm that extend as elongated dark brown spots greater than 1-2 cm (Chand *et al.*, 2002). A yellowing due to toxin production is sometimes observed

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extending from the lesion. Later such spots coalesce each other thus result blight on large leaf portion. As the disease progresses the spots join together forming large blotches that cover the leaves and eventually killing it. On leaves, conidia develop readily under humid conditions and spread over several centimeters before coalescing and inducing the death of the leaf tissue. An abundant production of conidia can be observed on old lesions under humid conditions and chlorotic streak is sometimes seen diffusing from the border of the lesion as a result of toxin production (Mercado Vergnes *et al.*, 2006 and Bockus *et al.*, 2010). Stunting and reduced tillering may be observed in heavily infected plants which may lead to premature death, resulting in white heads. Kernels become shriveled and roots become dark brown and rotted. Yields may be reduced due to root rot even though symptoms are not well-developed.

Pathogen and host range

Spot blotch is caused by *Bipolaris sorokiniana* (Sacc.) Shoem. Syn. *Drechslera sorokiniana (Sacc.) [Syn. Helminthosporium sativum,* teleomorph *Cochliobolus sativus]* Subram., and Jain, *Cochliobolus sativus, Drechslera* ex Dastur [anamorph *Bipolaris sorokiniana* (Sacc.) Shoem.] and several synonyms of the anamorph have been used like *Helminthosporium sorokinianum, Drechslera sorokiniana* and *Helminthosporium sativum* (Maraite *et al.*, 1998). The pathogen causing spot blotch is the same fungus that causes common root rot. Sometimes it is caused together with *Drechslera tritici- repentis (Died.) Shoem. [Syn. H. tritici- repentis* Died., *Pyrenophora tritici- repentis(Died.)Drechs.]* in teleomorph state respectively (Ruckstuhl, 1998). *Bipolaris sorokiniana* is characterized by thick-walled, elliptical conidia (60-120 µm ×12-20µm) with 5-9 cells. In axenic culture, the mycelium is composed of hyphae interwoven as a loose cottony mass and appears as white or light to dark grey depending on the isolates (Kumar *et al.,* 2002). These fungi are differentiated from the *Bipolaris* genus on the basis of morphological features of conidiophores and conidia. On the leaf, lesions are due to anamorph *Bipolaris sorokiniana*, characterized by long multicellular spores, whereas the ascospores of *Cochliobolus sativus* are formed in pseudothecia developed on the wheat residue. *B. sorokiniana* belongs to the division- *Eumycota*, subdivision-*Deuteromycotina*, class-*Hyphomycetes*, subclass-*Sporomycetidae*, order-*Moniliales* and family-*Dematiaceae.* It is considered as a semi-biotrophic fungus and has worldwide distribution. A key for distinguishing species of *Bipolaris* was reported (Subramanian, 1971). It affects small grain cereals, although rye is less susceptible and oats are seldom infected.

Another foliar blight disease, zonate eyespot (C.O. *Drechslera gigantea*) was reported (Chowdhury *et al.*, 2005) along with *B. sorokiniana* from infected wheat plants from Coochbehar, West Bengal. The conidiophores are dark brown, 3-6 septate and 180-350 µm × 10 µm in size. Conidia are straight, cylindrical with rounded ends, sub-hyaline and measure 330-490 µm ×15-20 µm in size. They are 6-8 septate and the middle cells are larger than the terminal ones.

Pathogen variability and aggressiveness

Historically, the spot blotch pathogen *B. sorokiniana* has been described as a variable fungus with many morphological (Christensen, 1925) and physiological (Tinline, 1962) variants. Part of the variability has been attributed to hetrokaryosis and parasexual mechanism (Tinline, 1958). The variability and aggressiveness of this pathogen seems to increase over time (Hetzler *et al.,* 1991: Jeger, 2004). Although variability in the isolates of *B. sorokiniana* have been reported at morphological (Chand *et al.,* 2003; Maraite *et al.,* 1998: Mishra, 1981) and pathological (Nelson, 1960: Jaiswal *et al.,* 2007) levels. The PCR based molecular markers RAPD has been successfully used to identify strains (Guzman *et al.*, 1999), to characterize races (Malvic *et al.,* 2001) and to analyse virulence (Chen *et al.,* 1995) in this pathogenic fungi. In such cases molecular markers are used for studying genetic variability in plant pathogens (Sharma *et al.,* 1999) RAPD offers very promising, versatile and informative molecular tool to detect genetic variation with population of plant pathogens (Prasad *et al.* 2012). Molecular characterization of pathogen variability in *B. sorokiniana* isolates causing spot blotch in wheat in India has also been reported (Saharan *et al.*, 2008).

Different aggressiveness behaviour of the pathogen to the host was observed during aggressiveness analysis by different researchers. In addition to morphological traits, *B. sorokiniana* varies in its pathogenicity on gramineous hosts. However, little information is available about aggressiveness of the *B. sorokiniana.* Sexual reproduction in *B. sorokiniana* is rare and reported only from Zambia (Raemaekers, 1987). As far as variability in asexual population is concerned, it is due to para-sexual recombination (Tinline, 1962). One isolate showed aggressiveness behaviour was observed (Mikhailova *et al.*, 2002). Aggressiveness behaviour of 11 isolates of *B. sorokiniana* collected from different geographical location in Russia, checked on 10 varieties of wheat showed significant difference in fungal strains behaviour. In another report (Duveiller and Altamirano, 2000), they isolated 27 isolates of *B. sorokiniana* (from roots, leaves and grains of spring wheat) collected from a single site in Mexico and found no clear difference between groups of isolates. The other workers also showed that isolates of *B. sorokiniana* possessed pathological variability (Nelson, 1960; Hetzler *et al.*, 1991). Ten isolates of *B. sorokiniana* (*Cochliobolus sativus*) from different geographical regions of Brazil were analyzed for their virulence on wheat cultivars, morphological characteristics, and growth rate on PDA. Variability in cultural characteristics was observed in the morphology and growth rate between the original isolates and the re-isolates. However, no relationship between morphological variability and virulence was observed among the ten-original isolates (Oliveira *et al.*, 1998). Chand *et al.*, 2003 demonstrated that the five groups of the isolates of *B. sorokiniana* differed for their morphological appearance. Similar observations were recorded (Rasmussen *et al.*, 2003) that the stability of resistant genetic strains remained essential considering that *B. sorokiniana*, the principal pathogen forms a continuum of strains differing in aggressiveness.

Epidemiology

The severity of the disease is directly influenced by tillage option, irrigation scheduling, soil fertility level, sowing density, crop growth stage, occurrence of late rains during crop cycle, heat stress during grain filling, late planting, high temperature and high relative humidity causing more than 12 hours duration of leaf wetness (Sharma and Duveiller, 2003). In field, infected seeds and soil serve as an important source for primary inoculum of spot blotch pathogen. Spot blotch pathogen may infect wheat right from first leaf stage and susceptibility of plants increases after flowering.

Spot blotch is seed transmitted disease and its conidia survive in the soil. Spot blotch is the most widely distributed disease of cereal crops (especially wheat and barley) in the subtropics, mainly in south Asia and some parts of South America. Ideal conditions for spot blotch development on the leaves are high relative humidity with high temperature and long periods (more than 12 to 18 hours) of leafs wetness caused by rainfall, irrigation, fog or dew. Conidia present on infected stubble and on the soil surface are dispersed by wind and initiate lesions on the leaves and stems later in the season. The most important factor, temperature plays a key role coupled with high humidity. Moderate to warm temperature range (18°C to 32°C) favours the growth of *B. sorokiniana.* Even at the end of the monsoon and in absence of rainfall, high relative humidity arising from high levels of soil residual moisture along with foggy days allows long hours of wetness on leaf blades that can last until late January in Indo-Gangetic Plains, creating ideal conditions for the establishment and multiplication of pathogen. There are various cycles of conidia production during the cropping season which lead to secondary infections after spreading through wind and water drops. Many scientists reported that disease was more severe at 28°C than at lower temperatures. Epidemiological studies have shown that timely sowing avoids the physiological stress that often coincides with the flowering stage which in turn reduces spot blotch (Duveiller *et al.*, 2005).

Toxin production

On the basis of morphological, physiological and genetic basis, differences in *Bipolaris sorokiniana* strains and least virulent isolates of *B. sorokiniana* have been detected showing difference in symptoms on wheat genotypes with culture filtrates of this fungal pathogen (Gayad, 1961). The fungus produces sesquiterpenoid toxins that are synthesized from Farnesol. About 20 compounds related to *Helminthosporol* have been isolated from different species of the genus *Bipolaris* (Kachlicki *et al.,* 1995). The "*Helminthosporol*" is a toxin, produce by B. *sorokiniana*, which may be used to evaluate wheat genotypes *in situ.* A new toxin '*Bipolaroxin*' in culture filtrate of *B. sorokiniana* has been detected and found non host specific.

Disease assessment

Field evaluation of resistance is based on visual assessment of the progress of the disease from the lower levels of the canopy. Disease intensity was noted under natural infection of spot blotch based on percent area infected. First reading was taken at anthesis stage (Zadoks Scale 69) and was repeated twice at 73 (every week) and 83 (every day) growth stage (Zadoks *et al.*, 1974).

The most effective system consists of using a double-digit scale (00-99) developed as a modification of Saari and Prescott's severity scale (Saari and Prescott, 1975). The first digit (D_1) indicates disease progress in the canopy height from ground level; the second digit (D_2) refers to measured severity based on diseased leaf area. Both D_1 and D_2 are scored on a scale of 1-9. For each score, the percentage of disease severity is estimated based on the following formula:

$$\text{Severity } (\%) = (D_1/9) \times (D_2/9) \times 100$$

Because the disease evolves very rapidly in areas affected by the spot blotch, it is often necessary to record several individual disease scores per plot at 3 to 7 day intervals over a 3 to 4 week period between anthesis and the dough stage, depending upon the seedling date (Duveiller and Sharma, 2009). The area under the disease progress curve (AUDPC) can be calculated using the percentage severity estimates corresponding to three to four recordings as shown below.

$$AUDPC = \sum_{i=1}^{n-1} [(X_i + X_{i+1}) / 2] (t_{i+1} - t_i)$$

where, X_i = severity on the i^{th} date, t_i= i^{th} day and n=number of dates on which the disease recorded. AUDPC (% /day) measures the extent of the disease as well as its rate of progress. Later, a new double digit method (0-9) was proposed which is based on per cent leaf area covered due to blight in case of flag and penultimate leaf to flag leaf (F-1) at dough stage. The digit towards right side indicates score of flag leaf whereas left digit gives the score of F-1 leaf.

According to this scale the two digits (left and right) represent the percentage of the leaf area infected on the flag and flag-1 leaf, respectively (Singh *et al.,* 2005). These two leaves are green at milk stage and contribute most to the grain filling process thus affecting directly to the grain yield (Kumar *et al.*, 1998). Based on the disease score values obtained at three different stages (cereal growth stages as per decimal scale at an interval of 7-10 days (between milk stage to late dough stage), the genotypes were categorized as immune or no blight (00), resistant (HLB score 01-23), moderately resistant (34-45), moderately susceptible (56-68), susceptible (78-89) and highly susceptible (89-99) to make double digit scale widely applicable for recording of disease even in breeding populations. The uniformity in disease recording following double digit scale along with rating scales to categorize genotypes/ cultivars is important and need to be implemented at all levels.

Yield losses

Yield losses due to foliar blights are variable and in last two decades spot blotch has emerged as serious concerns for wheat cultivation in the developing world. The disease causes significant yield losses overall 22 per cent to complete failure of crop under severe epidemics. In India, losses due to diseases may be 10-50 per cent which can be devastating for farmers in the Eastern Gangetic Plains (EGPs) and depends on the level of resistance in a cultivar against leaf blight and weather conditions. Spot blotch has been considered as a major constraint to wheat yields in South Asia due to reduction in 1000-grain weight and grain yield (Singh *et al.,* 2007). On an average, a South Asian country loses 20 per cent of crop yield through leaf disease. Grain yield losses due to foliar blight vary greatly, depending on wheat crop husbandry. Diseased wheat plots in Mexico without fungicides yielded 43 per cent less (Villareal *et al.*, 1995). In farmers' fields in Bangladesh, the average losses due to these foliar blights were estimated to be 15 per cent (Alam *et al.*, 1998). In Turkey, *B. sorokiniana* has been observed to be widespread in the sub crown internodes and crowns of wheat (Eken and Demirci, 1998).The pathogen also causes grain yield losses up to 10, 15, and 20 per cent through common root rot and seedling blight in countries like Scotland, Canada, and Brazil, respectively. At higher latitudes, such as the Canadian and US prairies (Gonzalez and Trevathan, 2000; Fernandez and Jefferson, 2004) and in parts of Australia (Lehmensiek *et al.*, 2004), *B. sorokiniana* is a dominant pathogen among fungi, causing common root rot and resulting in losses of up to 19 per cent. Earlier studies on wheat diseases have reported impressively high yield losses and suggested that sizable area of wheat is at risk to specific diseases or pests. Grain infections by this fungus in years that were favorable for the disease were detected to be as high as 70 per cent (Sharma *et al.* 2005). In Nepal, it was shown that spot blotch induced grain yield losses of 52 per cent under soil nutrient stress comrade with 26 per cent under optimum fertilization and spot blotch continues to causes substantial grain yield reductions under resource-limited farming conditions (Sharma and Duveiller, 2006). Besides, the usefulness of the information generated on spot blotch disease in wheat should find a place in promoting or advancing breeding material at each level to curtail the yield losses in future genotypes.

Disease management

Though the spot blotch disease can be controlled by a number of ways but integrated management is the best option. It includes the use of disease resistant varieties, cultural management, crop rotation, seed treatment, biological control and foliar fungicides. Earlier reports on each aspect of disease management have been discussed in detail along with future strategies to be followed for sustaining the productivity.

Improving host resistance

The first crosses to incorporate spot blotch resistance were made about three decades ago. These crosses involved moderately resistant cultivars, such as BH 1146 from Brazil. However, the level of resistance in progenies was inadequate when tests were carried out at Poza Rica, Mexico. In the mid-1980s, wheat genotypes carrying resistance to scab were obtained from the Yangtze River Valley of China, also showed varying levels of spot blotch resistance when tested at Poza Rica. These Chinese lines included Suzhoe 1 to 10, Wuhan 1 to 3, Shanghai 1 to 8 and certain Ningmai and Yangmai lines. About the same time, the wide crossing programme at CIMMYT produced resistant lines, which contained *Thinopyrum curvifolium* in their pedigree (Villareal *et al.*, 1995). Some of these lines and their derivatives are showing good resistance and appear to be promising in Bangladesh, low-land Bolivia and Nepal. Resistance in wheat genotypes such as Sabuf, Chirya 1 and Cugap, appear to be controlled by two to three genes. Whereas, Chinese lines namely; Longmai 10 and Yangmai 6 may carry polygenic resistance with high narrow sense heritability (Sharma *et al.*, 1997). A key problem with selection for spot blotch resistance is the negative correlation of disease severity with heading date and plant height (Duveiller and Gilchrist, 1994). Therefore, care must be taken if short types with early maturity are required. Current strategy followed at CIMMYT is to combine resistances from these diverse sources. Identification of some highly resistant lines from such crosses indicate that resistance is additive in nature. The mode of inheritance of resistance to the disease was studied in F_1 and F_2 generations in crosses using two resistant (VEE 'S' and HD 2206) and three susceptible varieties (HP 1633, K 8962 and Hork 'S') of spring wheat and scored every plant using the double digit scale formulated by Kumar *et al.*,(1998).

The growth stage of plants at which the spot blotch infection appears is an important factor to decide the extent of losses in grain yield. Information on the extent of the genetic variability, heritability and other genetic parameters of spot blotch resistance with other agro-morphology attributes, a pre-requisite for genetic improvement through systematic breeding programme, has been generated (Singh *et al*., 2007a). Another study was undertaken on character association analysis to estimate the nature of magnitude of correlation between yield components and leaf blight scores. Estimates of direct and indirect effects through path analysis identify the role of disease resistance and other morphological attributes including yield components, which directly or indirectly influence the grain yield in bread wheat (Singh *et al*., 2008).

A study carried out in 57 environments and confirms the low disease severity of a few genotypes showing their values in improving spot blotch resistance of the commercial cultivars in South Asia. Another study conducted at most of these sites in the same years, commercial cultivars had shown higher disease severity including susceptible check (Sharma *et al*., 2007). These results demonstrate that newer wheat genotypes in South Asia possess improved resistance over old commercial cultivars and confirm previous findings based on data from limited environments that included several resistant genotypes (Sharma *et al*., 2004, Joshi *et al*., 2004, Singh *et al.,* 2007). A few genotypes with lower disease severity (Chirya 7, Yangmai 6 and Chirya 1) had relatively lower grain yield and grain weight, and later maturing compared to check genotype which has been developed in South Asia. However, the genotype with the highest grain yield and grain weight (Altar-84/*Ae. sq.* (224)// Yaco) also had low disease severity. This shows progress in combining spot blotch resistance and high grain yield, which was not possible earlier. Dubin *et al.* (1998) had reported that high yielding wheat cultivars during early 1990s in India, Nepal and Bangladesh were susceptible to spot blotch. Still high yielding recently developed commercial wheat cultivars in the region with low to intermediate levels of resistance showed up to 20 per cent yield loss due to spot blotch (Siddique *et al*., 2006). Identification of high yielding and spot blotch resistant genotypes in this study offers opportunity to further increase the yield of the commercial cultivars by improving resistance through selective breeding. Kumar *et al.,* (2013) observed that Chirya 3, Chirya 7 and Chirya 1 were resistant both at seedling and adult plant stage and two genotypes viz., Milan/Shanghai 7 and Shanghai 4 were moderately resistant when tested at different locations of India. Genotype, K 8027 had also been studied earlier (Dubin *et al*., 1998). They reported that the leading commercial wheat cultivars of South Asia in early 1990s had much higher spot blotch severity than K 8027, which showed good level of resistance. The report also shows that a few of the recently developed wheat genotypes have resistance level equal to or better than K 8027, besides showing higher yield and grain size and were early maturing. These findings demonstrate that improvement achieved in the region is due to combined efforts at international level in improving spot blotch resistance of wheat cultivars in the Eastern Gangetic Plains of South Asia. Also, it shows that the best sources of spot blotch resistance are coming not only from the wide crosses alone, but also from the traditional hexaploid wheat. This confirms that spot blotch resistant wheat genotypes are becoming more acceptable agronomically, and are available for direct use in breeding programs to develop commercial cultivars. The results further substantiate the usefulness of the regional spot blotch resistance monitoring nursery as a vehicle for introducing new sources of spot blotch resistance that are agronomically acceptable and provide high and stable yields (Sharma *et al*., 2004a). The results revealed that segregation in all the three (RxS) crosses followed a 1 resistant: 15 susceptible ratio, wherein, it was concluded that the resistance is controlled by two pairs of complementary recessive genes. Besides, the genetics of leaf blight (*B. sorokiniana*) resistance in durum wheat by crossing two resistant genotypes with two susceptible genotypes suggested that susceptibility is governed by two dominant genes with complementary effect. The resistant reaction is expressed only when at least one of the two genes were in homozygous recessive form.

Sources of spot blotch resistance have been identified over the years and governed by one or more genes, and their origins can be differentiated into three categories: Latin America, China and wild relatives of wheat or alien species (Van Ginkel and Rajaram, 1998) and *Aegilops squarrosa* crosses had shown impressive resistance to spot blotch in Mexico. Some progress in transferring resistance genes from *Thinopyrum curvifolium, Elymus curvifolium* and *Triticum tauschii* to wheat germplasm has been achieved (Mujeeb-Kazi *et al*., 1996a, 1996b). Utilizing these alien sources in combination with Chinese resistance sources, outstanding lines such as Mayoor and the Chirya series were developed. Among 250 synthetic hexaploid (2n=6X=42) amphiploides of wheat some resistant stocks against *B. sorokiniana* have been identified. Other two resistant Brazilian varieties are BH 1146 and CNT 1 (Mehta, 1997). Earlier Chinese sources of resistance used at CIMMYT include Shanghai# 4, Suzhoe# 8, and Yangmai# 6. Spot blotch disease in wheat may also be tackled through a multipronged strategy that led to the development of new model sources of resistance as donors. As a result, many high yielding lines and spot blotch resistant lines were identified and shared with centers across zones in India (Singh *et al*., 2007). Besides, six new genetic stocks (LBRL 1, LBRL 4, LBRL 6, LBRL 11, LBRL 13 and DBW 46) possessing high level of leaf blight resistance in improved background have been developed and registered for use by the breeders across countries.

In wheat, somaclonal variants reported for various plant traits (Arun *et al.*, 2003) from immature embryos of two spring wheat varieties (HUW-206 and HUW-234) have displayed improved earliness, enhanced resistance to spot blotch disease and increased yield over parents established in regeneration. In Turkey, extensive studies were conducted by Liatukas and Ruzgas (2012) on resistance of European wheat varieties against *B. sorokiniana*. In South Asia, moderate success in breeding for spot blotch and foliar blight resistance has been reported (Bhandari *et al.*, 2003; Sharma *et al.*, 2004; Joshi *et al.*, 2004a; Siddique *et al.*, 2006; Singh *et al.*, 2007; Kumar *et al.*, 2013). Conventional breeding of wheat for selection of genotypes resistant for spot blotch has made limited progress in the past (Sharma *et al.*, 2004 & 2007, Singh *et al.*, 2008). However, there is still need for further exploration of sources imparting resistance to spot blotch.

Identification of QTLs and marker assisted selection

Many reports of tagging and mapping of several disease resistance genes and QTLs are available in wheat (Langridge *et al.*, 2001) however, only a few reports are available for spot blotch. The association of leaf tip necrosis with spot blotch resistance was established (Joshi *et al*, 2004). For this disease, the association of resistance with microsatellite markers in bulks of susceptible and resistant progeny lines was reported (Sharma *et al.* 2007). Later, stay green trait and erect leaf posture was also reported to have positive linkage with spot blotch resistance (Joshi *et al.*, 2007). These morphological markers are successfully being used in markers assisted selection of spot blotch resistance germplasm lines.

Through molecular analysis, four QTLs (QSB.bhu-2A, QSB.bhu-5B, QSB.bhu-2B and QSB.bhu-6D) for spot blotch resistance in the Chinese wheat variety, 'Yangmai 6' were mapped on chromosome 2A, 2B, 5B and 6D (Kumar *et al.*, 2009 & 2010). However, more information with respect to the identification of QTLs in different genetic backgrounds were generated when QTLs were mapped in two other resistance sources (Ning 8201 and Chirya 3) and to compare the chromosomal locations of QTLs with 'Yangmai 6' to identify diagnostic markers that can be used for marker assisted selection and to make an effective breeding programme.

Recently, Lillemo *et al.* (2013) found potential association of *Lr*34 and *Lr*46 with resistance to spot blotch. *Lr*34 was found to constitute the main locus for spot blotch resistance, and explained as much as 55 percent of the phenotypic variation in the mean disease data across the six environments. Based on the large effect, the spot blotch resistance at this locus was given the gene designation *Sb*1. Further, two minor QTLs were detected in the sub-population of RILs not containing *Lr*34. The first of these was located about 40cM distal to *Lr*34 on 7DS, and the other corresponded to *Lr*46 on 1BL. A major implication for wheat breeding is that *Lr*34 and *Lr*46, which are widely used in wheat breeding to improve resistance to rust diseases and powdery mildew, also have a beneficial effect on spot blotch. Molecular markers in wheat have been reported that showed association with spot blotch resistance (Virender *et al.*, 2012; Sonia *et al.*, 2013). There is urgent need to identify QTLs for spot blotch resistance and utilize in molecular breeding programmes to develop better yielding and disease resistant material in comparatively lesser time with more precision.

Agronomic practices

Information from different countries on managing foliar blight through manipulation of agronomic practices suggests that different mineral nutrients may reduce foliar blight (Krupinski and Tanaka, 2000; *Singh et al.*, 1998). Although soil moisture and soil nutrient stress occur together in the wheat fields of South Asia, little quantitative information is available on the effect of low soil moisture and poor soil fertility on foliar blight severity. There are some reports to indicate the role of potash in reducing spot blotch severity (Regmi *et al.*, 2002). Good crop husbandry and optimum agronomy may also reduce spot blotch disease severity up to certain level (Sharma *et al.*, 2006). Potassium helps to prevent disease development by hindering multiplication, development and survival of pathogen and controlling the internal metabolism of the plant and thus affecting food supply for the pathogen, as well as preventing the establishment of the pathogen and its spread within the plant (Perrenoud, 1990; Krupinsky *et al.*, 2000). Clearing or ploughing the stubble, grass weeds and volunteer cereals reduce inoculum similar to crop rotation (Diehl *et al.*, 1982).

Crop rotation favours beneficial soil organisms as well as promotes better plant nutrition. Crop rotation allows time for the decomposition of stubble on which pathogens carry over, and natural competitive organisms reduce the pathogens on the remaining residue while unrelated crops are being grown. As this pathogen has a wide host range, so there are some difficulties to find out the suitable non-host crop.

Seed treatment

Seeds are one of the important sources of primary infection. Therefore, seed treatment with a suitable fungicide reduces the carry over inoculum potential, but unless soil inoculums are reduced, seed treatment alone offers no benefit. Seed lots with less than 20 per cent infection should only be treated if there is a shortage of seed (Mehta, 1997). Seed treatment with Vitavax 200 B and Bavistin increased seed germination by 43 per cent and reduced seedling infection in Nepal (Sharma *et al.*, 2005). The seed treatment of a newly developed fungicidal formulation Vitavax 200 WS (Carboxin + Thiram 1:1) @ 2.0, 2.5 and 3.0 g per kg seed gave good results in reducing seedling mortality, incidence of foliar diseases at multilocation of India (Singh *et al.*, 2007).

Biological and chemical control

Bio-control of spot blotch has been attempted by several scientists with mixed responses. Successful antagonists against seed borne *B. sorokiniana* were *Chaetomium* sp., *Idriella bolleyi*, and *Gliocladium roseum* (Knudsen *et al.,* 1995).The antagonistic potential of *Chaetomium globosum* against *Drechslera sorokiniana* was first observed by Mandal *et al.*, (1999) which was further confirmed (Biswas *et al.*, 2000). The saprophytic Ascomycetes, *Chaetomium globosum* Kunze, is a potential antagonist of several soil and seed borne plant pathogens (Vannacci and Harman, 1987; Walther and Gindrat, 1988). A thorough study made by Agarwal *et al.*, (2004) has highlighted the potential antagonism of an antifungal metabolite produced by *C.globosum* against *C. sativus* both *in vitro* and *in vivo* conditions. Suppression of soil-borne fungi, including *Bipolaris sorokiniana* was observed in the presence of isothiocyanates released into soil by *Brassica* species (Kierkegaard *et al.,* 1996).

Despite the harmful effect of fungicides to human and environment, it has proved useful and economical in the control of spot blotch. Non systemic and systemic foliar fungicides belonging to the dithiocarbamates (*viz*; Mancozeb) and Triazoles (viz. Propiconazole, Tebuconazole, Flutriazol, Procloraz, and Triadimenol) and dicarboxymides (viz. Iprodione) are known to be effective. Foliar applications especially with systemic fungicides such as Tebuconazole, Epoxiconazole, Flutriazol, Cyproconazole, Flusilazole, Epoxiconazole and Metaconazole applied between heading and grain filing stages, have been proved to be cost effective.

Singh *et al.,* (2008) proposed that three foliar application of Propiconazole @ 0.1% after appearance of the disease significantly reduce the disease and increase yield tested over several locations of India. The foliar pathogen can be controlled with seed treating fungicides like Guazatine and Guazatine+ Imazalil (Schilder and Bergstrom, 1993).The other effective fungicide includes Captan, Mancozeb, Thiram, Pentachloronitrobenzene, Proline and Triademefone (Stack and McMuller, 1988; Mehta, 1993). The efficacy of some newly synthesized organotin compounds against *B. sorokiniana* has also been reported (Sarkar *et al.*, 2010).

It may be concluded that further studies on various aspects of this pathogen need attention from the researchers looking into the future threat in view of the climate change and also changing agronomy including tillage options and conservation agriculture. The search for new model donors and their use in hybridization programme for improving host resistance should continue to keep disease spread at its lowest level and improve yield by incorporation of useful genes. The pathogen variability and aggressiveness must be checked to avoid new race development and also to minimize the yield losses. The agronomic intervention namely timely planting, proper input application, crop geometry, fertilizer management and crop diversification have bigger role to play in managing this disease. The molecular approach for incorporation of resistance and also for pathogenic variability need to be explored and employed on larger scale to mitigate the problems of spot blotch disease in wheat. Integrating conventional breeding, molecular approach, need based application of fungicides and cultural options will offer eco-friendly and cost effective control of this disease in different parts of the world.

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