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Wheat Septoria Disease Management and Molecular Breeding Approaches in Ethiopia: A Review

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Review Article

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Abstract

Septoria tritici blotch (STB) caused by the fungus *Mycosphaerella graminicola*, is one of the most important foliar diseases of wheat (*T. aestivum* spp., *aestivum* L.) worldwide. The disease is pervasive and economically significant throughout Ethiopia's wheat-growing regions. Naturally susceptible wheat cultivars of STB disease were found in the Central Highlands of Ethiopia, where incidence (98%) and severity (97%) of the disease, as well as yield loss (41%), were documented. This disease has been managed using a variety of techniques, including cultural control, chemical control, and genetic controls have been utilized to control this disease and subsequently reduce yield losses. The lack of information on the diversity of diseases worldwide and in Ethiopia now hampers the screening and selection of wheat genotypes for disease resistance. In this review, wheat septoria disease management and molecular breeding approaches in Ethiopia were assessed.

Keywords: Disease Management; Molecular Breeding and Septoria Tritici Blotch

Abbreviations: STB: Septoria Tritici Blotch; SNNP: Southern Nations, Nationalities, and Peoples; MAS: Marker-assisted Selection; RFLP: Restriction Fragment Length Polymorphism; RAPD: Randomly Amplified Polymorphic DNA; AFLP: Amplified Fragment Length Polymorphism; SSR: Simple Sequence Repeats; SRAP: Sequence-related Amplified Polymorphisms; EST: Expressed Sequence Tags; DArT: Diversity Array Technology; SNP: Single Nucleotide Polymorphism.

Introduction

Wheat (*Triticum aestivum L.*) is among the most important staple food crops in Ethiopia produced at 1.89 million ha of land with an annual yield approximated to 5.78 million metric tons and wheat ranks third after Maize (Zea mays) and Teff (Eragrostis tef) in total production and fourth after Teff (Eragrostis tef), Maize (Zea mays) and Sorghum (Sorghum bicolor) in area coverage [1]. It is grown between 6 and 14° N latitudes and between 35 and42° E longitudes ranging in altitude from 1500 m to 3200 m above sea level (m.a.s.l). In Ethiopia, the most suitable area falls between 1700 and 2800 m.a.s.l. In Ethiopia, both common (bread) wheat (*Triticum aestivum L.*) and durum wheat (*Triticum turgidum ssp.* durum) is widely cultivated in Ethiopia for food, feed, and income generation.

It is used to make a variety of traditional and modern processed foods, including injera and other industrially processed foods like pasta and macaroni [2]. The straw is

a good source of animal feed and is also used for thatching roofs. Although the wheat cultivated areas, production and productivity of wheat in Ethiopia are showing an increasing trend, the production of wheat in the country is very insufficient to meet the increasing demand for food for the ever-increasing population; Ethiopia's wheat production self-sufficiency is only 75 percent and the remaining25 percent wheat is imported commercially and through food aid [3]. Between 2005 and 2017 wheat production and productivity have increased throughout the country, It is grown exclusively under rain fed circumstances, and its output is overtaking that of all other grain crops in the country [4].

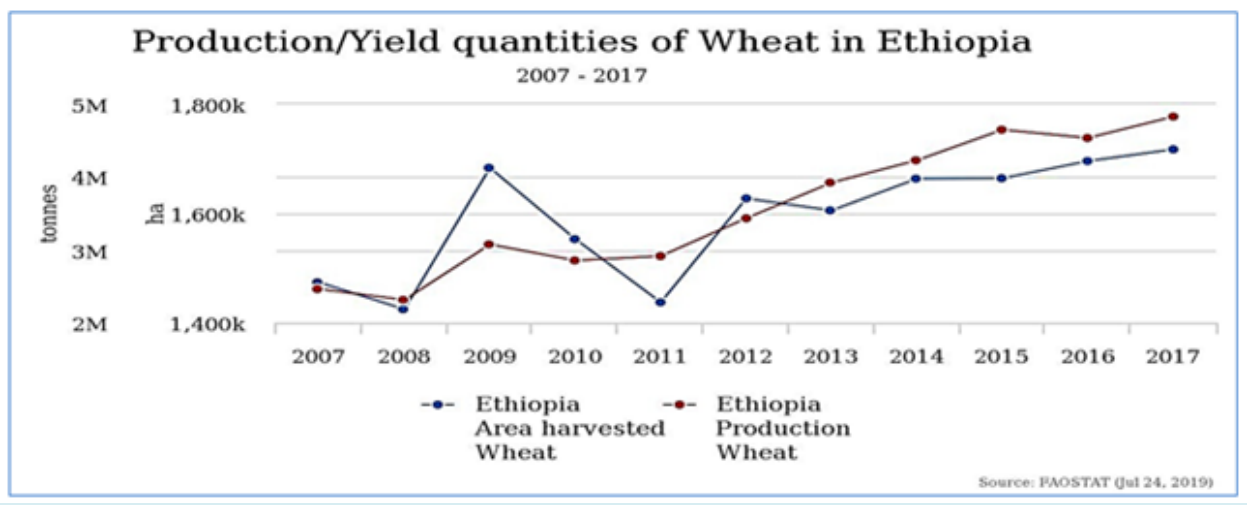

Figure 1: Wheat harvested area (ha) and production trend in Ethiopia from 2007 to 2017 source [5].

Oromia, Amhara, Tigray, and Southern Nations, Nationalities, and Peoples (SNNP) regional states are considered to be the primarily wheat-growing areas of the country accounting for more than 90% of national wheat production. Despite its incredible contributions, the average wheat productivity of the country is 2.8 t/ha; far below the global average of 3.5 t/ha [5]. The low productivity is because of both biotic and abiotic factors. Among these, diseases play a significant role in yield reduction [6]. In Ethiopia, wheat is susceptible to morethan 30 types of diseases which highly affect its yield [6,7]. *Septoria tritici* blotch, caused by the fungus Zymo*septoria tritici* (formerly: *Mycosphaerella graminicola or Septoria tritici*) is becoming the major wheat devastating foliar disease globally including in Ethiopia [6,8,9]. Under favorable environmental conditions, can cause relevant yield loss [7]. Both durum wheat (*Triticum turgidum* sub. *durum* Desf.) and bread wheat (*Triticum aestivum* L.)are affected by *Septoria tritici* [10].

The disease is economically significant and widespread throughout Ethiopia's wheat-growing regions across surveyed locations in the highest STB prevalence (100%) was found in the highlands of Wollo, Ethiopia, with the lowest STB prevalence (33%) found in various locations [11,12], It is the most destructive disease in West and South West Shewa zones and the overall distribution of the disease reached 100% [6,13]. In the Central Highlands of Ethiopia at Holeta naturally evolved susceptible varieties observed the highest STB disease incidence (98 %), disease severity (97%), and (41%) yield loss [8,14]. STB is the major disease limiting wheat yield in the most potential areas of the wheat production zone of Ethiopia, Arsi, and Bales [6]. In 2014 Data generated autumn season disease survey showed that STB and leaf rust are the two important diseases constraining wheat production in the Arsi, and Bale areas of Ethiopia [15]. Economic losses due to STB infections can result not only from losses in grain yield but also in quality as, under severe epidemics, the kernels of vulnerable wheat cultivars are shriveled.

For many years, rusts were the most threatening fungal wheat disease in Ethiopia, and therefore, breeding programs were mainly focused on the introduction and improvement of wheat genotypes resistant to rust Susceptibility of prevalent commercial wheat cultivars to STB resulted in severe epidemics in the major wheat-growing provinces of Ethiopia, Arsi and Bales [6]. Thus, the knowledge On-resistance spectra of wheat genotypes cultivated in various parts of Ethiopia, and on virulence patterns of *M. graminicola* populations are required to identify sources of resistance to STB and to replace the susceptible wheat cultivars with resistant genotypes throughout the country.

Biology of the Causative Agent of Septoria Tritici Blotch

Septoria Tritici Blotch (STB) of Wheat

Fungi show much morphological diversity, different growth forms include single-celled yeast, multicellular and tip- growing hyphae, and asexual and sexual spores [16]. *Zymoseptoria tritici* (formerly *Mycosphaerella graminicola*) is a major fungal pathogen of wheat that causes Septoria tritici blotch (STB) disease [9,17]. The STB is able to infect diploid, tetraploid, and hexaploid wheat species and infections occur during all stages of plant development but, infection on the flag leaves can cause the mostsevere losses by reducing grain test weight [18].

Septoria tritici blotch (STB) is principally a foliar disease and the primary infection may begin with airborne or rain splashes. Air borne ascospores (sexual) and splash-borne pycnidiospores (asexual). Ascospores are the main source of primary inoculum at the beginning of an epidemic and contribute to epidemic development during the season. Pycnidiospores are the main driver of polycyclic epidemics during the wheat growing season and can travel short distances while ascospores can travel long distances. The disease development depends on favorable conditions such as frequent rain and moderate temperature, traditional agricultural practices, availability of inoculum, and the presenceof susceptible cultivars [10]. Moisture is required for all stages of infection germination penetration, development of the mycelium within the plant tissue, and subsequent pycnidial formation [7,10].

Disease Cycle and Symptoms of STB

Disease Cycle

The disease cycle of STB begins with a windborne or rain splash from nearby or further away infected wheat debris. During the wheat-growing season, sexual spores (ascospores) from pseudothecia and asexual spores (pycnidiospores)from pycnidia are released and disseminated by airborne or rain splash and can establish infections in the right conditions [19]. The most favorable conditions for the propagation of this disease within crops are a combination of wind and moisture. In Ethiopia, the intensity of STB disease increases from June to November, when wheat is growing, and the disease's distribution is heavily influenced by temperature and other environmental factors [10]. The fungus thrives by feeding on crop residues, primarily leaf and stubble, and hence endures from season to season. Sexual reproduction contributes significantly to the *M. graminicola* population's genetic diversity, resulting in high biological fitness [20].

Ascospores are the major inoculum for infection and are commonly transmitted in the autumn [21,22]. When the fungus comes into contact with the leaves shortly after the seedlings sprout in thefall, the biotrophic development stage begins. When spores settle on a leaf, they germinate and develop into filamentous hyphae, which enter the host via stomata, other natural openings, or wounds [23]. The fungus grows slowly after penetration, without producing haustoria or other apparent feeding structures, and the plant stays symptomless for 8–11 days [24-26]. The fungus gets its nutrition from the plant, and its hyphae will spread throughout the plant.

Disease Symptoms

Septoria tritici blotch appears earlier in the growing season more frequently on lower leaves than on top leaves [27,28]. According to research, STB has an inverse association with plant height; tall wheatcultivars are less affected than dwarf wheat varieties [29,30]. Additionally, STB is present on the glumes and rachis. Tiny, tan-colored necrotic tissue lesions with a linear or rectangular appearance and frequently bordered by leaf veins are among the signs of STB. The first observable symptoms of the disease are little chlorotic patches on the lower leaf tips. Over time, these chlorotic areas develop into light-brown necrotic lesions. The leaf tissue will turn a light gray color as the necrotic lesions spread [24,31]. If environmental conditions are favorable and there is a lot of rain, the necrotic lesions will spread and the leaf tissue will appear light gray in color [32]. Fungus pycnidia or spore-producing bodies are the black spots on necrotic areas. The best in-field indicator of the disease is the presence of tiny, black pycnidia in lesions [28,33]. Pycnidia's size varies between cultivars and is influenced by both their quantity and overall density. The pycnidia themselves may become smaller as the number of pycnidia on the leaf rises [34].

Disease Assessment

For the quick implementation of disease management measures, research on the genetic and pathogenicity variability of the pathogen, and/or evaluations of germplasm resistance, disease rating is applied. When determining the severity of septoria on wheat, the percentage of diseased (or necrotic) leaf area, the density of pycnidia, and their combinations are typically utilized [35,36]. Previous research evaluated the severity of septoria using exceedingly labor- intensive, expensive, and time-consuming sample preparation techniques [37]. Developed standard diagrams for measuring the percentage of the affected area using an electronic scanner, while Rosielle AA [38] utilized a television scanner to create a scale to measure the amount of pycnidial covering on leaves.

However, the quick and hands-free visual assessment method is popular for determining the severity of septoria. There have been many different kinds of visual rating scoring scales produced so far. For evaluating the severity of foliar diseases in wheat, barley, and triticale [39] created a 0–9 scale. This scale has since been upgraded into a double-digit (00–99) scoring system that only expresses the vertical progression of the disease and its severity [35]. Additionally, CSA [40] created a six-point STB severity grading system based on pycnidia density, which is used to categorize plants.

Yield Loss Assessments of Septoria Tritici Blotch on Wheat in Ethiopia

The majority of the country's wheat is thought to be grown in Oromia, Amhara, Tigray, and the Southern Nations, Nationalities, and Peoples (SNNP) regional states. The majority of the country's wheat production is produced in Oromia (57.4%), Amhara (27.4%), SNNP (8.7%), Tigray (6.2%), and other regions (0.7%) [41]. Almost every section of the region can grow wheat, including agro-pastoral and pastoral regions like Afar, Gambela, and Somalia. The Oromia and Amhara areas do, however, produce the majority (85%) of Ethiopia's domestic wheat. Dueto the existence of sizable farms in the Bale and Arsi zone, the majority of the country's wheat-growing regions, the Oromia region ranks first in terms of production. Thus, Ethiopia's two wheat-growing regions are referred to as the Belt of Wheat Production Areas [4,42,43].

Ethiopia's present wheat productivity is much below the global average, despite its major contributions to the improvement of livelihoods for a large portion of the population [5]. Low productivity is correlated with biotic and abiotic factors as well as a lack of adoption of progressive agricultural practices. Ethiopian wheat is susceptible to over 30 diseases, many of which have a big impact on production [6,7]. Wheat can be afflicted by a number of diseases, including powdery mildew (*Blumeria graminis*), rust infections (*P. striiformis, P. graminis*, and *P. triticina*), Fusarium head blight (*Fusarium spp*.), Septoria tritici blotch (Zymomyces septoria), and others.

The Septoria tritici blotch disease (STB) is economically significant and pervasive throughout Ethiopia's wheat-growing regions, with the highest STB prevalence (100%) found in the highlands of Wollo, Ethiopia [6,12,13,44]. In the Central Highlands of Ethiopia naturally sensitive cultivars, STB disease incidence (98%) and severity (97%) were reported along with yield loss (41%) [8,45]. Because sensitive wheat type's kernels shrink during severe epidemics, STB infections may result in economic losses not just in terms of grain output but also in terms of quality.

Due to the susceptibility of common commercial wheat cultivars to STB, severe epidemics emerged in Ethiopia's key wheat-growing provinces of Arsi and Bales [6]. To identify sources of STB resistance and replace susceptible wheat cultivars with resistant genotypes throughout Ethiopia, information of resistance spectra of wheat genotypes cultivated in various parts of the country, as well as virulence patterns of *M. graminicola* populations,is required.

Towards Breeding Wheat for Septoria Tritici Blotch Disease Resistance

Plants use a combination of weapons from two arsenals to defend themselves against pathogens: (i) structural characteristics that serve as physical barriers and stop the pathogen from entering and spreading through the plant, and (ii) biochemical reactions that take place in the plant's cells and tissues and produce substances that are either toxic tothe pathogen or create conditions that inhibit pathogen growth in the plant. The structural traits and metabolic processes utilized by plants to defend themselves vary depending on the host-pathogen system. Furthermore, different combinations can occur even when a particular host and pathogen are used, depending on the age, type, and circumstances of the plant, as well as the organs and tissues that are affected as well as the nutritional status and weather [46]. To manage *Septoria tritici* blotch, an integrated approach that incorporates variety selection, cultural practice, crop rotation, bio-control fungicides, and deployment of genetic resistance has been employed are the most effective way [47,48].

Cultural Control

Effective long-term STB disease management under Ethiopian conditions has not yet been achieved [49]. There are numerous disease management strategies that are recommended to control this STB in wheat fields.During the growth season, infected plants release septoria tritici spores into the air, and between growing seasons, infected straw and other crop debris do the same. The frequency and severity of STB can be decreased by rotating non-host crops and eliminating wheat crop leftovers. The amount of inoculum that can start a new disease cycle can be reduced by clearing crop debris and thorough plowing. Other cultural techniques for managing STB disease include planting sensitive cultivars late, using cultivar combinations, and intercropping wheat with other crops [35,47,50,51].

Chemical Control

Fungicides are one of the most important components of a disease control strategy in wheat. Some of the fungicides used against STB are protectants like dithiocarbamates

(Maneb, Manzate, Mancozeb, Zineb) and systemic fungicides such as benomyl (Benlate) [35]. However, the procedure necessitates the use of fungicides on a regular basis, making it prohibitively expensive for small growers. Ethiopian farmers are another example [52-54].

Genetic Control

In Ethiopia, the majority of wheat genotypes are susceptible to Septoria tritici blotch (STB), and resistance breeding has been unsuccessful. Almost all high-yielding wheat cultivars grown in Ethiopia are now susceptible to STB foliar disease. The principal line of defense against this disease is genetic resistance, particularly for resource-poor smallholder farmers in developing countries [44]. Planting cultivars with durable genetic resistance is the most cost-effective, long-lasting, and environmentally friendly way to control Septoria tritici blotch. Finding and using sources of resistance are top priorities in most breeding programs [55].

Genetic Resistance to Septoria Tritici Blotch

There are different genetic mechanisms for STB disease resistance breeding programs to select and improve both qualitative and quantitative traits. Breeding for qualitative disease resistance is controlled by one or two large-effect alleles, called resistance (R) genes, and are further referred to as major genes [46,56]. Qualitative disease resistance, race-specific vertical resistance based on main genes, generally exhibits gene-for-gene interactions and often results in the recognition of physiological races or pathotypes and quickly degrades due to the rapid evolution of new pathogen races [57]. Most qualitative resistances are unlikely to be durable and some formerly effective genes have been overcome by the evolution of pathogen virulence. The breedingmethod for horizontal or vertical/race-specific resistance is similar to the methodology used for other complex traits such as grain yield [56].

Qualitative resistance is strong and is usually controlled by major genes with a powerful effect While for STB disease-resistant breeding use of major genes is not likely to be effective in the long term due to the rapid breakdown of some resistance genes, so it would be best to select for quantitative resistance or at least to pyramid several STB genes into a single cultivar since some of the most resistant cultivars seem to contain multiple STB genes [58,59].

Major gene pyramiding provides more durable resistance to multiple pathogen races into a single line [56]. Successful implementation of major genes relies on identifying the useful sources of the genes, finding the linked markers, confirming the effect in different genetic backgrounds, and finally, deploying said major genes [56,60]. Major gene implementation is further complicated when it comes to selecting multiple major genes simultaneously for gene pyramiding. Horizontal or minor gene resistance is defined as a non-race-specific or general resistance to a range of pathogens or pests [61] as a result of many genes expression with minor additive effects. As it is controlled by the cooperative effects of numerous genes horizontal resistance is important to control a broad range of pathogen races [62,63].

The minor non-race specific genes often show intermediate responses and typically combinations of more than three genes are required to attain a commercially acceptable level of resistance. The presence of horizontal genes slows down the rate of disease development. Similar to qualitative resistance, selecting for quantitative resistance can be completed throughout the breeding process. The majority of variation in STB field resistance is dictated by quantitative resistance, and the well-defined progressin STB disease-resistant breeding over the last 30 years is thought to have resulted from the slow accumulation of minor genes. The symptoms of STB disease, chlorosis, necrosis, and pycnidia, have recently been discovered to be genetically controlled in different ways [64].

Because it relies on multi-resistant alleles, breeding for quantitative or horizontal resistance conferred by a combination of minor and major genes produces more durable resistance in breeding lines. Breeding for quantitative or horizontal resistance necessitates multiple breeding cycles to gradually improve resistance [56,65]. In exact resistance breeding, both qualitative and quantitative types of resistance are frequently combined. Major genes are easy to manage, but quantitative or horizontal resistance is more difficult to select and complex, but it is expected to last longer, making it useful in resistance breeding [56,66].

The quantitative nature of phenotypes displayed by the host-pathogen interaction has frequently led to the identification of STB resistance genes using QTL mapping techniques [67]. To confer resistance, the plant has a dominant resistance (R) gene that encodes a product that recognizes a pathogenicity factor (produced by a dominant Avirulent or Avr gene) in the pathogen [68]. The pathogen is not recognized by the plant if the R gene is missing in the plant and/or the avirulence gene is missing in the pathogen. This activates the pathogen virulent gene, making the plant susceptible [69] (Table 1).

Resistance or susceptibility gene in the plant		
Virulence or a virulence gene in the pathogen	R(resistant) dominant	r(susceptible) recessive
A(avirulent) dominant	AR(-)	Ar(+)
A(virulent) recessive	aR(+)	ar(+)

Table 1: Summary of host–pathogen reaction types based on the gene-for-gene concept.
-Signs indicate incompatible (resistant) reaction and therefore no infection,
+Signs indicate compatible (Susceptible) reaction and therefore infection develops. Source: [46,62].

The term 'QTL' as a qualitative gene has been used in the literature when a large percentage of genotypic variation is explained by the QTL and/or a specific interaction with one or more isolates is observed. QTL are quantitative geneswith low heritability, and small genetic and accumulative effects in classical genetics [20]. In wheat, adult plant resistance genes express partial STB resistance phenotypes except under very specific conditionsand this is characterized by less and slower pathogen growth without a necrotic response. In crop plants, there are a variety of resistance screening methods. Effective disease resistance selection in plant populations necessitates precise,cost-effective screening approaches that allow thousands of plants to be tested quickly. Field testing under natural disease pressure and greenhouse/growth room screening procedures in which plants are inoculated with specific pathogen strains are two common disease screening techniques [24].

Greenhouse Seedling inoculation allows for rapid assessment of disease reactions, reduction of some sources of environmental variation through the use of characterized pathogen strains and defined inoculum concentrations, and avoidance of confounding effects from other pests or diseases and seedling screening allows researchers to assess the efficacy of resistance against a diverse range of strains [70,71]. Two indicators were utilized for STB disease severity in the extensive investigation of the interaction between *M. graminicola* isolates and host cultivars: necrosis and the presence of pycnidia, both of which were scored as percentages coverage of leaf area [72].

Marker-Assisted Breeding

Wheat breeding's ultimate goal is genetic gain in terms of measurable parameters such as agronomic performance, disease resistance, and grain quality. In most cases, selection involves evaluating a breeding population in field or greenhouse trials for one or more traits. Plant breeding purposes to produce new varieties with more necessary gene combinations. The breeding method, picking desirable plants for traits with higher heritability begins in early generations. However, for traits with low heritability, the assortment is frequently delayed until the lines become more homozygous in later generations [73,74]. Phenotype evaluation for agronomic traits, disease resistance, and grain quality as well as laboratory tests for qualityor other traits, are used in the selection of larger plants. When the breeding populations become homozygous, they canbe gathered in bulk and confirmed in replicated field trials. The entire process takes a long time around 5–10 years forbest elite lines to be identified. While conventional breeding has the potential to improve yields for a long time further,nowadays technologies such as biotechnology will be compulsory to maximize the probability of success chances in breeding for many traits [74-77].

Marker characters are characters that can be easily identified, easily detected by phenotype, or molecular techniques during genetic analysis referred to as a marker. Markers associated with variations in DNA fragments generated by restriction endonuclease enzymes are called DNA markers or genetic markers [78]. DNA marker technology is one area of the new technologies in biotechnology that holds great promise for plant breeding [79]. Development of this technology in the 1980s changed the fate of plant breeding. Different types of molecular markers have been developed and accelerated crop improvement. The evolution of DNA marker technology made in molecular plant breeding, genetics, genomic selection, and genome editing has contributed to a more comprehensive understanding of molecular markers and made a deeper understanding of the diversity available for crops and greatly complemented breeding stratagems [80].

Marker-assisted selection (MAS) is the use of DNA marker technology in plant breeding and is a component of the new discipline of molecular breeding. The discovery of molecular techniques opened the way for the study of the genetics of disease resistance at the DNA level. Molecular breeding, or MAS, refers to the technique of using DNA markers that are tightly linked to phenotypic traits to assist in a selection scheme for a particular breeding objective [81]. Molecular markers are so helpful for quick and precise identification of Zymoseptoria resistance genes in a large set of wheat germplasms to develop broad and /or durable resistant wheat materials for effective control of the disease [9]. The molecular mechanism of breeding disease resistance in plants is essential for devising sophisticated breeding

strategies leading toward crop protection. Trait-linked DNA markers have been identified for numerous traits in wheat, including disease resistance and grain quality. Using such markers in MAS gives considerable advantages to wheat breeding when compared to traditional phenotypic selection and rigorous grain quality analyses. Early development of desirable traits in the breeding program, as well as marker-assisted backcrossing to transmit agronomically significant genes from wild relatives to cultivated wheat, are among the advantages.

The scale of breeding programs also highlights the difficulties of incorporating a relatively expensive technology like MAS. The primary advantages of MAS over traditional phenotypic selection are that it may be simpler than phenotypic screening, saving time, resources, and selection can be done at the seedling stage [76]. This could be useful for a variety of traits, particularly those expressed later in development. Unwanted plant genotypes can thus be quickly eliminated, and single plants can be selected. Because single-plant selection is unreliable due to environmental factors, plant families or plots are grown using conventional screening methods for many traits. Individual plants can be selected using MAS based on their genotype.

Conventional phenotypic screening cannot distinguish between homozygous and heterozygous plants for most traits. Breeders can take advantage of these advantages to speed up the breeding process. Target genotypes can be selected more effectively, allowing certain traits to be fast-tracked, resulting in faster line development and variety release. Markers can also be used in place of phenotyping, allowing selection in off-season nurseries and making it more cost-effective to grow more generations per year [76,82,83]. Another advantage of using MAS is that the total number of lines that must be tested can be reduced. Because many lines can be discarded after MAS early in a breeding scheme, it allows for more efficient use of glasshouse and/or field space, which is often limited because only important breeding material is kept. Many molecular marker systems are restriction fragment length polymorphism (RFLP), randomly amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP®), simple sequence repeats (SSR), sequence-related amplified polymorphisms (SRAP), expressed sequence tags (EST), Diversity Array Technology (DArT) and single nucleotide polymorphism (SNP) have been developed in wheat and subsequently employed to locate loci associated with qualitative and quantitative trait loci including for STB resistance [84-87].

In earlier years, several investigations identified STB resistance genes using molecular methods. The first three qualitative STB resistance genes to be discovered were Stb1, Stb2, and Stb3 [88]. STB resistance wasonce assumed to be a quantitative, polygenic trait. Stb6 was discovered on the short arm of chromosome 3A in the cultivar Flame. This is the only STB-resistant gene known to interact with an Avr gene in the pathogen through a gene-for-gene interaction between certain R genes in the host. Later research revealed Stb6 to be among the most common STB-resistant genes in European wheat [89,90]. Stb16q is the gene of particular interest, which has shown effectiveness against all Z. tritici isolates tested thus far, and certain QTLs have been identified at or near the locus of qualitative genes, including Stb6, which is present in multiple sources of resistance. There are 21 stb genes that have already been identified and mapped, and they play important roles in the regulation of genetic diversity and in the development of qualitative resistance. Since there are few avirulent *Z. tritici* isolates, it has been shown that many STB resistance genes are genotype-specific [88].

There are currently several molecular markers associated with these genes that can be utilized for marker-assisted selection. Various septoria disease resistance genes have been identified in wheat by MAS (Table 2).

Stb gene	Original cultivar source	SSR Markers	Linkage distance (cM)	Location	Reference
Stb 1	Bulgaria 88	*Xbarc74*	2.7 cM prox	5BL	[91]
		Xgwm335	7.4 cM prox	5BL	
Stb 2	Veranopolis	*Xbarc008*	5 cM	1BS	[92]
		Xwmc230	Tight	1BS	
		Xwmc406	6 cM	1BS	
Stb 3	Israel 493	*Xwmc83*	3cM	7AS	[86]
Stb 4	Tadinia	*Xgwm111*	0.7cM	7DS	[93]
Stb 5	Synthetic 6x	*Xgwm44*	6-7cM	7DS	[94]
Stb 6	Flame	*Xgwm369*	Flanking	3AS	[89]
Stb 7	ST6	*Xwmc313*	0.3cM	4AL	[95]

Stb 8	Synthetic W7984	*Xgwm146*	3.5cM	7BL	[96]
		Xgwm577	5.3 cM	7BL	
Stb 9	Courtot	*Xwmc317*	7cM	6AS	[97]
Stb10	Kavkaz-K4500	*Xgwm848*	Flanking	1D	[98]
Stb11	TE9111	*Xbarc008*	Flanking	1BS	[66]
		Xbarc137	Flanking	1BS	
Stb12	Kavkaz-K4500	*Xwmc219*	0.8cM distal	4AL	[98]
Stb13	Salamouni	*Xwmc396*	7-9cM	7BL	[99]
Stb 14	Salamouni	*Xwmc623*	5cM	3B	[99]
		Xwmc500	2cM	3BS	
Stb 16	M3 synthetic W7976	*Xwmc494*	1-5 cM	3D	[90]
Stb 17	M3 synthetic W7976	*Xhbg247*	1-5 cM	5A	[90]
Stb 18	Balance	*Xgpw5176*	1-5 cM	6DS	[70]
Stb 18	WW2451	*Xgpw3087*	1-5 cM	6DS	
StbWW	WW1842,WW2449,	Xbarc119b	0.9–4.1cM	1BS	[100]
TmStb1	MDR043(T.Monococcum)	Xbarc174	23.5cM	7A	[101]

Table 2: List of wheat resistance genes against STB disease and closely linked molecular markers.
Note: *Stb* 1-TmStb1 *Z tritici* blotch resistance genes against *Z tritici* blotch. A, B, and D = A, B, and D genomes of bread wheat, S= short arm, and L= long arm of a chromosome Source: [88,102].

Stb16 holds promise for future breeding of effective and long-lasting STB resistance. Single qualitative resistance genes in *Z. tritici* have easily overcome so quantitative resistance, on the other hand, is thought to be more durable. This is due to the pathogen facing less selection pressure as a result of the smaller resistance effects of individual QTLs. Furthermore, because quantitative resistance is frequently polygenic, mutation of one gene does not always result in complete disease resistance [103,104]. Understanding host-pathogen interaction, STB resistance inheritance, STB resistance loci localization, and the identification of molecular markers associated with STB resistance in common wheat have all made significant progress in recent years. This has occurred in a number of countries around the world. However, the use of molecular tools in *Zymoseptoria tritici* resistance breeding is severely lacking in Ethiopia. In Ethiopia, research is currently beingconducted to use tightly linked markers to screen for *Zymoseptoria tritici* resistance genes in wheat (*Triticum aestivum* L.). The technique is very efficient, economical, and fast to select the resistant genotypes which may take several seasons and years in field or greenhouse germplasm evaluations. Thus, developing countries including Ethiopia shall start the use of modern molecular tools in their crop improvement program [9,105].

Conclusion

Wheat (*Triticum aestivum L.*) is among the most important staple food crops in Ethiopia. Regardless of its incredible contributions, the average wheat productivity of the country is far below the global average. The low productivity is because of both biotic and abiotic factors. Among these, diseases play a significant role in yield reduction. In Ethiopia, wheat is susceptible to more than 30 types of diseases which highly affect its yield. *Septoria tritici* blotch, caused by the fungus Zymo*septoria tritici* is becoming the major wheat devastating foliar disease globally including in Ethiopia. The disease is economically significant and widespread throughout Ethiopia's wheat-growing regions where there is under favorable environmental conditions can cause relevant yield losses and reduced grain quality. The fungus persists on dead leaves and other plant residues to initiate primary infection. Screening and selection of wheat genotypes for resistance to disease are currently hampered by the dearth of knowledge on the variability of pathogens in the world as well as in Ethiopia. Plant breeding has made remarkable progress in crop improvement, which must be maintained. Although the impact on resistant breeding has been minimal, Marker-assisted selection could greatly assist plant breeders in achieving this goal. Marker-assisted selection provides new solutions for selecting and maintaining desirable genotypes. Marker-assisted selection can be performed in early segregating populations and at early stages of plant development for pyramiding the resistance genes, with the ultimate goal of producing varieties with durable or multiple disease resistance.

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