



Epidemiology and molecular characterization of quantitative trait loci (QTLs) for resistance to common rust (*Puccinia sorghi*) and gray leaf spot (*Cercospora zae maydis*) diseases of maize in Ethiopia

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Abstract

Maize (*Zea mays* L.) is an important component of farming systems and staple food crop in sub-Saharan Africa. In Ethiopia maize is a staple food and one of the main sources of calories in the major maize producing regions. It is cultivated on about 1.7 million hectares of land. The national average yield of maize under subsistence production is about 2200kg/ha. This is too much below the world's average yield. This low yield is attributed to foliar diseases and insect pests such as stalk borer. One of the bottle necks in developing countries like Ethiopia which have lowered the yielding ability of maize is the usage of inferior genes which are susceptible to diseases, insects, weeds, low yield and quality. Another is lack of adequate investment and skilled manpower to improve varieties for high yield and disease resistance, diminishing land and water resources and environmental stresses. The most common potentially economic diseases on maize in Ethiopia are common rust and gray leaf spot. Despite the presence of food shortage in Ethiopia, every year a heavy toll of maize yield is taken by these pathogens. For example, 23% yield reduction by common rust and 37% loss by gray leaf spot were recorded. Genomic research can provide new tools and resources to revolutionize crop genetic improvement and production. Recognizing the enormous potential of DNA markers in plant pathology and breeding, many agricultural research centers with plant pathology and breeding institutes in developed countries have adopted the capacity for marker development and marker-assisted selection (MAS) and due to rapid developments in marker technology, statistical methodology for identifying quantitative trait loci (QTLs) and the jargon used by molecular biologists, the utility of DNA markers in plant pathology and breeding is clearly understood by molecular biologists. But these technologies are scanty in Ethiopia. Therefore, in this review epidemiology of these pathogens and molecular approaches helpful in boosting maize productivity were discussed. Hence, this information can help plant pathologists, plant breeders and geneticist to promote further studies in this new research area in Ethiopia.

Key words: Epidemiology, Genomic research, molecular biology, QTLs, Common rust, Gray Leaf Spot, Maize.

Introduction

Currently the world population is alarmingly increasing leading to enhanced increase of global food demand. Especially in developing world like Africa the quest for food self sufficiency and food security is a commendable question. In order to balance the global population increase with the global food demand, it is a must to use improved agricultural technologies that help in boosting crop production and productivity (FAO, 2011).

The world's population is estimated to grow from 7 billion people to day to 9.4 billion in 2050. Maize (*Zea mays* L.) is both an exciting model organism in plant genetics and also the most important crop worldwide for food, animal feed and bioenergy production (Bello *et al.*, 2010; Randjelovic *et al.*, 2011; Christian *et al.*, 2012). It is an important food crop in Africa, for example it provides over 30% of the dietary calories in East Africa (Salasya *et al.*, 1998). But many African

countries experience maize shortages which affect approximately 100 million people (Alexander and Bindiganavile, 2004).

Over 70% of maize in Africa is produced by resource poor small-scale farmers (Salasya *et al.*, 1998) and the average maize yield in Africa stood at 1.3 t/ha compared to 3.0 t/ha elsewhere (FAO, 2006). This low grain yield can be attributed to a number of constraints which include both biotic stress (diseases, pests and lack of suitable varieties) and abiotic stresses (low soil fertility and lack of capital to purchase farm inputs) (Salasya *et al.*, 1998; Bello *et al.*, 2010; Veigal *et al.*, 2012).

Generally, maize production in tropical Africa is constrained by a number of stress factors including a complex of pests and diseases that significantly reduce the quantity and quality of production (Bello *et al.*, 2010). Grain yield losses ranging from 10-70% have been reported due to some of the major diseases which depend on factors such as genetic constitution of the cultivars and stage of growth at the time of infections (Bello *et al.*, 2010; Bello *et al.*, 2012). Foliar diseases, mainly gray leaf spot (GLS) (*Cercospora zea maydis*), Northern corn leaf blight (NCLB) (*Exserohilum turcicum*) and common rust (*Puccinia sorghi*) are the most important diseases in maize production. Chemical control of these diseases is unfeasible due to high costs and environmental concerns (Bello *et al.*, 2012).

In Africa maize is used as both human and animal food, eaten directly as grilled cobs or as various products of maize flour. It is easily stored after drying or milling (Polaszek and Khan, 1998). In Eastern Africa, for instance, 3.9% of the cultivated land is under maize production with grain yields of 700 to 1800 kg /ha as opposed to 7437 kg /ha in the USA (Mosisa *et al.*, 2007). In general, maize in Africa is grown on a small-scale by farmers for local consumption, and yields tend to be low, averaging less than half that of Asia and Latin America (Assefa *et al.*, 2008; Semagn *et al.*, 2012).

In Ethiopia maize is a staple food and one of the main sources of calories in the major maize producing regions. It is cultivated on about 1.7 million hectares of land. However, maize varieties mostly grown in the highlands altitude (1,700 to

2,400 m.a.s.l) of Ethiopia are local cultivars (Legesse *et al.*, 2007). The national average yield of maize under subsistence production is about 2200kg/ha (CSA, 2007). This is too much below the world's average yield (Soboksa *et al.*, 2008). This low yield is attributed to foliar diseases, weeds and insect pests such as stalk borer (Dagne *et al.*, 2008; Bekeko, 2013).

Gray leaf spot (GLS) caused by the fungal pathogen *Cercospora zea-maydis* (Tehon and Daniels, 1925), is one of the major disease constraints to maize production in many parts of the World including Ethiopia. It had significantly contributed to yield losses of about 37% in the western part of Ethiopia. When susceptible genotypes are affected, it may lead to epidemics and yield losses of over 37% can be observed (Dagne *et al.*, 2008). Resistance to grey leaf spot disease is generally quantitative in nature (Balint-Kurti *et al.*, 2008), and it has been suggested that an understanding of the molecular basis of quantitative disease resistance requires exploitation of maize genetic diversity combined with improved phenotyping approaches (Poland *et al.*, 2009; Rafalski, 2010).

Common rust caused by *Puccinia sorghi* is another common fungal disease of maize in Ethiopia in medium to high altitude zones. Common rust may cause extensive yellowing and premature desiccation of maize foliage, resulting in leaf necrosis, and complete destruction of photosynthetic areas. In extreme cases, heavy rust infestations may result in stunting, incomplete ear tip fill, and pustules on ear husks, reducing marketability and yield. On average a yield reduction of 23% was noted due to common rust in eastern high lands of Ethiopia (Fininsa, 2001).

Maize yield is highly variable in rainfed environments of Ethiopia and it is still very low (often <2 t/ha), for example the average national maize yield in Ethiopia is 2.2 t/ha. That is too much below the genetic potential of the crop and the average yields of other Asian and Latin American countries (Mosisa *et al.*, 2007; Veiga *et al.*, 2012). Therefore, developing and deploying maize varieties combining high yield potential and tolerance to major foliar diseases, is the need of the hour to reduce the risks associated with planting under rainfed conditions in highland parts of the country (Brummer *et al.*, 2011).

Hence the quest for improved grain yield and

disease tolerance/ resistance maize varieties therefore become imperative for profitable maize production. Thus the use of host plant resistance/ tolerance remains the most economically viable and practical means of controlling disease epidemics (Bello *et al.*, 2012; Martin *et al.*, 2012).

Maize production trends in the world

By 2020 maize production in industrialized and developing countries will surpass that of wheat and rice and it has increased since 1997 by 45% at the global level and by 72% in developing countries (FAO, 2006). Within the developing world the demand of maize for food will be the greatest in sub-Saharan Africa (40 million tons) followed by Latin America (30 million tons), and then South and Southeast Asia (25 million tons). This can be achieved when high yielding and disease resistant varieties are used by farmers and commercial maize producers (FAO, 2011; Ali and Yan, 2012).

It is one of the most important cereals broadly adapted worldwide (Christian *et al.*, 2012). In Ethiopia, it is grown in the lowlands, the mid-altitudes and the highland regions. It is an important field crop in terms of area coverage, production and utilization for food and feed purposes. However, maize varieties mostly grown in the highlands (altitude = 1,700–2,400 masl.) of Ethiopia are local cultivars. They are low yielding, vulnerable to biotic and abiotic constraints and also exhibit undesirable agronomic performances such as late maturity and susceptibility to root and stalk lodging (Legesse *et al.*, 2012). Enhancement of maize production and productivity can be achieved through identification of potentially superior inbred line combinations in the form of hybrids (Bernardo, 1999; Saleh *et al.*, 2002).

Hybrid maize production

In maize, hybrid breeding remains the method of choice for attaining maximum genetic gain from the effects of heterosis. Nevertheless, identification of parental inbred lines leading to superior hybrid combinations is a crucial factor (Hallauer *et al.*, 1989). Such activities using conventional breeding methods are expensive and time consuming. Furthermore, the large number of possible hybrid combinations to be produced from a relatively small number of inbred lines, render the evaluation of all possible combinations unfeasible (Bernardo, 1992; Betran

et al., 2003; Bello *et al.*, 2012).

The efficiency of hybrid breeding program could be increased if the inbred lines per se could be screened for genetic diversity using molecular markers and superior crosses are accurately predicted prior to field evaluation for yield and disease resistance (Melchinger *et al.*, 1999; Martin *et al.*, 2012; Semagn *et al.*, 2012).

Molecular Markers and QTLs in maize Breeding

Molecular markers are used to meet a number of objectives including identification of QTLs, genetic diversity analysis and prediction of hybrid performances in different crop species (Melchinger, 1999; Reif *et al.*, 2003; Christian *et al.*, 2012). They are not influenced by environmental factors and are also fast, efficient between genotypes at the DNA level and more sensitive than field testing to detect large numbers of distinct differences. However, one should not overlook the importance of field testing across years and locations to identify phenotypically desirable hybrid combinations (Melchinger, 1999; Ali and Yan, 2012).

Currently several molecular marker techniques are available serving various purposes in crops. Amplified fragment length polymorphism (AFLP) is one of the well known molecular marker systems relying on polymerase chain reaction (PCR) technique for DNA amplification. It requires no prior sequence knowledge and can detect large number of genetic loci than restricted fragment length polymorphism (RFLP), random amplified polymorphic DNA (RAPD) and simple sequence repeat (SSR) markers (Pejic *et al.*, 1998; Beyene *et al.*, 2005; Prasanna and Pixley, 2010; Semagn *et al.*, 2012; Zhang *et al.*, 2012).

Single nucleotide polymorphism (SNP) markers have highly automated DNA scoring potential than AFLPs and SSR (Suliman-Pollatschek *et al.*, 2002); however, they are expensive and demand high technology input and special instruments are required for many SNP genotyping technologies (Ching and Rafalski, 2002). It is also known that the AFLP and microsatellite (SSR) markers have lower cost (Garcia *et al.*, 2004). In maize, AFLP and SSR techniques have been applied to genome mapping (Ajmone-Marsan *et al.*, 2001), DNA fingerprinting (Oliveira *et al.*, 2004; Zhang *et al.*, 2012), genetic diversity studies (Garcia *et al.*, 2004) and hybrid performance prediction (Sheng and Rui, 2000 ;

Barbosa *et al.*, 2003). Previous studies conducted to assess genetic diversity and to predict hybrid performance in maize were mostly focused on temperate germplasm (Melchinger, 1999; Rakshit *et al.*, 2012; Semagn *et al.*, 2012).

Molecular marker-assisted breeding is the way forward in effectively meeting the greater challenge of developing cultivars with combinations of adaptive traits (e.g., drought, heat tolerance; water logging, drought tolerance; a biotic and biotic stress tolerance). The success of such a strategy strongly depends on the ability to accurately phenotype a large number of genotypes (Vargas *et al.*, 2006; Veiga *et al.*, 2012). Appropriate stress phenotyping platforms are needed to enable high-throughput screening of genotypes in multi-location field trials, besides identification of new secondary traits that more precisely describe the level of disease resistance in tropical maize (Ininda *et al.*, 2004; Veiga *et al.*, 2012). But these technologies are not available in Ethiopia. As a result the yield of maize is still too much below the genetic potential of the crop under farmers' condition even in potential regions (Legesse *et al.*, 2007). Biotic stress tolerance in itself is not sufficient to ensure adoption; farmers require maize varieties that also offer resistance to regionally important diseases and insect-pests, and responsiveness to favorable condition in years in which stress is not severe (Al-Khafagi *et al.*, 2013).

QTL associated with resistance to common rust, GLS, and many other diseases) and insect-pests have been identified and mapped in maize using making MAS a potentially viable strategy to improve resistance to these biotic stresses. Projects on gene pyramiding, is an indicator that MAS can play an important role in breeding for disease resistance in maize (Ojo *et al.*, 2007; Randjelovic *et al.*, 2011; Kumar and Nadagoud, 2012). Concerted efforts are now required for developing breeder-ready, low-cost QTLs markers for resistance to major diseases of maize, such as common rust and GLS allowing rapid introgression of an appropriate suite of resistances into elite, high-yielding, abiotic stress-tolerant lines. Integrating molecular marker technologies such as MAS into breeding strategies could become increasingly important in the coming years, to realize genetic gains with greater speed and precision (Ojo *et al.*, 2007). The prom-

ise of MAS for improving polygenic traits in a quick time-frame and in a cost-effective manner is still elusive. There is a wider appreciation that simply demonstrating that a complex trait can be mapped to approximate genomic locations using DNA markers would not serve the ultimate goal of trait improvement. In facing the challenge of improving several lines for quantitative traits, MAS strategies use DNA markers as a key selection step to maximize their impact (Ininda *et al.*, 2004; Ojo *et al.*, 2007).

Recognizing the enormous potential of DNA markers in plant pathology and breeding, many agricultural research centers in plant pathology and breeding institutes in developed countries have adopted the capacity for marker development and marker-assisted selection (MAS) and due to rapid developments in marker technology, statistical methodology for identifying quantitative trait loci (QTLs) and the jargon used by molecular biologists, the utility of DNA markers in plant breeding is clearly understood by molecular biologists (Setti *et al.*, 2011; Francisco *et al.*, 2012).

Application and utilization of heterotic patterns in standard grain quality maize had significant influence on improvement of breeding in yield increase, making more efficient testing of hybrids and increasing the probability of identifying hybrids with desirable traits (Kumar and Nadagoud, 2012). In this connection the analysis of GCA and SCA has become increasingly important to plant breeders because of the widespread use of hybrid cultivars in maize crops (Jackson *et al.*, 2011; Christian *et al.*, 2012).

Genomic position, number and magnitude of QTLs affecting genetic variation for a number of physiological traits at the whole plant level, in F2:3 families derived from a cross between two maize inbreds showing contrasting expression for some disease tolerance related parameters have been identified (Orsini *et al.*, 2012). The information thus obtained provides valuable information on the feasibility of using QTLs disease resistance in a marker-assisted selection scheme to improve disease resistance in maize (Betran *et al.*, 2003; Martin *et al.*, 2012). The identification of disease-resistant maize cultivars and incorporation of resistance in hybrids can increase yields, lower Production costs, and reduce use of pesticides (Assefa *et al.*, 2008; Orsini *et al.*, 2012).

One of the bottle necks in Ethiopia that have lowered the yielding ability of maize is the usage of inferior genes which are susceptible to diseases, insects, weeds, low yield and quality. Another is lack of adequate investment to improve varieties and yield, diminishing land and water resources and environmental stresses (Legesse *et al.*, 2007). Therefore, it is very important to search technologies that helps in filling this gap in utilizing DNA markers, concept of polymorphism, linkage analysis and map construction, the principles of QTL analysis and how markers may be applied in breeding programs using MAS in selecting disease resistant QTLs for common rust and gray leaf (Garcia *et al.*, 2004). Using AFLP, SNP and SSR markers, some information on tropical maize germplasm is present for QTLs but the genotypes studied were of lowland tropical origin (Sheng and Rui 2000; Barbosa *et al.*, 2003; Garcia *et al.*, 2004; Brito *et al.*, 2012). No such information is available in Ethiopia on tropical highland maize germplasm serving breeding programs for yield stability and disease resistance.

Maize breeding program has a narrow genetic basis for disease resistance and yield in highland parts of Ethiopia (Legesse *et al.*, 2007). And also the resistant genes for GLS and common rust were not investigated except for some hybrids which were released for mid altitude areas where these diseases are not sever. In nature these pathogens are highly variable that makes their management complex (Danson *et al.*, 2006; Brito *et al.*, 2012).

Therefore, it is highly important to explore resistant genes to over come these foliar diseases of maize in highland areas of Ethiopia using QTLs including their pattern of epidemic dynamics under field condition. Knowledge of epidemiological features of plant diseases provides useful information for understanding the biology of their causal agents, and is the basis for the establishment, planning and monitoring of effective disease management strategies (Jeger, 2004). But such information is not available for these pathogens in Ethiopia except the investigation made for common rust in eastern highlands of Ethiopia on local cultivars by Fininsa *et al.* (2001).

Most disease resistance used in maize is quantitative in nature, i.e. incomplete but suffi-

cient to protect yield (Christian *et al.*, 2012; Orsini *et al.*, 2012). Quantitative resistance is generally extremely durable, but very little is known in Ethiopia about its molecular or physiological basis therefore, characterizing genomic regions conferring quantitative resistance (also known as quantitative trait loci or QTL) to common rust and gray leaf spot (GLS) diseases has significant importance in maize productivity to ensure food security and food self sufficiency which the country has envisioned. Validation of candidate QTL conferring partial resistance would present marker-assisted selection as a potentially viable strategy to improve host resistance in maize. But quantitative trait loci (QTL) conditioning partial-resistance to these foliar pathogens have not been investigated in Ethiopia.

Generally, in Ethiopia so far, no attempt was made in make use of molecular markers in studying high yielding and disease resistant maize cultivars except the investigation made by Beyene *et al.* (2005), Legesse *et al.* (2008) and Dagne (2008) in which the genetic diversity of maize inbred lines from lowland and highland areas were genetically characterized into different heterotic groups based on their level of tolerance to low moisture and soil nitrogen level. In addition, investigation and characterization of QTLs in maize patho-breeding is poorly understood in the country.

As a result, the traditional breeding methods for yield and disease resistance are followed in maize breeding projects in the country which is costly and time consuming. Cognizant of these facts, this review is designed to promote further information on: epidemiology and molecular characterization of quantitative trait loci (QTLs) for resistance to common rust (*Puccinia sorghi*) and gray leaf spot (*Cercospora zea maydis*) diseases of maize in Ethiopia.

Epidemiology of Common Rust and GLS

Favorable conditions for early infection symptoms of GLS are similar to that of other foliar diseases, such as common rust. Knowing weather conditions under which it can develop is important to identify and potentially manage the disease. In common rust, young leaves are the most susceptible once. Infection occurs within three to six hours of moderate temperatures, between 60 and 75° F, heavy dews, or 95% or higher relative humidity (Bigirwa *et al.*, 2001).

In gray leaf spot wetted-leaf surfaces for 11 to 13 hours and 90% or higher relative humidity of the canopy for 12 to 13 hours favor GLS infection. Incidence often increases after summer rains. However, full lesion expression after initial infection is slow to develop. Summer-night temperatures above 70° F, heavy dews, fogs, and rainfall also contribute to the development of GLS. The fungal spores can remain dormant when development conditions are unfavorable but high relative humidity encourages GLS infection levels to become active when favorable conditions materialize.

These diseases are most severe and damaging during high relative humidity and prolonged late-season rains (Beckman and Payne, 1983). The extent of the damage has been found to be dependent on the hybrid affected and prevailing environmental conditions (Ward *et al.*, 1999). Increased incidence of common rust and GLS in Africa has been associated with continuous cultivation of maize, and use of susceptible maize cultivars (Gevers *et al.*, 1994; De Nazareno *et al.*, 1993; Dagne *et al.*, 2008).

Gray leaf spot (GLS), *Cercospora zae-maydis*, may begin appearing in the area due to environmental conditions that are favorable for disease development. Weather conditions greatly influence the infection of GLS, as the disease develops readily during prolonged periods of hot and humid weather and yield losses can vary between maize cultivars which help for seeking resistant genes among the populations (Beckman and Payne, 1983).

Knowledge of epidemiological features of plant diseases provides useful information for understanding the biology of their causal agents, and is the basis for the establishment, planning and monitoring of effective disease management strategies (Jeger, 2004). The first and more common approach to the epidemiological study of an epidemic is the analysis of its temporal dynamics through the description and interpretation of the disease progress curve (DPC). DPC measures the change with time in the amount of diseases in the population of host plants, and may be considered as the epidemic "Signature" in the sense that it integrates all host, pathogen and environmental factors occurring during the epidemic (Campbell and Madden, 1990; Agrios, 2005), which determine the final

amount of disease.

In plant disease epidemiological research, the pattern of the pathogen movement, sources of inoculum, direction of inoculum movement, the amount of initial inoculum and its rate of movement dictates the effect of the pathogen on the target crop and pathogens which have fast generation cycle and which are poly cyclic have a profound effect on the target crop (Savary, 2006).

Gray Leaf Spot (*Cercospora zae-maydis*)

Gray leaf spot (GLS) caused by the fungal pathogen *Cercospora zae-maydis* (Tehon and Daniels, 1925), is one of the major disease constraints to maize production in many parts of the World including Ethiopia. It had significantly contributed to yield losses of about 37% in the western part of the country. In Ethiopia when susceptible genotypes are affected, it may lead to epidemics and yield losses of over 37% (Dagne *et al.*, 2008). For instance, yield losses of between 30 and 60% due to GLS infection have been reported in South Africa (Ward *et al.*, 1999). GLS has a long latent period with 14 to 28 days after infection before lesions produce conidia under humid conditions, which can be seen as a grayish cast (Berger *et al.*, 2012).

Yield losses of maize attributed to GLS vary from 11 to 69% (Ward *et al.*, 1999), with estimated losses as high as 100% when severe epidemics contribute to loss of total photosynthetic leaf area, increased stalk lodging, and premature plant death (Latterell and Rossi, 1983). Under severe disease pressure a toxin called cercosporin is produced which causes extensive blighting of the upper leaves resulting in significant yield losses (Lipps, 1987). This disease is relatively a new disease in Ethiopia and its pattern of host pathogen interaction is not established in the country (Dagne *et al.*, 2008).

GLS disease epidemics have been managed conventionally through deep tillage to bury previous maize residue, fungicide application, and field hygiene (Ward *et al.*, 1999). However, these measures have not been efficient in the management of GLS (Bigirwa *et al.*, 2001). A reduction in conservation tillage would have to be universally adopted to have an economic impact on GLS epidemics (Lipps *et al.*, 1996). Fungicide application is costly and not practical in most operations for the resource-poor farmers. Most hybrids currently under production in Kenya, Brazil

and South Africa are susceptible to GLS (Ininda *et al.*, 2004; Derera *et al.*, 2008; Brito *et al.*, 2012). Availability and adoption of resistant hybrids would provide a cost-effective means of controlling GLS.

Development of improved maize lines with resistance to multiple foliar pathogens (including GLS, Turicum blight and common rust) has been commenced in Kenya, through the use of resistance sources from Kenya, CIMMYT, IITA and South Africa. This has been accomplished by introgressing resistance regions from donors into elite maize germplasm. But GLS disease resistance in these sources is quantitatively controlled, necessitating the search for molecular markers linked to quantitative trait loci for resistance to GLS that have aided breeding efforts by augmenting conventional phenotypic selection (Brilo *et al.*, 2012) but, such efforts were not made in Ethiopia.

Many studies have reported on how resistance to the disease is controlled. In some temperate adapted lines, the genetic basis of resistance to *C. zea-maydis* has been reported to be under additive genetic control, with some dominance effects (Coates genetic control, with some dominance effects (Coates and White, 1998; Gevers and Lake, 1994; Dagne *et al.*, 2008). Most of the sources of resistance to *C. zea-maydis* identified and used in maize have genes for resistance inherited in a quantitative manner (Gevers *et al.*, 1994; Lehmensiek *et al.*, 2001; Clements *et al.*, 2000). The genetic study of Ininda *et al.* (2004) using a generation mean analysis concluded that additive genetic effects accounted for 82 to 96% of the total variation in conditioning GLS resistance among generations, although dominance and epistasis provided some contribution.

Major resistance factors have been mapped to at least three different chromosomes, with some of the quantitative trait loci consistently expressed across environments and having large effects on GLS resistance (Clements *et al.*, 2000). A major constraint in breeding for GLS resistance is the high degree of genotype-environment interactions observed during artificial inoculation experiments. Molecular markers linked to QTLs that control resistance may be useful for plant breeders to support the introgression of the resistance alleles into elite - yielding inbred lines

(Danson *et al.*, 2006; Veigal *et al.*, 2012).

Common Rust (*Puccinia sorghi* Schw)

Common rust caused by *Puccinia sorghi* is a common fungal disease of maize in Ethiopia medium to high altitude zones (Fininsa, 2001). Common rust may cause extensive yellowing and premature desiccation of maize foliage, resulting in leaf necrosis, and complete destruction of photosynthetic areas. In extreme cases, heavy rust infestations may result in stunting, incomplete ear tip fill, and pustules on ear husks, reducing marketability and yield (Richter *et al.*, 1995). Conventionally, control of common rust disease has been through cultural and chemical measures. The major cultural method used is timing of the rainy seasons, while chemical sprays use strobilurin and sterol-inhibiting fungicides which have some systemic properties. However, these measures are limited by the unpredictable weather conditions, and the environmental side effects. In addition, chemicals require to be used in a program that minimizes the development of resistant strains of the rust fungus and to maximize efficacy. This increases the cost of production, hence putting an additional burden of resource poor farmers. Breeding for resistance has been identified as a better method of managing the common rust disease (Thomas *et al.*, 1998).

There are two types of resistance (*Rp*) genes which were found to be involved in race specific against *P. sorghi*: partial and race-specific. In some studies more than 25 dominant resistance and organized in complex loci at chromosomes 3, 4, and 10 (Hooker, 1985; Delaney *et al.*, 1998). Richter *et al.* (1995) found that within these complex loci, novel resistance specificities are generated by genetic re-assortment events, such as unequal crossing the over all gene conversion Danson *et al.* (2006). Pyramiding of multiple closely linked genes into "compound" genes has been proposed as a possible means of constructing more durable race specific resistance on the materials employed in generation menace inherited by complex loci against common rust in maize (Hu and Hulbert, 1996; Holland *et al.*, 2007). Depending on the analyses, the prevalent mode of gene action varies between additive and dominant for resistance against *P. sorghi* (Kim and Brewbaker, 1977).

Quantitative Trait Locus (QTL) Mapping

Appropriate selection of parents for the develo-

ment of mapping populations is pivotal to maximizing the power of quantitative trait loci detection. Trait genotypic variation within a family is indicative of the family's informativeness for genetic studies. Accurate prediction of the most useful parental combinations within a species would help guide quantitative genetics studies (Zwonitzer *et al.*, 2010; H-Y Hung *et al.*, 2012; Hallauer *et al.*, 1989).

Breeding for disease resistant varieties and availing high yielding seeds of both true and top cross hybrids to small scale farmers remains as the only feasible option to boost maize productivity. In maize, quantitative resistance has been widely used to confer partial and durable resistance for disease control. A large number of quantitative trait loci (QTL) for disease resistance have been mapped in maize genome, and clusters of QTL for various diseases were identified in some chromosomal regions (Wisser *et al.*, 2006).

An effective approach for studying complex and polygenic forms of disease resistance is known as "Quantitative Trait Locus" (QTL) mapping, which is based on the use of DNA markers (Edwards *et al.*, 1987; Semagn *et al.*, 2012). With QTL mapping, the roles of specific loci in genetically complex traits can be described, and fundamental questions that have vexed researchers in the field of plant pathology for decades can be addressed. Quantitative trait locus (QTL) mapping is a highly effective approach for studying genetically complex forms of plant disease resistance. With QTL mapping, the roles of specific resistance loci can be described, race-specificity of partial resistance genes can be assessed, and interactions between resistance genes, plant development, and the environment can be analyzed (Young, 1996; Wisser *et al.*, 2008; Semagn *et al.*, 2012).

Outstanding examples of QTL study include: quantitative resistance to the rice blast fungus, late blight of potato, gray leaf spot of maize, bacterial wilt of tomato, the soybean cyst nematode and stem rust of wheat (Orsini *et al.*, 2012). These studies provide insights into the number of quantitative resistance loci involved in complex disease resistance, epistatic and environmental interactions, race-specificity of partial resistance loci, interactions between pathogen biology, plant development and biochemistry, and the relationship between

qualitative and quantitative loci (Young, 1996; Orsini *et al.*, 2012; Veigal *et al.*, 2012; Zhang *et al.*, 2012). QTL mapping also provides a framework for marker-assisted selection of complex disease resistance characters and the positional cloning of partial resistance genes (Zwonitzer *et al.*, 2010; Martin *et al.*, 2012). Therefore, in order to reap multiple advantages from these noble techniques and boost maize production and productivity in the country, these techniques should be promoted in the National and Regional Agricultural Research Centers and Universities in Ethiopia.

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