Combining ability and nature of gene action in maize (*Zea mays* L) inbred lines for resistance to gray leaf spot disease (*Cercospora zeae maydis)* in Ethiopia

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ABSTRACT

Ten elite maize inbred lines were selected based on all over *per se* performance and gray leaf spot disease reaction. Crosses were made in a 10 × 10 half-diallel mating design to produce 45 F$_1$ single cross hybrids. The experiment was conducted at Bako national maize research center in 2015 and evaluation of the crosses were made at Bako and Jimma research centers in 2016 by using alpha lattice design with three replications including three commercial checks. All the necessary yield, agronomic and GLS disease data were recorded. In all the studied traits highly significant genotypic differences were observed indicating the existence of genetic variability among the crosses. Analysis of variance for the combining ability indicated GCA and SCA mean squares were significant at ($P < 0.001$) for all traits except for anthesis-silking interval, ear per plant, ear diameter, lesion length and width. The ratios of GCA/SCA variances for agronomic parameters and all disease parameters were greater than unity except for that of first disease appearance implying the predominance of additive gene actions. Among all inbred lines, P1, P4, P7, P8 and P9 were identified as desirable sources of resistant genes for GLS disease resistance with positive days of first disease appearance and negative disease incidence, severity and AUDPC values for GCA effects. From the analysis of epidemiological data and disease progress curves the Logistic model (R^2 = 96.5) better described the disease progress curves than the Gompertz model (R^2 = 92.5) indicating the presence of delayance in epidemics and the inflection point of the GLS. P1, P7 and P8 were identified as a good general combiners for yield, yield related traits and GLS disease parameters. Thus, these parents were recommended to be used in breeding programs with a purpose of developing high yielder and GLS resistant single cross hybrids. In conclusion this study identified potential high yielding and GLS resistant single cross hybrids (CML-395/CML-383, CML-395/Sc-22, CML-395/CML-197 and CML-383/CML-197). Therefore, it is recommended that these hybrids can be used for direct production where this disease is the most prevalent and/or for further breeding programs in generating novel hybrids for future use.

1. Introduction

Maize is an important component of farming systems and staple food crop in sub-Saharan Africa. It is a versatile crop with wider genetic variability and able to grow successfully throughout the world covering tropical, subtropical and temperate agro climatic conditions (Masuka et al., 2017). In Ethiopia it is a staple food crop and one of the main sources of calories in the major maize producing regions. It is cultivated on about 2.135 million hectares of land and the national average yield

of maize under subsistence production in Ethiopia is 3700 kg/ha (CSA, 2017). This is too much below the world's average yield which is over 6000 kg/ha. This low yield is attributed to several factors among which foliar diseases and insect pests are the major once (Ali and Yan, 2012; Abate et al., 2015).

Gray leaf spot (GLS) caused by the fungal pathogen *Cercospora zeae-maydis* is one of the major disease constraints to maize production in many parts of the World including Ethiopia. It is the most destructive foliar disease of maize, significantly reducing yields in many maize-

growing areas throughout the world (Roane et al., 1974; Berger et al., 2014). In severely affected regions, yield losses are estimated to be 10–25% annually, but losses as much as 100% due to severe deterioration of the leaves and stalk lodging have been recorded (Ward et al., 1999; Carson et al., 2002; Derera et al., 2008; Aschalew et al., 2012).

Direct yield losses due to GLS occur as a result of the reduction of the photosynthetic area of the plant. This pathogen is a newly introduced foliar disease of maize in Ethiopia. The disease was first observed in 1997 in the border of west Wollega and Ilu-Abbabora zones, of western Oromia, Ethiopia (Dagne et al., 2001). It has significantly contributed to yield loss of about 37% in the western part of the country. In Ethiopia when susceptible genotypes are affected, it may lead to epidemics and contributing to a yield of losses of over 37% (Dagne et al., 2008).

GLS disease epidemics have been managed conventionally through deep tillage to burry previous maize residue, fungicide application, and field hygiene (Ward et al., 1999). However, these measures have not been efficient in the management of GLS (Sibiya et al., 2013). 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. Availability and adoption of resistant hybrids would provide a cost-effective means of controlling GLS. Most of the sources of resistance to *C. zeae-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). Many studies have reported on how resistance to this disease is controlled. In some temperate adapted parents, the genetic basis of resistance to *C. zeae-maydis* has been reported to be under additive genetic control, with some dominance effects (Coates and White, 1998; Gevers et al., 1994; Dagne et al., 2008; Zhang et al., 2015).

Mostly disease resistance in maize is quantitative rather than qualitative in nature. Qualitative disease resistance is generally controlled by one gene or a few genes with major effects, whereas quantitative disease resistance (QDR) is generally controlled by many minor genes. Although rapid progress has been made in recent years in the genetic characterization of qualitative disease resistance in maize, progress in the understanding of the genetic and physiological processes underlying QDR has been limited due to their complexity and incomplete and variable expression (Berger et al., 2014; Benson et al., 2015; Yang et al., 2017).

Resistance to gray leaf spot is reported to be inherited quantitatively by genes that act primarily in an additive manner and is expressed as rate reducing resistance. Diallel crosses have been used in genetic research to determinate the inheritance of a trait among a set of genotypes to identify superior parents for hybrids development. It is also commonly utilized to determine gene action for quantitative traits (Hayman, 1954; Hallauer et al., 2010). Two parameters normally calculated from such studies include general combining ability (GCA) and specific combining ability (SCA).

GCA is the average performance of a parental genotype over several cross combinations and is associated with additive gene effects, while SCA reveals the average performance of crosses that perform better and is typically associated with non additive gene effects (dominance) (Derera et al., 2008; Sibiya et al., 2013). The variance of general combining ability GCA and specific combining ability SCA are related to the type of gene action involved. Variance for GCA includes additive portion while that of SCA includes non-additive portion of total variance arising largely from dominance and epistatic deviations (Sprague and Tatum, 1942). Breeding for resistance to *C. zeae maydis* has relied on partial resistance, a form of an incomplete or quantitative resistance characterized by slow epidemic build-up despite high infection type of a compatible host–pathogen interaction (Derera et al., 2008; Herman et al., 2013). Components associated with partial resistance to gray leaf spot of maize include prolonged latent and incubation periods, reduced infection rates, low sporulation and fewer and smaller lesions (Menkir and Ayodele, 2005; Gordon et al., 2006; Herman et al., 2011).

Understanding the genetics of components expressing partial resistance has enabled selection of this type of resistance possible in several host–pathogen systems based on component measurements (Gordon et al., 2006). Except the investigation made by Dagne et al. (2008), in Ethiopia little has been reported on the components expressing partial resistance to gray leaf spot of maize and possible applications in the selection and breeding of resistant genotypes. In any hybridization program, recognition of the best combination of two (or more) parental genotypes to maximize variance within related breeding populations, and as a result the chance of recognizing superior transgressive segregants in the segregating populations, are the most critical challenge to plant breeders. Since the combining ability was introduced in 1942, it has been widely adopted in plant breeding to compare performances of lines in hybrid combinations.

Estimating combining ability, the nature and magnitude of gene action is an important factor in developing an effective breeding program, which can be understood through combining ability analysis. This information is helpful to plant breeders, pathologists and geneticist for formulating hybrid breeding programs for better yield and disease resistance (Tester and Langridge, 2010). Currently in Ethiopia the most adopted commercial maize hybrids and composites by the farmers are becoming susceptible to this disease. This can strongly affect the lively hood of millions of farmers who are relaying on maize as staple food leading to failure of the food self sufficiency and food security envisioned by the country. Thus, searching for GLS resistant hybrids and composites remain the crux of the matter. Hence, the objectives of this study were to determine the combining ability and nature of gene action for resistance to GLS and identify resistant single cross hybrids for direct production or breeding. This paper presents results from field experiments of maize agronomic, breeding and genetics and pathological researches.

2. Materials and methods

2.1. Description of the study areas

This experiment was conducted during the 2015/2016 main season (May to October) at Bako National Maize Research Center (BNMRC) and Jimma Agricultural Research Center (JARC). Bako National Maize Research Center is located in East Wollega Zone of the Oromia National Regional State, Western Ethiopia at an altitude of 1650 m above sea level (m.a.s.l). It lies between 9°06′ North latitude and 37°09′ East longitude in the sub-humid agro-ecology of the country. During the experimental seasons, the rainy season covered the period from May to October and maximum rainfall was received in the months of July and August and the average annual rainfall was 944.4 mm. The mean, minimum and mean maximum temperatures were 12.3 and 29.8 °C, respectively. The soil is classified under the Nitosol order. Naturally, this area is exposed to high maize foliar disease pressure and mostly used as a hot spot area to screen new maize genotypes for the most foliar diseases (Tilahun et al., 2017; Dagne et al., 2008).

Jimma Agricultural Research Center is located in Oromia Regional State in the South West part of Jimma Zone at an altitude of 1750 m above sea level (m.a.s.l). It lies between 7°46′ North latitude and 36°00′ East longitude in the sub-humid agro-ecology of the country. During the experimental season, the average annual rainfall was 1536 mm. The mean minimum and mean maximum temperatures were 11.2 °C and 25.9 °C, respectively. Since it is a hot spot area for the most of foliar diseases it is the most recommended area to evaluate new maize genotypes for GLS resistance in the country (Tullu et al., 2003).

2.2. Experimental materials

Ten maize inbred lines with contrasting reaction to GLS were