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Ethiopian Sorghum [*Sorghum bicolor* (L.)] Landraces: Sources of Biotic and Abiotic Stress Resistance

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Abstract: **Sorghum [*sorghum bicolor* (L) Moench] is an important cereal and widely grown for food, feed, fodder and fuel in the semi-arid tropic's areas of the world. Different works were done in sorghum breeding but production and productivity gap are still there. The existence of tremendous amount of sorghum variability exhibiting native genetic variation made Ethiopia as genetic resource reservoir ranking first in contributing germplasm collection worldwide. The relationship between a plant and a pest is very complex. However, the ability of a pest or pathogen to cause disease in or damage to a plant depends on different factors. Plant varieties within a species can differ in their ability to defend themselves. Its Understandable that the presence and magnitude of genetic variability is a pillar for developing tiptop variety in breeding program. Ethiopian sorghum landraces exhibit native genetic potential for sources of drought, salinity, Al-toxicity tolerance, pest resistance, as sources of nutritional value, high energy, fodder quality, malting and processing quality, NUE and WUE are an opportunity and considerable starting point for exploiting noble gene in the development of sorghum cultivars with resistance to these important stresses. Therefore, reviewing the genetic diversity of Ethiopian Sorghum landraces for sources of biotic and abiotic stress resistance is the main objective of this review paper. It is important to adequately collect, characterize and preserve existing genetic potentials of sorghum landraces from untouched areas of Ethiopia before it is invaded and destroyed this dynamic world.**

Keywords: **Variability, Tolerance, Resistance, landraces, biotic, abiotic, Al-toxicity, NUE, WUE.**

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1. INTRODUCTION

Sorghum [*Sorghum bicolor* (L.) Moench, 2n=2x=20, C_4 plant] is the most important grain crop globally (FAO, 2018, Dicko *et al*., 2006). Its self-pollinated monocotyledon crop with the degree of often cross pollination up to 30% depending on panicle type (Poehlman and Sleper, 1995). Sorghum is an indigenous crop of Ethiopia where tremendous amount of variability exists in the country (Adugna, 2007), having a diversity of both domesticated and wild relatives which revealed Ethiopia as center of origin and diversity (Mekibeb, 2009) supported by Vavilonian center of origin and diversity (Vavilov, 1951). From the world sorghum grain production more than half of the produced is used for human consumption in developing countries. It is the main staple food crop for more than 500 million people in Africa, Asia and Latin America particularly in semi-arid tropical regions where drought is the major limitations to food production (Ejeta, 2005). Ethiopian sorghum landraces exhibit native genetic variation for drought resistance (Borrel *et al*., 2000), having huge source of high lysine (Singh and Axtell, 1973), good grain quality and resistance to disease and insect (Yilma, 1991), post flowering drought tolerance (stay-green trait) (Borrel *et al*., 2000), source of zera zeras sorghum popular at ICRISAT still today in developing food type hybrid (Reddy *et al*., 2004). Sorghum, is a C_4 plant, has clear advantages over other grain crops because of its ability to return economic yields in hotter and drier environments than rice (*Oryza sativa*), wheat (*Triticum aestivum*) and maize (*Zea mays*) (Bryden *et al*., 2009; Reddy *et al*., 2012).

Stress tolerance is the ability to be relaxed and composed when faced with difficulties. Having positive stress tolerance is being able to stay calm without getting carried away by strong emotions of helplessness and hopelessness. In addition, Stress tolerance is the threshold at which an individual can effectively and consistently deal with and manage stressful situations. Stress is a normal biochemical reaction that occurs when the prefrontal cortex of the brain secretes and regulates a stress hormone called dopamine. A small amount of stress can be beneficial to a person by increasing focus on routine tasks and/or trigger warnings against potential threats. However, high levels of stress can impair cognitive function (i.e., concentration), interfere with relationships at home and/or work, and lead to detrimental future health issues. Stress-tolerant plants establish a new metabolic homeostasis in response to stress and thereby can continue to grow without suffering stress-induced injury (Mahajan and Tuteja, 2005).

Tolerance mechanisms are coordinated and fine-tuned by adjusting growth, development, and cellular and molecular activities (Levitt, 1980). Resistance is the ability of a plant variety to restrict the growth and development of a specified pest or pathogen and/or the damage they cause when compared to susceptible plant varieties under similar environmental conditions and pest or pathogen pressure. Resistant varieties may exhibit some disease symptoms or damage under heavy pest or pathogen pressure. Two levels of resistance are defined: High resistance (HR): plant varieties that highly restrict the growth and development of the specified pest or pathogen under normal pest or pathogen pressure when compared to susceptible varieties. These plant varieties may, however, exhibit some symptoms or damage under heavy pest or pathogen pressure. Intermediate resistance (IR): plant varieties that restrict the growth and development of the specified pest or pathogen, but may exhibit a greater range of symptoms or damage compared to highly resistant varieties. Intermediate resistant plant varieties will still show less severe symptoms or damage than susceptible plant varieties when grown under similar environmental conditions and/or pest or pathogen pressure. Susceptibility is the inability of a plant variety to restrict the growth and development of a specified pest or pathogen (Mahajan and Tuteja, 2005). Generally, despite the versatile and multitude importance of the sorghum; however, reaching the full genetic potential of the crop is a gap because of biotic and abiotic stresses like; drought, stem borer, grain mold and the parasitic weed “striga” are some of them. Therefore, reviewing the genetic diversity of Ethiopian Sorghum landraces for sources of biotic and abiotic stress resistance is the main objective of this paper.

2. LITERATURE REVIEW

Sorghum Genetic variability as source of Drought Tolerance

The effect of drought stress depends on the plant developmental stage at the onset of stress. Drought stress can occur at any stage of crop growth stages (Rosenow and Clark, 1995; Rosenow *et al*., 1996). Sorghum is known for its ability to tolerate water stress, both intermittent and terminal stress. This is mostly correlated to its root system (Tsuji *et al.*, 2003). Water-stress responses in sorghum can be of physiological, morphological and phenological in nature. Sorghum genotypes differ in their degree of drought tolerance, especially with respect to the timing of stress. Sorghum genotypes that exhibit good tolerance during one developmental stage may be susceptible to drought during other growth stages (Akram *et al.*, 2011). Such genotypic variation with respect to responses to water stress allows for farmers to select varieties which best suit local farming conditions and hence making sorghum suitable to a range of conditions. Ability to maintain key physiological processes, such as photosynthesis, during drought stress is indicative of the potential to sustain productivity under water deficit. Sorghum exhibits physiological responses that allow a continued growth under water stress (Dugas *et al*., 2011). Delayed senescence, high chlorophyll content and chlorophyll fluorescence as well as low canopy temperature and high transpiration efficiency are physiological traits that confer drought tolerance to sorghum (Harris *et al*., 2006; Kapanigowda *et al*., 2013). From a crop improvement perspective, manipulating these traits can increase drought tolerance in sorghum. Currently efforts are focused on improving crop genotypes for drought-prone area by evaluating various growth attributes, physiological, biochemical and agronomic performances of different Stay-Green (SG) sorghum accessions. Ethiopian sorghum landraces exhibit native genetic variation for drought resistance yet not exploited in development of sorghum cultivars with resistance to these important stresses. For instance, Afeso and Sorcoll 163/07 sorghum accessions showed better stress tolerance and the Stay green (SG) property in Ahmara lowland areas recorded maximum grain yield per hectare (Zelalem *et al*., 2015). Line B35 is a BC1 derivative of IS12555 dura sorghum from Ethiopia (Harris *et al*., 2007) shows distinct responses to drought at both pre- and post-flowering stages (Rosenow *et al*., 1996), being highly resistant to post-flowering drought (stay-green trait), with a relatively low yield. In contrast, line E36-1 is a high-yielding breeding line assigned to the Guinea caudatum hybrid race of Ethiopian origin (Haussmann *et al.*, 2002). Hence, these Ethiopian materials are the best suggested for improvement in terminal drought areas, serving as donor for high yielder but susceptible to drought prone areas of recipient parents at ICRISAT and USA (Edema and Amoling, 2015).

In Ethiopia, being tremendous genetic resource sorghum for drought tolerance landraces are existed, the breeding strategy in Ethiopia mainly focused on screening the landraces and verities in drought prone areas. For instance, areas such as Werer, Kobo and Miesso representative used as dry lowland areas for verification of drought tolerant land races or variety before release (EIAR, 2014).

Sorghum Genetic variability as source of Salinity Tolerance

Salinity toxicity in crops is caused by the presence of high levels of soluble salts in the soil solution, namely the Na+ cation and probably to a lesser extent Cl. Salinity affects approximately 830 million ha worldwide and is becoming an increasing problem in regions where saline water is used for irrigation. There are many areas with varying degree of salinity in India, Africa and countries in West Asia. Salinity retards seed germination and root emergence causes ion toxicity, osmotic stress and mineral deficiencies which adversely affect photosynthetic, physiological and biochemical processes limiting crop yield (Krishnamurthy *et al.*, 2007; Kausar *et al*., 2014).

The whole plant is more than the sum of its cells. It is only a small proportion of cells within the root that exist in relation to the external salinity. Most cells in a plant are not exposed directly to the external salinity but to the result of how this interacts with the processes governing uptake and partitioning of ions in the plant as a whole. The 'external' salinity for most cells in the plant is the apoplast immediately surrounding them. The timescale over which this leaf environment develops is very different to the timescale of imposition of most salinity regimes in laboratory experiments. The list of gene products that contribute to the concentration of salt in the compartments within, and surrounding, a photosynthesising cell in a plant is legion. It is perhaps possible that salt tolerant plants have evolved ways to co-ordinate the functioning of all these different genes (Cherry *et al.*, 2012).

In a single-celled organism it is necessary only to consider those processes that act at the cellular level. In a plant with its roots in the soil and its leaves in the air the tissue, organ and plant levels of organisation are of at least equal concern. This means: the perception of a salinity stress, the discrimination of this from other stresses than can elicit similar effects (such as water deficit), signalling to tell the rest of the plant that there is this stress, and the coordination of activities that produce the tolerant phenotype. In a whole organism the different cells of the different tissues perform different functions that contribute to the survival of that organism Cells in the root and the shoot (and celIs in different tissues at a finer level) do not do the same thing neither do they behave in the same way. This is central to how a complex organism copes with its environment (Cherry *et al.*, 2012). The genetic differences can be exploited to search varieties for salt tolerance by rapid screening methods using different growth parameters such as relative shoot growth, leaf blades, sheaths, leaf water potential, osmotic potential, nitrate reduction activity and relative water contents (Munns and Tester, 2008).

Sorghum is grown in arid and semiarid regions of the world and is a moderately salt tolerant crop (Gates, 2009). Currently, different strategies are being adopted for alleviating the adverse effects of salinity such as screening of cultivars of different crop plants. Indeed, molecular marker techniques are being utilized to find out DNA marker linked with salt tolerance and crop stability as genetic differences are basis for improvement in plants (Akber *et al*., 2009). Many genetic variations in sorghum cultivars are present in response to salinity tolerance under their genetic control (Netondo *et al*., 2004; Krishnamurthy *et al*., 2007). According to Tigabu *et al*. (2012) laboratory experiment shows that genotype ICSV-111 showed greater salt tolerance during germination stages while Teshale and 76T1#23 were better salt tolerant during seedling growth stages. Similarly, study done by Asfaw (2011) on effects of Salinity on Seedling Biomass Production and Relative Water Content of Twenty Sorghum accessions found the following accessions acc. 235461, acc. 69239, acc. 223550, acc. 69029 and acc. 23403 were salt tolerant during seedling biomass production and in Relative Water Content (RWC). Recently study done by Hailu *et al.* (2020) reported two sorghum genotypes namely Meko and 76T1#23 were good seed yielder compared to the national average and better tolerant compared to the tested sorghum varieties in the two consecutive cropping seasons.

Sorghum Genetic variability as source of Aluminum toxicity Tolerance

Aluminum (Al) toxicity is a major abiotic constraint on sorghum production and productivity worldwide (Magalhaes *et al*., 2004). Moreover, over 40% of the arable lands are acidic. Aluminum toxicity is widely prevalent in many countries of East Africa (Tanzania, Kenya) and Latin America (Colombia, Venezuela, Brazil, Bolivia, Peru, etc). Aluminum in acidic soil inhibits water and mineral uptake and consequently, reduces plant vigor and yield. Hanning *et al.* (1992) described the mechanisms of tolerance to acid soils and indicated that it is generally controlled by polygenic genes in crop plants. In sorghum, the AltSB locus, located on chromosome 3, was first identified as a major determinant for Al tolerance in the sorghum line SC283, explaining 80% of the phenotypic variation. Root organic acid release into the rhizosphere resulting in the formation of stable, non-toxic complexes with Al has long been hypothesized as a major physiological mechanism of tolerance via root Al exclusion in plants (Ma *et al*., 2001).

Sorghum Genetic variability as source of Nutritional value

Sorghum being one of the major food crops in the world has predominant role in meeting the dietary energy and micro-nutrient requirements particularly in the low income group populations; thus improving sorghum nutrition quality is of paramount importance. In sorghum breeding, it is necessary to identify germplasm that breeders can use to improve not only yield, but also mineral concentration, total starch, and sugar content. High genetic variability for protein content has been reported by different scholars. A study on limited number of germplasm lines and hybrid parents in sorghum did not show appreciable variability for β-carotene content in sorghum (Reddy *et al.,* 2004 and 2005). Similar is the case with yellow endosperm lines wherein the β-carotene did not exceed 1.1 ppm. For phenotyping for this trait, spectro-photometry can be followed but estimation using High-Performance Liquid Chromatography (HPLC) gives more accurate information (Reddy *et al.,* 2004). According to Shegro *et al.* (2012) genetic diversity in nutritional composition was observed among the sorghum landrace accessions (acc.) studied. High values were seen in acc. 228741 (total starch), acc. 228739 (amylose and amylose to amylopectin ratio), acc. 223525 (amylopectin and Fe), acc. 229831 (total sugar), acc. 69127 (Ca and K), acc. 223558 (Mn, P, and Mg), and acc. 223555 (Zn and protein). Accessions with high concentration of the most important mineral elements, protein content, and total starch and its components are potential genetic sources for the future development of improved lines in Ethiopia and similar environments.

Sorghum Genetic variability as Source of High Energy Sorghum

Sorghum has distinct advantage as energy sorghum because of its high biomass production and adaptation across semi-arid tropical environments. Hence, this crop is widely believed as a model bio-fuel and feed stock owing to its adaptation and ease of handling segregating generations. Sorghum biomass yields vary between 15 and 25 t/ha, but have been reported to be as high as 40 t/ha (Rooney *et al.,* 2004). Sorghum is a very robust plant that not only produces high biomass but also accumulates large quantities of sugars in the stalks that can be used for biofuel production without scarifying the grains. Sweet sorghum or high energy sorghum can also thrive under moderate water stress conditions (Reddy *et al*., 2004 & 2008), on marginal lands and with little external inputs (Rao *et al*., 2009). It also can be grown successfully in degraded and marginal lands contaminated with heavy metals (Zhuang *et al*., 2009). Thus, energy sorghum (both biomass and sweet sorghum) is well suited for land of low productivity or at higher risk for drought or water logging stress and is unlikely to replace food crops from higher quality land (Rao *et al*., 2010). Specific traits of interest are stalk sugars accumulation, biomass yield, post flowering drought adaptation, water use efficiency, non-lodging and cell wall composition. According to Disasa *et al.* (2017) a significant variation was observed for ^{0}Brix among the collections ranging from 11.8 to 22.5 % with a mean value of 17.7 % and also Significant variation was observed among the sites of collections. Collections from northern Ethiopia (South Tigray, North Wello and South Wello) had the highest ^{0}Brix values and were significantly higher than the rest of the regions such as Hararge, West Shewa, East Wollega and Gojam. Also, this study confirmed that similar results from India shows diversity among sweet sorghum genotypes from India with ^{0}Brix value with wide ranged (Reddy *et al.,* 2005). And showed that the mean value of ^{0}Brix obtained in Ethiopian genotypes was higher than most of globally known sweet sorghum varieties such as L-Tian (Guan *et al*., 2011), R9188 (Ritter *et al*., 2008) and SS79 (Shiringani *et al.,* 2010). So, Sweet sorghum accession from Ethiopia have the potential to be developed into commercial varieties, and the wide variation in ^{0}Brix content will serve as a good genetic base in the development of modern cultivar for sugar-related traits through hybridization. Generally, we can say that Ethiopian sweet sorghum genotypes can be used as sources for high energy genotypes.

Sorghum Genetic variability as Source of Fodder quality

Sorghum is a versatile species with potential for high biomass production. It can be used as a source of forage for livestock in the arid and semi-arid tropics. The demand for fodder has increased because of recent efforts to increase milk and meat production, which necessitates increased quantity and quality of green and dry fodder. In semi-arid situations, sorghum can be the major supplier of fodder, and its role becomes important during winter and summer months.

Extensive market survey of fodder trading in India has shown that the ratio of stover to grain price is narrowing and is now about 0.5 (Sharma *et al*., 2010). Additionally, price premiums are paid for higher quality stover and a difference of about 1 percentage unit in stover digestibility was associated with a price premium of about 5% (Blümmel and Rao, 2006). Phenotyping for stover fodder quality of pipelined and release tested hybrids and open-pollinated varieties has shown that about 5 units difference in stover digestibility exists that can be exploited without detriment to grain and stover yield (Blümmel *et al.*, 2010). Price premium for such stover is 25 to 30%. Near Infrared Spectroscopy (NIRS) platforms were developed and validated to phenotype for stover quality in multidimensional crop improvement programs (Sharma *et al*., 2010). The dry stalks are controlled by a simple dominant gene, D; juiciness is recessive (House, 1985). Stay-green QTL introgression can improve stover digestibility by 3 to 5 percentage units without detriment to grain and stover yields, in addition to improving drought resistance of sorghum cultivars and their water use efficiency. Brown mid-rib introgressions improved stover quality similarly, but had a depressing effect on grain and stover yields. Fortification and densification work has shown that sorghum stover based feed blocks, feed mash and feed pellets have the potential to increase average milk yields (currently <4 kg day -1) by 3- to 4-fold (12 to 16 kg day) (Anandan *et al*., 2010). The effect of such intensification on natural resource usage and greenhouse gas emission is dramatic. For example, an increase in average daily milk yield from 4 to 6 kg would reduce methane emission from Indian dairy by more than 1 million tons per year (Blümmel *et al*., 2010). According to Aruna *et al.* (2015) presence of heritable variation for both fodder yield and quality traits and their independence suggest that simultaneous improvement of fodder yield and quality is possible. Additionally, genotypes HC308 and SEVS4 were the best combiners for most fodder yield parameters such as plant height, leaf number etc. and for some of the fodder quality traits, such as low lignin (HC308). The brown midrib genotypes, EC582508 and EC582510, were good combiners for early flowering, IVOMD and low lignin concentration, and can be used as a source of genes to improve fodder quality in terms of digestibility. Keller was a good combiner for early flowering and fodder quality traits such as high IVOMD and low lignin. Nizamabad forage was a good combiner for CP and early flowering. These have potential for crossing with HC308 and SEVS4 for improvement of forage sorghum for animal feed. Breeding programs can be designed to utilize these lines for improving biomass/fodder yield and quality, and multiple crosses involving these parents would result in identification of superior segregants with favorable genes for most traits associated with fodder yield and quality (Aruna *et al.*, 2015).

Sorghum Genetic variability as source of Malting and Processing Quality

Understanding the malting properties of sorghum varieties and identifying varieties that yield malts with highest levels of enzyme (α-Amylase and β-Amylase) activity is key to adoption of sorghum in the malting industry. Sorghum has been malted for centuries and is used for the production of baby food and traditional alcoholic and nonalcoholic beverages. Both α-Amylase and β-Amylase are needed to hydrolyze starch and produce fermentable sugars in these processes. However, improvements and standardization of malting procedures and of malt evaluation techniques need to be made. Malting properties were investigated for 16 sorghum varieties using a germinator method (which mimics the pneumatic malting process) and for six sorghum varieties using a jar method (which mimics the floor malting process). Density of caryopses decreased for all sorghum after malting. Dry matter losses ranged from 8 to 19%. α-Amylase activity determined by calorimetric assay ranged from 25 to 183 U/g, with two cultivars having activity levels similar to that of commercial barley malt. Reduction in pasting viscosity was significantly correlated with α-Amylase activity. Sorghum diastatic (SDU) power was positively correlated to α-Amylase activity in cultivars with SDU values >30. β-Amylase activity was low, ranging from 11 to 41 U/g. The jar malting method yielded malts with lower dry matter losses and low levels of α-Amylase and β-Amylase activity, except for one cultivar (Beta *et al*., 1995). According to Shegro *et al.* (2012) report, the highest total sugar content was 14.93% found in accession 229831 followed by accession 223548 (14.09%). The lowest was 5.25% and recorded in accession 223558. These values were lower than those reported by Sabramanian *et al.* (1987) and higher than those reported by Arora and Luthra (1972). So, those accessions may have good potential for further use as dual-purpose sorghum types for grain and sugar production and may be used in sorghum improvement programs for incorporation of this trait into breeding lines.

Sorghum Genetic variability as source of Nitrogen use Efficiency

Sorghum is grown in a range of soils where nutrient deficiency in particular nitrogen is common. There are number of studies establishing variability in nitrogen use efficiency (NUE) in sorghum. Gardner *et al.* (1994) demonstrated that among the sorghum cultivars studied, M 35-1 was consistently high in NUE. They also found plants with fewer, larger and thicker leaves and that lower dark respiration rates are related to NUE and can be used as a selection criterion in breeding. Interestingly, sorghum possesses biological nitrification inhibition that reduces nitrogen losses from soil. Study done in Northern Ethiopia shows that as nitrogen fertilization increased both biomass and grain yields and NUE attributes, it is advisable that farmers in north-eastern Ethiopia should apply N fertilizer to increase the yield and quality of sorghum. And Genotype ICSV111 and 76T1#23 are important cultivars in north-eastern Ethiopia where farmers cannot afford to apply large amounts of inorganic fertilizers, as these cultivars are N use efficient and give higher yields on nitrogen poor soils (Bayu *et al.*, 2012). According to Bayu *et al.* (2012) the difference in NUE between efficient and inefficient cultivars was large enough to indicate that success in increasing sorghum yield on nitrogen poor soils could be achieved by screening genotypes for NUE. So, the future breeding work can use these cultivars as sources for gene to develop varieties with best nitrogen use efficiency.

Sorghum Genetic variability as Source of Water use efficiency

Sorghum is a C_4 plant with an extensive and fibrous root system enabling it to draw moisture from deep layers of soil. It requires less moisture for growth compared to other major cereal crops; for example, in some studies sorghum required 332 kg of water per kg of accumulated dry matter whereas maize required 368 kg of water, barley (*Hordeum vulgare*) required 434kg and wheat required 514 kg (House, 1985). Maman *et al.* (2003) showed clearly that yields of pearl millet (*Pennisetum glaucum*) were 1.9 and 3.9 t ha in 2000 and 2001 compared to 4.1 and 5.0t ha^{-1} of sorghum in 2000 and 2001 respectively under similar water use conditions (336 and 370 mm in pearl millet; and 330 and 374 mm in sorghum in 2000 and 2001 respectively). In another study involving sorghum, maize and soybean, sorghum was found to be the most consistent water use efficient crop between the two years of varying environmental conditions with rainfall received from crop emergence to physiological maturity of 10.1 inches in 2009 and 16.4 inches in 2010 in Nebraska, USA (Rees *et al.*, 2006). Similarly sweet sorghum gives higher biomass per unit of water used compared to maize or sugarcane (*Saccharum officinarum*) (Reddy *et al.*, 2008).

Sorghum Genetic variability as Source of Pest Resistance

Anthracnose resistance

Sorghum anthracnose, caused by *Colletotrichum sublineolum Henn*., is found in most sorghum producing regions of Ethiopia (Chala *et al.*, 2010). The disease can be successfully managed using resistant varieties; however, the pathogen population is highly variable which reduces the longevity of resistant sources (Marley *et al.*, 2001); new sources of resistance are needed and germplasm collections have been an important resource for resistance (Erpelding, 2010). Sorghum has its origin in Africa and the greatest genetic diversity in native sorghum is found in Ethiopia (Sleper and Poehlman, 2006); this centre of origin could also serve as a center of diversity for host plant resistance to anthracnose as sorghum is a diverse crop providing ample opportunity to look for sources of resistance (Erpelding, 2010). In the meanwhile, the use of resistant cultivars is considered the most cost effective and efficient option in combating sorghum anthracnose. Hence, searching for possible sources of resistance and breeding for disease resistance are important tasks for researchers engaged in finding effective and sustainable means of controlling anthracnose (Chala and Tronsmo, 2012). For instance, in Southern Ethiopia considerable variation in response of 56 sorghum accessions collected from different regions of Ethiopia showed significantly lower disease levels compared to the susceptible checks, indicating that germplasm from Ethiopia may be useful sources of anthracnose resistance (Chala and Tronsmo, 2012). Similarly, Erpelding (2010) identified 44 lines which were developed at USA from Ethiopian source showed high frequency of resistance to anthracnose; suggests that Ethiopian germplasm could be an important source of anthracnose resistant accessions. Chala *et al.* (2010) also identified resistant germplasm from Ethiopia and indicated that Ethiopia is an important source of resistance to anthracnose for sorghum improvement. These all reports suggest that, the potential Ethiopian sorghum germplasm may have in serving as sources of resistance in future breeding programs. However, Even though Ethiopia is native to sorghum where greatest genetic diversity of the crop for host plant resistance to anthracnose is found (Chala *et al.*, 2010), the variability of C. sublineolum (Afanador *et al.*, 2003) diverse nature of the farming system and climatic condition under which sorghum is grown in Ethiopia (Berhanu and Beyene, 2015; Chala *et al.*, 2010), limits the breeding progress to develop anthracnose resistant varieties that could be used across locations. Hence, the identified resistant materials need to be tested across locations before the deployment of resistance in breeding programs (Girma, 1995). Currently, in national sorghum improvement program source of anthracnose and other foliar disease resistant were identified. Sorghum landraces from Western and South Western parts of the country were resistant to multiple leaf disease including anthracnose (Prasada and Mengesha, 1981; Dilooshi *et al.*, 2016) these locations are serving as sorghum screening under natural condition (hot spot area) in national sorghum improvement program particularly for disease resistance breeding.

Panicle Disease Resistance

In the past, panicle diseases of sorghum such as grain mold, smut and ergot were recognized as major production constraints (Reddy *et al.*, 2004). Grain mold resistant Zera zera genotypes were identified and still in use as a donor parent to develop grain mold resistant varieties in world including Ethiopia. Reliable screening techniques and resistant genotypes to grain mold, smut are identified and efforts are underway to exploit the genetic potential of the resistant lines to develop mold resistant varieties and explore the possibility of developing smut resistant male-sterile female parents (A-lines) that could be used in the hybrid sorghum seed production (Girma, 1995). The Western of parts of Ethiopian regions harbors a unique set of sorghum germplasm adapted to conditions not conventional to sorghum grown in other parts of the world. Accessions from the region and parts of South Western possess unique resistance to multiple leaf and grain diseases (Dilooshi *et al.*, 2016). Though the region is conducive for growing variety of sorghum as the primary choice and variants of sorghum sources serving as global germplasm such as Zere-Zera sorghum (Prasada and Mengesha, 1981), warm temperature, high rain fall a near humidity (100%) agro-ecology of the area is challenging sorghum breeding due to grain mold and various leaf diseases (Dilooshi *et al.*, 2016) received favorable environment for development. Ethiopian national sorghum research program and other regional research centers has been conducted sorghum breeding in this agro-ecologies, particularly on leaf and grain mold resistance breeding. For instance, Bako (BARC), Asosa (AARC), Pawe (PARC) and Jimma Agricultural Research Center (JARC) has been conducted a lot of sorghum breeding trials particularly for leaf and grain mold diseases. Since today, Only from BARC, AARC and JARC foliar and grain disease resistant varieties like Chemeda, Gemedi, Lalo, Dano, Adukara, Asosa-1 and Aba melko were released and under production (ECVR, 2014; EIAR, 2014).

Striga Resistance

Striga species (witch weed), a root parasitic (obligate parasite) flowering plant, is common in Sub Saharan Africa (SSA) causing severe constraints to crop production diverting essential nutrients from crop such as sorghum (Hayelom, 2014). It affects the life of more than 100 million people in Africa and cause economic damage equivalent 1 billion $ US per year (Labrad *et al.*, 2008; Waruru, 2013). It has broad host range and affects important cereal crops such as sorghum, maize, peal millet, Finger millet, and upland rice (Hayelom, 2014).

Striga is known by ‘Akenchira’, ‘Metselem’ local name (Fischer, 2006) in Ethiopia which is serious the problem in dry lowland agroecologies characterized by erratic rain fall, low soil fertility and fragile ecosystem (EIAR, 2014). Annually, sorghum loss by striga in SSA is estimated 22-27 %, while Ethiopia shares 25% estimated to US$75 million (AATF, 2011). In Africa, relatively Ethiopia has strong sorghum breeding program on striga (AATF, 2011). Ethiopia becoming strong with collaborative research work focused on the introduction of varieties/lines that combine high yield and Striga resistance has been a high priority thematic area of research (Adugna, 2007). Such germplasm has been introduced from ICRISAT and International sorghum and millet (INTSORMIL) collaborative research and evaluations have been made in Striga prone areas. Over the years the apparently available Striga resistant varieties and lines have been introduced and tested in hot spot areas. Well, known two Striga resistant sorghum varieties, Gubiye (P9401) and Abshir (P9403), initially introduced from Purdue University, USA, were released for commercial production in Striga infested areas of the country. Furthermore, a new back crossing program has been started in collaboration with the Purdue University to introgress the Striga resistance gene(s) from the introduced resistance sources (SRN 39 and Framida) into the otherwise better yielding locally adapted sorghum cultivars (Adugna, 2007).

Insect Tolerance

Nearly 150 insect species have been reported as pests on sorghum, of which sorghum shoot fly (*Atherigona soccata*), stem borers (*Chilo partellus* and *Busseola fusca*), sugarcane aphid (*Melanaphis sacchari*), sorghum midge (*Stenodiplosis sorghicola*) and head bugs (*Calocoris angustatus* and *Eurystylus oldi*) are the major pests worldwide. In-fester row, artificial infestation and no-choice cage screening techniques have been standardized to evaluate sorghum germplasm, breeding material and mapping populations for resistance to insect pests (Sharma *et al*., 1997). Large-scale screening of the sorghum germplasm at ICRISAT has resulted in identification of several lines with reasonable levels of resistance to shoot fly, stem borer, midge and head bugs (Sharma *et al*., 2003).

Sources of resistance to insects in sorghum have been used in the breeding program, and many varieties with resistance to insect pests have been developed (Sharma *et al*., 2005). Cultivars with resistance to midge have been released in India and Myanmar, but are cultivated on a limited area due to non-availability of seed. However, these lines have been used by the seed industry to develop midge-resistant hybrids in Australia and USA. Resistance to midge and shoot fly has been transferred into maintainer lines and used by the NARS partners and the industry in developing improved varieties in different regions (Ashok *et al*., 2011).

Wild relatives of sorghum belonging to Parasorghum and Stiposorghum have shown high levels of resistance to shoot fly, stem borer and sorghum midge (Sharma and Franzmann, 2001; Kamala *et al.*, 2012), and have diverse mechanisms of resistance to insects. These can be used to transfer resistance genes into the cultivars. Polymorphic simple sequence repeat (SSR) loci associated with resistance to shoot fly and the traits associated with resistance to this insect have been identified (Folkertsma *et al*., 2005), and are now being transferred into the locally adapted hybrid parental lines via SSR based marker-assisted selection (MAS). While host plant resistance is an effective tool to manage midge in sorghum, there is need to develop other tools of integrated pest management (IPM) for managing white grubs, shoot fly and stem borer and sprays for head bugs in sorghum (Sharma, 2006).

According to Tetreault *et al*. (2019) study inheritance of Sugarcane Aphid resistance was determined, susceptible (A/BCK60) and resistant (RTx2783) sorghum lines were cross-pollinated and screened for resistance in the F2 generation. And finally the study confirmed both RTx2783 and F1 plants were highly resistant based on the relatively small amount of sugarcane aphid induced damage observed over the time course. Conversely, genotype BCK60 was shown to be highly susceptible to sugarcane aphid based upon the greater amounts of aphid induced damage observed and the greater rate of change in damage than the resistant line and F1 hybrids. So, the breeding program can use this sorghum lines as sources of sugarcane Aphid resistance parental lines for the development of a new variety which can resistance sugarcane aphid for highly prone sorghum production areas.

3. CONCLUSION

Knowledge and understanding of the presence and magnitude of genetic variability is a pillar for developing tiptop variety in breeding program. Ethiopian sorghum landraces exhibit native genetic potential for sources of drought, salinity, Al-toxicity tolerance, pest resistance, as sources of nutritional value, high energy, fodder quality, malting and processing quality, NUE and WUE are an opportunity and considerable starting point for exploiting noble gene in the development of sorghum cultivars with resistance to these important stresses. Phenological with molecular data are the best and trust-able method for skillful characterization of germplasm resources. With the advent of high throughput molecular marker technologies, it is possible to characterize larger number of germplasms with limited time and resources. It is important to adequately collect, characterize and preserve existing genetic potentials of sorghum landraces from untouched areas of Ethiopia before it is invaded and destroyed this dynamic world.

DISCLOSURE STATEMENT

The author declares no competing interests

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