Chapter 5
Genomic Designing for Biotic Stress Resistance in Sorghum

B. Fakrudin, T. N. Lakshmidevamma, J. Ugalat, Raghavendra Gunnaiah, J. Khan, S. P. Gautham Suresh, K. A. Apoorva, M. Doddamani, S. Kadam, K. Rashmi, M. N. Mamathashree, K. Omkar Babu, A. Hadimani, M. Faizan, Gopalareddy Prakash, and Anurag Gowda

Abstract Sorghum (*Sorghum bicolor* (L.) Moench) is an immensely valuable staple cereal crop across semi-arid tropical regions of the world and is regarded as a nutritionally potential crop compared to other cereals with high fibre content, minerals and slow digestibility. A multitude of bacterial, fungal and viral pathogens and several insect pests cause significant losses in yield and quality of sorghum. Management of these biotic stresses using chemicals is quite expensive and environmentally not sustainable. Developing host-plant resistance and use of resistant cultivars has great promise in this direction. Repository of genetic resources and the wild gene pool in sorghum that harbor many biotic resistant genes serve as a rich source to develop resistant cultivars. Crossing programs involving several resistance sources resulted in many resistant varieties, hybrids and parents. The genetic barriers between wild and cultivated sorghum species are still challenging to transfer resistant genes. However, with the recent advances in genomic tools, next generation sequencing/re-sequencing technologies, genetic engineering, more genomic data is being utilized in the sorghum breeding programs. These advanced molecular tools have helped to unravel the genetic architecture and provide a deeper understanding of the marker-trait associations. A maximum number of individuals in the mapping population coupled with large-scale genotyping with markers like SNPs would capture more recombination events, leading to high resolution of QTL

B. Fakrudin (✉) · T. N. Lakshmidevamma · J. Ugalat · R. Gunnaiah · S. P. Gautham Suresh · K. A. Apoorva · M. Doddamani · S. Kadam · K. Rashmi · M. N. Mamathashree · A. Hadimani · M. Faizan · G. Prakash · A. Gowda
Department of Biotechnology and Crop Improvement, College of Horticulture, University of Horticultural Sciences Campus, Bengaluru 560065, India
e-mail: bfakrudin@uhsbagalkot.edu.in

J. Khan
Center for Cellular and Molecular Platforms, National Center for Biological Sciences, Bengaluru 560065, India

K. Omkar Babu
Acharya Nagarjuna University, Guntur, Andhra Pradesh, India

C. Kole (ed.), *Genomic Designing for Biotic Stress Resistant Cereal Crops*,
https://doi.org/10.1007/978-3-030-75879-0_5

mapping. Marker-assisted selection can now be efficiently used for pyramiding multiple resistance genes/QTLs which can accelerate the varietal development process, resulting in durable resistance with great impact on the sorghum yield stability and sustainability. This chapter provides an overview of biotic stresses in sorghum, their impact, various breeding strategies and genomics assisted tools in prospecting sorghum biotic stress resistance besides highlighting the recent concepts and future perspectives for genomic designing.

Keywords Sorghum · Biotic stresses · Nutritionally potential · Host-plant resistance · GWAS · QTL

5.1 Introduction

Sorghum (*Sorghum bicolor* (L.) Moench), the fifth major cereal crop of the world with a small genome size of 750 Mbp, is a native of Africa and possesses enormous genetic potential as a food crop, especially in disadvantaged marginal situations of the world human habitats (Paterson et al. 2009; Zhang et al. 2017b). It is known to be grown since five thousand years and as a crop of the semi-arid regions, it is being utilized as food and forage for the cattle. Much recently this crop has sustainably prospected for biofuel manufacturing (Calvino and Messing 2012). The food security necessitates a deeper understanding of the food production dynamics in the environmentally challenging situations where sorghum is being cultivated (Mundia et al. 2019). The factors that significantly limit sorghum production comprise adverse weather, poor soil fertility and most importantly the pests and diseases. Insect pests and diseases significantly affect crop yields, grain quality, marketability and its utilization as food and fodder (Savary et al. 2012) which in turn influence the food supply, if measures are not taken (Reynolds et al. 2016). The yield loss in sorghum due to biotic stresses covering all stages is anywhere between 30 and 100 % (Singh and Bandyopadhyay 2000). Global sorghum production at about 57.50 million tons during 2019–20 is expected to increase by 3.94% to meet the demand (Miller magazine 2020). Developing sorghum cultivars resistant to various biotic stresses is critical to sustaining its production to meet the present food, fodder and industrial requirements. Deployment of resistant cultivars to overcome biotic stresses can augment the solution for low productivity of cultivars. Knowledge of the genetic resources/gene pool of sorghum as the source of genes for stresses is crucial to develop biotic resistant cultivars (Kumar et al. 2014). Owing to the faster evolution and development of counter-resistance genes in pathogens and insect-pests to evade the host resistance, it is highly challenging to develop durable, long-lasting resistance through conventional approaches (Witcombe and Hash 2000). An integrated approach involving plant breeding and genomics tools could increase the efficiency and precision of resistance breeding, this has to happen on sustainable pace across different tropical and sub-tropical situations (Perez-de-Castro et al. 2012). The availability of mapping populations, molecular

markers and genetic maps in sorghum over the last two decades offered ample opportunities for the identification of genomic regions/quantitative trait loci (QTLs) associated with traits of interest, especially those associated with biotic stresses. The modern molecular tools can achieve introgression of several resistant genes/QTLs into a single cultivar through molecular breeding strategies. Marker assisted selection (MAS) has enhanced the selection efficiency in some of the important traits related to resistance against insect pests and pathogens (Dormatey et al. 2020).

Functional genomics tools coupled with diverse genetic backgrounds having broad resistance can be used to provide critical insights into the biotic stress responses (Cuevas et al. 2019). Indeed, the relevance of the sorghum functional genomics is increased with the advent of next-generation sequencing techniques (Paterson et al. 2009). Functional genomics along with the developments in genome sequencing, QTL mapping, RNA-sequencing, and bioinformatics allow a deeper understanding of the genetics of resistance both in plant and pathogen as well as insect pests (Andersen et al. 2018). The RNA-interference (RNAi) in imparting resistance to biotic stresses is becoming practically relevant in sorghum and other millets due to affordability of the technology (Banerjee et al. 2017; Majumdar et al. 2017; Zhang et al. 2017a). Transcription factors (TF), the proteins crucial in governing transcriptional regulation during the entire crop period, can function as switches to control the expression of genes involved in mediating biotic stress resistance. Characterization of transcription factor genes critically involved in plant stress responses and their introgression is vital for enhanced biotic stress resistance in sorghum.

The biotic stress management systems depend on various control approaches such as genetic, physical, chemical, cultural and biological, among others. However, the use of stress-resistant varieties can lead to enhanced ecological fitness, reduced pesticide usage and sustainable production system, resulting in increased yields and grain quality/end-use traits (Singh et al. 2004a). A multidisciplinary and multipronged approach with synergistic integration of morphological and molecular approaches i.e., plant breeding in combination with genomics tools would accelerate and maximize the efficiency of breeding programs for developing biotic stress resistance in sorghum (Dormatey et al. 2020).

5.2 Different Biotic Stresses

Sorghum is affected by various biotic factors including multiple insect-pests, diseases and parasitic weeds that cause significant economic losses.

5.2.1 Major Diseases of Sorghum

Major diseases of sorghum are grain mold, anthracnose (*Colletotrichum sublineolum*), ergot (*Claviceps sorghi* and *C. africana*), downy mildew (*Peronosclerospora sorghi*), sorghum rust (*Puccinia purpurea*), charcoal rot/stalk rot (*Macrophomina phaseolina*), bacterial leaf spot (*Pseudomonas syringae* pv. *syringae*), leaf blight (*Helminthosporium turcicum*) and head smut (*Sporisorium reilianum*). *Striga* spp., a parasitic weed is one of the most devastating constraints that can cause a cent per cent yield loss under severe infestation (Esele 1995).

5.2.1.1 Grain Mold

Grain mold is the most devastating disease of sorghum with global distribution. More severe in the *kharif* season, especially, in white-grain sorghum, which is being grown widely in Asia and Africa for food. Grain mold is less severe on colored grain sorghum being grown widely in United States of America (USA), Argentina, Australia and Mexico for feed purpose. It is a complex disease caused by more than 40 pathogenic and opportunistic fungi from several genera, including the most common species *Fusarium thapsinum* (Klittich et al. 1997; Cuevas et al. 2019). *Fusarium* spp., *Alternaria* spp., *Curvularia* spp. and *Colletotrichum* spp. were the most principal fungi reported in grain mold (Williams and Rao 1981; Navi et al. 2005). The disease develops with the infection and colonization of spikelet followed by grain colonization leading to the deterioration of seed (Bandyopadhyay et al. 2000). Fungi secrete enzymes that degrade starch in endosperm and germ tissues (Hodges et al. 2000). A devastating effect of grain mold on grain yield, quality, market value and eventually on the grain-based products with an annual loss of US$ 50–80 million was estimated in India (Das 2019).

5.2.1.2 Anthracnose

Anthracnose caused by *Colletotrichum sublineolum* Henn. is one among the most economically damaging sorghum diseases that affect leaves, stems and grain, with significant grain yield reduction over 50–86% (Cota et al. 2017). An estimated grain yield loss of more than 50% was observed in susceptible sorghum cultivars under severe anthracnose epiphytotic in Georgia (Harris et al. 1964). The disease gets aggravated under warm and humid conditions (Tsedaley et al. 2016). Symptoms include the development of small spherical spots on leaves and leaf midribs with red, orange, purple or tan colored wide margins having straw-colored centers. In case of disease severity, the spots increase in number and conjoin covering the entire leaf surface and stem leading to premature plant death. In the centers of the spots, small black fruiting bodies (acervuli) develop (Tesso et al. 2012). A direct

negative impact on grain yield can be envisaged as the infection in later stages of development, is seen on the rachis, panicle branches and seeds.

5.2.1.3 Ergot or Sugary Disease

Ergot is caused by the fungi of the genus *Claviceps*, i.e., *Claviceps sorghi or Sphacelia sorghi*. Over 40 species of *Claviceps* have been reported, major include *C. sorghicola*, *C. africana* and *C. purpurea* (Pazoutova and Frederickson 2005). The infection starts with the sclerotium production within the floret and only the ovaries are infected. Ergot infects unfertilized ovaries individually within a panicle. Male sterile lines are highly susceptible. Severe infection is seen under high rainfall, high humidity, cloudy weather during anthesis and in cool night temperature conditions. The two noticeable signs of the disease are droplets of honeydew oozing from infected florets and the growth of fungal sclerotia. The hard textured sclerotia developed from sphacelia protrude few millimeters outside the glumes. The major threat from ergot is the infection and contamination of the harvested grains by toxic alkaloids present in the sclerotia (Wegulo and Carlson 2011). Major types of ergot alkaloids produced are clavine alkaloids, D-lysergic acid and its derivatives, and ergopeptines which cause a group of symptoms called "ergotism" (Hulvova et al. 2013).

5.2.1.4 Downy Mildew

Downy mildew of sorghum is caused by *Peronosclerospora sorghi.* The disease is manifested as downy whitish growth on the lower leaf surface followed by whitish streaks on both the leaf surfaces. Tissues alongside the white streaks slit later resulting in leaf shredding. Primary infection of the disease is through oospores present in the soil, mycelium in seeds and secondary infection is through air-borne sporangia. Crop rotation with other crops viz., pulses and oilseeds and removal of the infected plants can prevent the secondary spread of the disease (Tesso et al. 2012).

5.2.1.5 Rust

Sorghum rust caused by *Puccinia purpurea*, is of significance as it predisposes sorghum to other diseases such as stalk rot. The disease is manifested as small reddish-brown specks on the lower leaf surface and pustules (uredospori) on both the leaf surfaces as purplish spots which later rupture to release a reddish powdery mass of uredospores. Primary infection is through long cycled rust and secondary infection is by wind-born uridospores. Infection can be minimized through the destruction of the alternate host, *Oxalis corniculata* and spray of mancozeb (Hooker 1985).

5.2.1.6 Charcoal Rot or Stalk Rot

Charcoal rot caused by a soil-borne fungus, *Macrophomina phaseolina*, is a major fungal disease of sorghum worldwide with great destructive potential causing substantial losses in economic yield levels ranging between 14.2 and 46.6% (Mughogho and Pande 1983). After infection, the infected stalk will split open and consequently results in longitudinal shredding of the pith tissue into fibers and disintegration. The stem breaks down to the ground resulting in premature stem lodging that negatively affects the grain and fodder quality. The disease is primarily infected from the soil, weed hosts and can be aggravated by rain or irrigated water (Ghosh et al. 2018).

5.2.1.7 Bacterial Leaf Spot

Bacterial leaf spot is caused by *Pseudomonas syringae* pv. *syringae*. Symptoms include initial water-soaked lesion on the lower leaves which grow and mature, and become elliptical to circular developing red or brown margins. As lesions dry, the centers become light-colored. Most commonly found in the spring season since it is dispersed by rain and wind and becomes insignificant in summer seasons (Te-Beest et al. 2004).

5.2.1.8 Leaf Blight

Causal organism of this disease is *Helminthosporium turcicum* (Syn. *Exserhilum turcicum*). Yield losses can approach 50%. Symptoms of the disease are manifested as small reddish or tan spots that can enlarge to long elliptical reddish-purple or tan lesions of 12 mm wide and 2.5–15 cm long. Sporulation of the fungus on lesions often gives them a dark grey or olive appearance on the surface. The fungus can survive on grasses, on residue and seeds (Lu et al. 2018).

5.2.2 Insect Pests of Sorghum

More than 150 species of insect pests infest sorghum. The key pests are shoot-fly (*Atherigona soccata*), sorghum gall midge (*Stenodiplosis sorghicola*), stem borer (*Chilo partellus*), aphids (*Rhopalosiphum maidis* and *Melanaphis sacchari*), jowar ear head bug (*Calocoris angustatus*), shoot bug (*Peregrinus maidis*), red-headed hairy caterpillar (*Amsacta albistriga*) and ear head caterpillar (*Helicoverpa armigera*) causing significant damage to the crop (Sharma et al. 2006).

5.2.2.1 Shoot-Fly

The shoot-fly (*Atherigona soccata* Rondani) is one of the prominent threats for sorghum production in Asia, Africa and American continent (Sharma et al. 2003). Sorghum shoot-fly, the most devastating pest, alone is responsible for 5% loss out of 12% total insect losses. Grain yield reduction of about 50% (Jotwani et al. 1979) and a still more devastating damage with loss up to 90% was reported (Jotwani et al. 1970). High susceptibility is seen in the early stages of crop growth (5–25 days), especially in the late sown crop during rainy season, whereas, the early-sown crop is more affected during the post-rainy season (Mohammed et al. 2016). Female shoot-fly lays eggs singly on the surface of the leaf, parallel to the mid-rib. The larvae cut the growing point of the apical shoot resulting in a dead heart symptom. Larvae feed on the decaying tissue which may lead to seedling mortality and the crop gets damaged within 1–4 weeks after seedling emergence, present a rosette appearance and fail to produce any grain (Mohammed et al. 2016). Pesticides are being used to control shoot infestation in sorghum crop (Sharma et al. 2007).

5.2.2.2 Sorghum Gall Midge

Sorghum gall midge (*Stenodiplosis sorghicola* Coquillett) is an ubiquitous damaging pest of grain sorghum all over the globe (Young and Teetes 1977). A crop loss of 10–15% was reported and in severity, this can cause cent per cent damage to developing kernels in all the sorghum growing areas (Sharma and Teetes 1995). Eggs hatch and feed on the ovaries resulting in chaffy grains. Certain varieties may be particularly susceptible to egg lay in pre-flowering spikelets (Franzmann and Vaschina 1989). Sorghum midge can be managed by uniform regional planting, such that, all sorghum varieties flower within 7–14 days or through insecticide spray at anthesis. Genetic resistance mechanism that increases non-preference of florets for sorghum midge is eco-friendly and a durable approach.

5.2.2.3 Sorghum Stem Borer

Sorghum stem borer (*Chilo partellus* Swinehoe) infestation begins from over a month after sowing. The larvae feed on the surface of leaf sheath and leaf whorls, bore into the midrib and the shoot which later feed on the internal tissues causing extensive tunnelling and results in 'dead heart' formation and consequent killing of young plants. Larvae also infest ear heads and cause tunneling leading to chaffy ear heads and poor grain development. Chemical control includes soil application of phorate or carbofuran at the time of sowing. Many parasitoids viz., green lacewing, ladybird beetle, spider, fire ant, reduviid bug, robber fly, black drongo, big-eyed bug, earwig, ground beetle, pentatomid bug, praying mantis, *Dicyphus hesperus* etc. are effective against stem borer. Greenleaf desmodium can also be used as a control strategy against stem borers in sorghum (Khan et al. 2006).

5.2.2.4 Aphid

Both sorghum aphid (*Rhopalosiphum maidis* Fitch) and sugarcane aphid (*Melanaphis sacchari*) are common in several sorghum growing countries (Singh et al. 2004a). The severity of aphid damage is up to 77% reduction in grain yields (Van Rensburg and Hamburg 1975). Aphids usually attack newly emerged leaves, wherein, the adult and nymphs cause the damage throughout the growing period by piercing and sucking sorghum juice which eventually slows down plant growth leading to plant death. Sorghum is reported to be a preferred host for sugarcane aphid (Bowling et al. 2016). Aphids produce honeydew in plenty on which sooty molds grow, which further hinder grain harvesting and grain quality (Wang et al. 2013). Leaf extracts from neem seed or dursban found to be effective in controlling aphids (Diarisso et al. 2005). Insecticides viz., dimethoate 30 EC and imidacloprid formulations are reported to be most effective in reducing the aphid population.

5.2.2.5 Jowar Ear Head Bug

Jowar ear head bug (*Calocoris angustatus*) is a vigorous, small yellowish-green bug that infests the crop from ear head emergence to dough stage and causes about 54–89% reduction in grain yield levels. During ear head formation, ear head bugs are usually seen covering over the ear heads. Both nymphs as well as adults suck the milky juice from ear heads or developing grains, as a consequence the grains shrink and turn black color leading to chaffy or crinkled grains. Older grains show distinct feeding punctures that reduce grain quality (Sharma 1985).

5.2.2.6 Shoot Bug

Shoot bug (*Peregrinus maidis*) is a sporadic pest of sorghum that can cause heavy damage under favorable conditions. Nymphs and adults suck the sap from young leaves and leaf sheath resulting in unhealthy plants, with reduced plant vigor and yellowing. Under severe infestation, the leaves wither from top-down and later turn reddish finally leading to plant death. The infestation generally leads to twisting of leaves and seldom of panicles emergence—collectively results in over 41% yield toll in India (Subbarayudu 2002). Deep summer ploughing, collection and destruction of larvae, crop rotation with non-host crops, timely sowing, destruction of alternate host plants, field sanitation, rogueing, early uprooting and burning of infested plants can reduce the incidence of pest.

5.2.2.7 Red Headed Hairy Caterpillar

Red headed hairy caterpillar (*Amsacta albistriga, A. moorei*), a polyphagous pest is highly injurious to young sorghum seedlings. Caterpillars are voracious feeders

which feed on leaves by scrapping the under surface of tender leaflets besides flowers and main stem in later stages independently, they spread across fields, which lead to severe crop damage and yield loss (Nagarajan et al. 1957). Use of light traps and digging trenches around the infested field and dusting with insecticide can reduce the pest infestation.

5.2.2.8 Ear Head Caterpillar

The adult ear head caterpillar (*Helicoverpa armigera*) is a medium-sized moth. Caterpillars feed till grain hardening stage and are covered in the inner branches of the ear. Compact panicles are more prone to heavy damage and damaged ears could be easily spotted in the field by their chalky appearance (Bora et al. 1994).

5.3 Genetic Resources of Resistance Genes

The sorghum germplasm resources can stand rounds of intense selection to meet diverse requirements of plant breeding due to its rich genetic diversity that stems from five basic races - *Bicolor, Guinea, Caudatum, Kafir*, *Durra* and 10 intermediate races that include -*Guinea-bicolor, Durra-bicolor, Caudatum-bicolor, Guinea-caudatum, Kafir-bicolor, Guinea-kafir, Guinea-durra, Durra-caudatum, Kafir-caudatum, Kafir-durra* (Harlan and de Wet 1972; Venkateswaran et al. 2019). The rich genetic diversity in the gene pool 1 (GP-1) and gene pool 2 (GP-2) and their cross-compatibility with *Sorghum bicolor* have led to the development of successful hybrids. Most significantly, *S. bicolor* subspp. *verticilliflorum* and *S. propinquum* have contributed for yield per se and *S. halepense* has contributed genes for crop duration (Dweikat 2005; Aruna and Cheruku 2019). Wild species, harbouring genes, which are resistant against striga are *arundinaceum, virgatum* and *verticilliflorum* (Cox et al. 1984; Bramel-Cox and Cox 1988). Other potentially useful traits in sorghum's GP-1 and GP-2 include *S. bicolor* subspp. *drummondii* for allelopathic properties and resistance to ergot and nematodes, and *S. halepense* conferring resistance to multiple pests (Dweikat 2005; Baerson et al. 2008). Further, the gene pool 3 (GP-3) of sorghum has enormous potential in gaining grain yield advantage through introgression of specific genes and it is envisaged that the diversity in GP-3 would be of particular use in breeding sorghum for climate change eventualities and dreaded insect pests of sorghum (Venkateswaran 2003; Kamala et al. 2009) (Fig. 1).

The concept of core collection facilitates thorough characterization of accessions for various traits of interest and thereby maximizing the use of the germplasm. The core collection consists of a subset of accessions from the entire collection, capturing most of the species diversity. Further, Upadhyaya and Ortiz (2001) postulated the concept of mini core collection with 10% core collection accessions. Repeated evaluation of the reference collection, core collection and mini-core

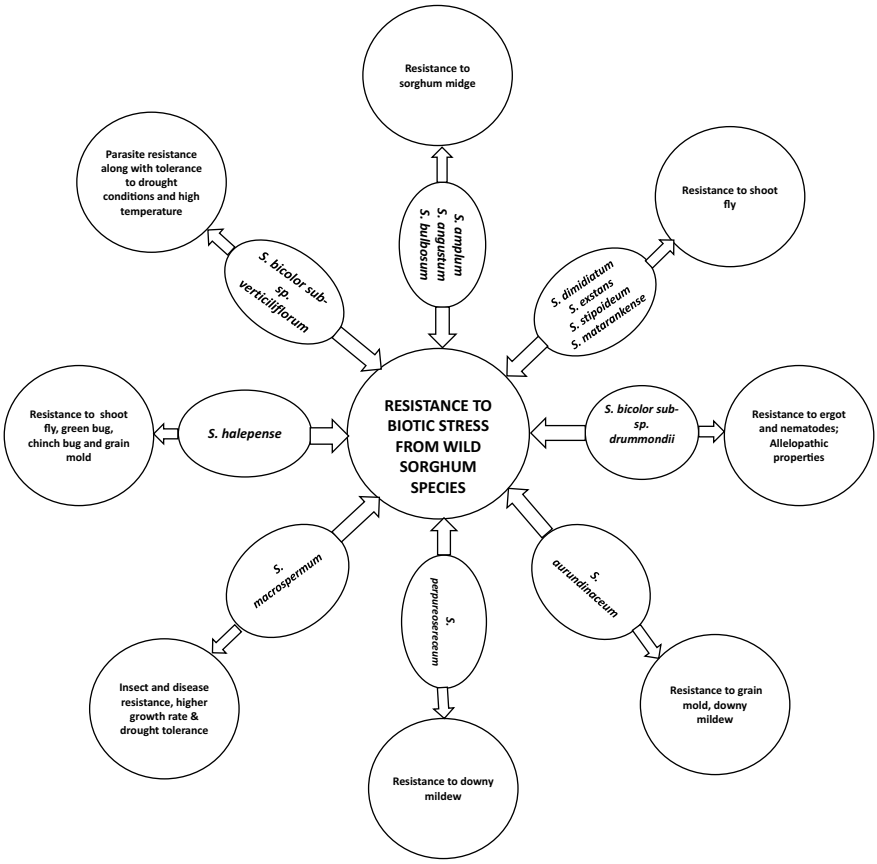

Fig. 5.1 Resistance to biotic stress from wild sorghum species. The genus *Sorghum* consists of 25 diverse species, among which few wild species confer resistance to major pests and diseases of sorghum. *S. bicolor subsp. verticiliflorum* gives high yield along with tolerance to drought conditions and high temperatures (Bramel-Cox and Cox 1998; Rich et al. 2004). *S. bicolor subsp. drummandii* has allelopathic properties to ergot disease and nematodes (Mojtahedi et al. 1993; Tsukiboshi et al. 1998). The species *S. amplum, S. angustum, and S. bulbosum* are a source of resistance sorghum midge (Sharma and Franzman 2001). *S. dimidiatum, S. extans, S. stipoideum*, and *S. matarankense* are a source of resistance to major pest of sorghum, shoot fly (Nwanze et al. 1995; Kamala et al. 2009). *S. perpureosereceum* confers resistance to downey mildew (Sharma 2010). *S. halepnse* is resistant to shoot fly, green bug and chinch bug (Nwanze et al. 1995; Dweikat 2005). *S. aurundinaceum* is resistant to and grain mold and downey mildew (Mohan et al. 2008). *S. macrospermum* has resistance to many pests and diseases along with higher growth rate and significant aboveground Dhurrin content under drought conditions (Kuhlman et al. 2008; Cowan et al. 2020)

collections of sorghum germplasm resulted in the identification of accessions useful in breeding for various biotic stresses. These include, ***Grain mold***: White-grained four guinea race accessions and a set of 50 sorghum mini core accessions have been reported to be resistant to grain mold (Sharma et al. 2010). ***Anthracnose***: a set of 13 accessions including IS10302, IS19153, IS20956 and IS24218, recorded minimal mean disease scores (Sharma et al. 2012). ***Leaf blight***: IS2906, IS18417, IS18425, IS18758, IS19667 and IS19669 (Reddy et al. 2004); besides a set of 27 accessions of mini core recorded resistance with a mean disease score of 2 (Sharma et al. 2012); ***Rust***: IS3413, IS13896, IS18417, IS21454 and IS29016; IS473, IS23521, IS23684, IS24503, IS26737 and IS33023 with mean disease severity of 3.8% (Reddy et al. 2004; Sharma et al. 2012); ***Downy mildew***: IS3547, IS20450, IS23992, IS27697, IS28449, IS28747, IS30400 and IS31714, (Reddy et al. 2004; Sharma et al. 2012); ***Potyvirus spp***.: IS7679 and IS20740 (Seifers et al. 2012); Further, accessions such as IS2058, IS18758, IS3547, IS14332, IS17141, IS2333, IS14387, IS3413, IS14390, IS21454 have shown multiple disease resistance (Reddy et al. 2008; Sharma et al. 2010, 2012).

5.4 Traditional Breeding for Disease and Pest Resistance

Insect pests and diseases cause considerable loss in grain and fodder yield levels besides the quality of produce. Resistant cultivars that are genetically superior form the cheapest method for minimizing the yield toll. Breeding for host plant genetic resistance is a continuous process in terms of searching for source accessions that are resistant to ever-evolving new races of the pathogens (Singh and Bandyopadhyay 2000; Mohammed et al. 2016). Classical breeding methods such as introduction, selection, backcrossing, pedigree method, recurrent selection schemes continue to play vital roles in evolving resistant cultivars. All through the history of the plant breeding, the crop wild relatives have been the sources of resistance genes (Hariprasanna and Rakshit 2016). However, a multidisciplinary approach to utilize these crop wild relatives is critical in achieving success (Kamala et al. 2016; Ananda et al. 2020). Sorghum germplasm with rich and diverse crop wild relatives offers an excellent opportunity to improve the deficient agronomically superior cultivars/hybrids. In sorghum, wild relatives such as chaeto, hetero, stipo, and parasorghum have been potential sources of biotic stress tolerant genes (Kamala et al. 2002).

5.4.1 Traditional Breeding Research for Diseases Resistance

5.4.1.1 Grain Mold

Grain mold being a disease complex, its development mechanisms are fairly described (Waniska et al. 2001). Both major and minor genes with additive and epistatic effects coupled with significant genotype X environment (GXE) interaction have been reported (Stenhouse et al. 1997; Rodriguez-Herrera et al. 2000). Limited success in resistant cultivar development to this disease could be attributed to complex genetics, mechanisms governing resistance and high influence of the environment (Audilakshmi et al. 2011). The conventional breeding prospected 'grain hardness' to improve grain mold resistance in white-grained sorghum used for human consumption in Asian and African counties (Das et al. 2020) and this approach has been successful in developing cultivars with high yield and resistance to grain mold through an expanded systematic screening and selection in segregating progenies of specifically planned crosses (Reddy et al. 2000). The resistant sorghums belonging to the guinea race with open panicles, large glume coverage along with grain hardness need to be involved in the crosses (Reddy et al. 2000). Germplasm from Sudan and Ethiopia which possessed desirable quality with white grains as well as less susceptibility to grain mold under natural conditions was utilized in the development of variety CSV 4, which further served as restorer parent for several hybrids viz., CSH 5, CSH 6 and CSH 9 in India (Ashok Kumar et al. 2011b). Accessions such as E 35-1, CS 3541, SC 108-3, SC 108-4-8 and SC 120 continue to be parents of choice in widening the genetic base of grain mold resistance in sorghum improvement programs of India and Africa (Reddy et al. 2000; Ashok Kumar et al. 2011b).

Pedigree breeding followed by multi location testing led to the identification of many advanced breeding lines which were used to develop high yielding grain mold resistant varieties and hybrids, such as SEPON 77, M 90038 and SEPON 82 × S 34. Many grain mold resistant lines with dwarf and earliness sorghum segments, grain and glumes traits from guinea along with semi-compact heads were developed through pedigree breeding (Stenhouse et al. 1997). A grain mold resistant population was developed with white-grained, color-grained lines coupled with higher grain yielding ability into genetic male-sterility (ms3) background. Repeated half-sib family selections and cycles of random mating resulted in pinning down of several superior lines with resistance, which eventually contributed to the release of grain mold resistant varieties and hybrids in India (Ashok Kumar et al. 2011a). Germplasm sources with wide adaptability and high grain quality along with the grain mold resistance are available. Resistant lines viz., ICSB392, ICSB403, ICSB383, IS13817, IS8614, IS10646, IS25060, IS21599 and IS23585 have been used extensively in the breeding programmes (Reddy et al. 2005).

5.4.1.2 Ergot

Ergot resistant trials, with susceptible A-lines and R-lines, concerning to incidence and severity of the disease revealed Tx2737 as a popular R-line. A male-fertile accession from Ethiopia, IS8525 with high levels of resistance was considered as a potential source for host-plant resistance strategies. Five CMS-lines were crossed with five pollinator lines without fertility restorer genes, wherein, the pollinator lines on an average had low (7–10%) and the CMS female lines had very high (62–82%) ergot severities (Reed et al. 2002). Further, pollen traits such as genetic architecture, pollen quantity and pollen viability have significant correlations with the ergot resistance. The genetic correlations studied among different traits have also have pointed at possibilities of common genetic factors controlling these traits (Parh et al. 2008). Three male-sterile lines in sorghum exhibited noteworthy differences in ovary colonization rates after inoculation (Komolong et al. 2003). Further, ergot severity with high heritability behaved quantitatively and the possible effect of floral traits need to be understood, as the resistance donor was having a short, narrow stigma, least or no stigma.

5.4.1.3 Charcoal Rot or Stalk Rot

Stalk rot resistance in sorghum is associated with a delay in leaf and plant death. Different genetic control mechanisms within SC599-11E for non-senescence and charcoal rot resistance envisaged that these two forms of resistance are not different pointers of the same trait (Tenkouano et al. 1993). The component traits—internode number was associated with two QTLs on linkage group B, the length of infection associated QTL on linkage group D and two QTLs associated with per cent lodging on linkage group I (Reddy et al. 2008; Patil 2011). Stalk rot-resistant sorghum genotypes were unaffected by the pathogen-mediated yield retardation (Bandara et al. 2019). High-temperature stress decreased chlorophyll and *F*v/*F*m. Genotypes PI533946, IS26749, IS23992, RTx7000, and SC35 had the maximum *F*v/*F*m and the genotypes IS19262, SC35, PI576380 and IS27912 had resistance to both pathogens (Perumal et al. 2020).

5.4.1.4 Downy Mildew

Concerted efforts to search and characterize the resistant sources for downy mildew by using the dual approach of sandwich inoculation technique and green-house screening revealed high-level resistance to the disease in a set of six accessions viz., IS28747, IS27697, IS31714, IS28449, IS23992 and IS30400 out of 242 germplasm accessions of sorghum mini-core collection from diverse geographies (Sharma et al. 2010; Rashid et al. 2018).

5.4.1.5 Rust

Eight loci with a significant effect on rust resistance with a total phenotypic variation explained (PVE), varied from 6.8 to 42.6% (Tao et al. 1998). Of the 12 sorghum varieties screened, a local cultivar 'Tetron' was reported to be highly resistant with zero yield loss compared to 40% yield reduction in 97 MW 6129 (NVT11 4). Impact of this disease on seed germination was also observed (Abera and Alemayehu 2012). A set of 13 advanced breeding lines generated from a cross between UPCA-S1 and Numbu revealed significant G × E interaction on leaf rust disease severity.

5.4.1.6 Multiple Disease Resistance

Field studies have revealed that an effective screening strategy can identify resistance sources to multiple pathogens in sorghum germplasm as vast genetic diversity to individual component traits exist across its species and subspecies (Prom et al. 2012). The development of several diseases simultaneously on a susceptible sorghum grown as a mixed stand with either maize or resistant sorghum found to be a good strategy (Ngugi et al. 2001). Over 242 sorghum mini-core collection evaluated to identify resistant ones for anthracnose and leaf-blight diseases resulted in 13 accessions resistant to anthracnose and 27 to leaf blight (Kimball et al. 2019). These accessions with resistance to multiple diseases would be potential sources for sorghum disease resistance breeding programs (Upadhyaya et al. 2013a). Parental genotypes such as 234112, Bt-623, 226057 and 210903 with positive genetic combining ability (GCA) effects -Bt-623 × Gemedi, 210903 × 234112, 210903 × 71708, 74222 × 234112, 74222 × 226057, 234112 × 71708, 226057 × 214852 and 226057 × 214852 with positive specific combining ability (SCA) effects for grain yield and the desirable families: 174222 × 234112, Gemedi × 71708, Bt-623 × 234112, Bt-623 × Gemedi, 226057 × 71708, Chemeda × 71708, and Gemedi × 71708 with negative SCA effect and low anthracnose severity were forwarded as promising populations for resistance breeding (Mengistu et al. 2019).

5.4.2 Traditional Breeding Research for Resistance to Insect Pests

5.4.2.1 Shoot-Fly

Shoot-fly resistance is a complex trait, that depends on the interplay of many component traits of plant, insect and environment. Developing genetically superior resistant cultivars offers a sustainable pest management system with enhanced grain

quality (Sharma et al. 2005; Mohammed et al. 2016). Resistance is manifested in the form of non-preference for oviposition (Dhillon et al. 2006). Systematic screening and further evaluation of sorghum germplasm led to identification of resistant accessions (Sharma et al. 2014a). Use of these resistant accessions in crossing programs led to the development of several shoot-fly resistant (SFR) varieties and hybrids (Kumar et al. 2014). Shoot-fly resistant superior advanced breeding lines such as IS2122, IS18551, IS2146, IS1054, IS2312, SFCR151, ICSV705 and SFCR125 were derived from germplasm (Riyazaddin et al. 2015). Rigorous breeding efforts have evolved cultivars that are significantly tolerant to shoot-fly incidence. Germplasm after infestation by the shoot-fly recovered in varying proportions. The accessions, CSV 22 and RSV 1093 revealed high grain yield potential in addition to shoot-fly resistance, while Phule Yashoda, RSV 1235, IS 2312, and ICSV 574 were high yielding with moderate resistance (Sharma et al. 2015). Similarly, another set with 10 parents, 45 F_1's along with their reciprocals screened for shoot-fly resistance and inferred that the genotypes ICSV 700, ICSV 25019 were useful (Mohammed et al. 2016).

The morphological traits allied with an expression of resistance/susceptibility to shoot-fly exhibited significant GCA effects. The interlard-fishmeal technique used to increase shoot-fly abundance at seedling stage of susceptible cultivars such as Swarna was effective and successful (Chamarthi et al. 2011). In a successful effort, a trait-based pedigree breeding approach was used to develop *kharif* and *rabi* sorghum grain types in both agronomically superior genotypes and genotypes with specific traits of importance. New sources of resistance such as IS923, IS5072, IS1057, IS1071, IS4664, IS1082, IS4663, IS1096, IS2394, IS5636, IS5470 and IS18369 have been mined to infuse and breed for shoot-fly resistance in sorghums (Kumar et al. 2014). A comparative study indicated that upregulation of total soluble sugar, total phenol, prussic acid and chlorophyll play a dominant role to impart resistance in the susceptible sorghum genotypes (Kumari et al. 2020; Salama et al. 2020).

5.4.2.2 Sorghum Gall Midge

Sorghum gall midge was first reported in 1953 in 'Nunaba' varieties from West Africa (Bowden and Neve 1953). Efficient management requires combining several strategies that suppress midge damage and abundance in the field. Resistance to this pest has been attributed to the traits long glumes and non-anthesis. Field tests have suggested that 'Nunaba' varieties were resistant under choice conditions in the presence of an alternative host, but susceptible in the absence of a more favorable host (Passlow 1965). Spikelet flowering time and morphology have a direct influence on the per se resistance. Genotypes that displayed resistance under no-choice conditions in glasshouse and field trials were reported to deploy an antixenosis resistance mechanism (Franzmann 1988). The mechanism of resistance to midge has been recognized as reduced egg-lay (Franzmann 1988; Sharma and Vidyasagar 1994). Midge resistant sorghum hybrids gave higher yields and greater

returns than susceptible hybrids under the same insecticidal spray regime (Teetes et al. 1986). There is little clear evidence on the exact chemical or physical components that affect the antibiosis mechanism of resistance in sorghum. Association between tannins and midge resistance is also noted (Santos and Carmo 1974; Sharma 1985, 1993). The hybrid breeding approach has been successful to achieve resistance (Boozaya-Angoon et al. 1984).

5.4.2.3 Sorghum Stem Borer

Larva of stem borer crawls and feeds on tender leaves that become folded, causing typical "shot hole" symptom. Sorghum genotype IS18573 displayed antibiosis to stem borer in terms of reduced survival and development (Kumar et al. 2006). Induced resistance in sorghum genotypes against stem borer infestation included elevated expression of peroxidase (POD), polyphenol oxidase (PPO), hydrogen peroxide (H_2O_2) and malondialdehyde (MDA) (Hussain et al. 2014).

5.4.2.4 Aphid

Aphid has emerged as a potential threat to sorghum. Resistance to this pest was assessed by testing 23 genotypes for tolerance to antixenosis and antibiosis and was compared with the known resistant cultivar 'TX 2783' and the susceptible 'KS 585'. The entries viz., AG1201, AG1301, W844-E, and DKS 37-07 expressed all three forms of resistance to aphids, while H13073 exhibited antibiosis and tolerance (Paudyal et al. 2019). Screening of a diverse set of sorghum genotypes resulted in the identification of several lines with moderate levels of resistance to aphid damage.

5.4.3 Traditional Breeding for Resistance to Striga

Witchweed (*Striga* spp.) infestation is an obstacle to sorghum cultivation and it inflicts both grain and biomass production. Over 20–100% yield reduction has been recorded in Asian and African countries (Ejeta and Gressel 2007; Parker 2009). Co-evolution of sorghum with striga in Africa might have resulted in inherent resistance, which is of scope as a breeding strategy (Shayanowako et al. 2018). Complex interactions between host, parasite and the physical environment have restricted the exploitation of resistance to striga (Ejeta and Gressel 2007). Several novel techniques have been employed to identify unique resistance sources to striga followed by introgression of these genes into selected cultivars with multiple resistance mechanisms. Several high yielding cultivars with striga resistance have been deployed in many African countries (Ejeta and Gressel 2007; Mbuvi et al. 2017). Over 25 sorghum accessions screened for *Striga hermonthica* were shown

resistance along with yield in Nigeria, identified SRN39, Sepon82, Danyana and SAMSORG40 as the top four resistant accessions to *S. hermonthica* (Afolayan et al. 2020). Seeds of acetolactate synthase herbicide-tolerant mutant recorded fewest *Striga* attachments (Tuinstra et al. 2009). Introgression of major quantitative trait loci (QTLs) governing resistance to striga or major genes/transcription factor genes involved are identified, and genetic engineering approach is an effective way forward for their effective transfer and integration (Gressel 2010). Such resistance is difficult to overcome by the parasitic weeds and could be easily backcrossed into local varieties (Wang et al. 2009).

5.4.4 Morphological and Biochemical Markers in Disease and Insect Pest Resistance

Effective screening techniques and availability of biochemical, morphological or DNA markers associated or genetically linked to a specific disease or pest resistance, or at least to the specific component traits, would go a long way in sorghum breeding. Morphological and biochemical markers play a crucial role in the diagnosis and management of various biotic stresses in sorghum. Several phenolic compounds viz., allelochemicals like p-coumarates, p-hydroxybenzoates, flavanols and phytoalexins (3-deoxyanthocyanidins) have a key role in biotic stress resistance (Weir et al. 2004). Higher contents of proanthocyanidins, flavan-4-ols and 3-deoxyanthocyanidins (3-DAs) are involved in host plant resistance. 3-DAs are considered as better markers for resistance to biotic stresses as they associate with resistance to all biotic stresses (Dicko et al. 2005). The peroxidases (POXs) play a vital role against biotic and abiotic stress resistance by forming physical barriers through the synthesis of cell-wall polymers (lignin and suberin) (Cui et al. 1996).

5.4.4.1 Diseases

Antifungal proteins viz., chitinases, glucanases, sormatin and ribosome-inhibiting proteins play a significant role in imparting resistance to grain mold (Rodríguez-Herrera et al. 1999; Bueso et al. 2000). Further, traits like kernel hardness and pericarp color were found to be associated with grain mold resistance (Menkir et al. 1996). Traits such as kernel hardness with red pericarp, tan plant color kernels, high tannins along with a pigmented testa, as well as the pericarp intensifier (*I*) gene can enhance grain mold resistance (Esele 1995; Waniska et al. 2001). Involvement of peroxidases in fungal resistance was also inferred (Luthra et al. 1988).

5.4.4.2 Insect Pests

Insect/pest infestation in sorghum produces prussic acid or hydrocyanide (HCN), a toxic chemical which shows fatal response to herbivores. Two enzymes viz., glycosidase and hydroxynitrile lyases produce HCN from cyanogenic glycosides after mechanical stress or insect feeding (Freeman and Beattie 2008). Salicylic acid, jasmonic acid and abscisic acid, auxin and gibberellic acid are envisaged as defense responses to greenbug feeding (Park et al. 2006). Increased secondary metabolites also take part in shoot-fly resistance mechanism (Sharma et al. 2007). Biotic stress resistance in sorghum shoot-fly infestation is attributed in the form of tolerance, antixenosis (non-preference) and antibiosis which make them repellent to insects for feeding, shelter, egg laying and survival (Chamarthi et al. 2011; Mohammed et al. 2016). Biochemical factors like p-hydroxy benzaldehyde, luteolin, cinnamic acid and apigenin were connected with expression of shoot-fly resistance (Chamarthi et al. 2012). Further, polyphenol oxidase and peroxidase activities were upregulated in resistant genotypes which might have helped plants to tolerate infestation by shoot-fly (Padmaja et al. 2014). The pivotal role of total chlorophyll content, peroxidase and polyphenol activity in imparting resistance to shoot-fly was also noted (Singh et al. 2004b).

Shoot-fly resistance is associated with leaf glossiness and trichomes besides pigmentation and epicuticular wax (Dhillon et al. 2006; Kumar et al. 2014; Kiranmayee et al. 2015). The associated traits include reduced dead hearts incidence, improved leaf glossiness and reduced oviposition incidence (Anandan et al. 2009). Flies are reflected by the glossiness of leaves, larval movement on the surface of leaves is inhibited by dense trichomes, in turn acting as a physical barrier between the leaf and fly to prevent egg deposition (antixenosis). High seedling vigor leads to rapid growth of seedlings which hinder the larvae movement to the central leaf whorl thereby, reducing the frequency of dead hearts (Satish et al. 2009). Glumes of spikelets of gall midge resistant varieties are more tightly closed than those in susceptible varieties. A correlation between tannins and midge resistance was also noted (Santos and Carmo 1974; Sharma 1985, 1993). Spikelet morphology might be associated with antixenosis resistance mechanism (Henzell et al. 1994). A positive association between midge resistance and small glume size has been observed in sorghum (Jadhav and Jadhav 1978).

5.5 A Brief Account of Molecular Mapping of Resistance Genes and QTLs

Identification and mapping of major QTLs associated with disease resistance in sorghum pave way for the transfer of QTLs to varieties or parental lines to be used in breeding. Fine mapping of the QTLs would be revamped through the establishment of highly saturated genetic maps, restriction-site associated DNA

sequencing (RAD-seq) and single nucleotide polymorphisms (SNPs) (Zou et al. 2012). Six collinear independent component maps of sorghum were created and integrated into a single resource through the amalgamation of the component maps (Mace et al. 2009). A set of five genetic linkage maps based on RFLP markers were integrated to 10 linkage groups (Xu et al. 1994; Subudhi and Nguyen 2000). Thereafter, various research groups saturated the linkage maps with amplified fragment length polymorphism (AFLP) markers (Ramu et al. 2009). Over 323 RFLPs and 143 simple sequence repeats (SSRs) were utilized for the construction of high-density linkage map (Bhattramakki et al. 2000; Bowers et al. 2003). Later, AFLPs, SSRs and RFLPs markers constituting 2926 markers were further used to saturate the former map (Menz et al. 2002). EST-SSRs and candidate genes-based SSR markers have been used in constructing linkage maps (Ramu et al. 2009; Reddy et al. 2012; Zou et al. 2012).

5.5.1 Mapping Populations

Different research groups across the globe have developed specific bi-parental mapping populations that have paved the way for the identification and mapping of QTLs associated with resistance to several pests and diseases in sorghum. In general cross between two, sometimes more parents are involved in obtaining mapping populations. The parents selected and the mating design for the development of the mapping populations largely depend on the purpose of the study. F_2, F_2-derived F_3 (F_2:F_3), recombinant inbred lines (RILs), backcross inbred lines (BILs), near-isogenic lines (NILs), doubled haploids (DHs), multi-parent advanced generation intercross (MAGIC), chromosomal segment substitution lines (CSSLs), nested association mapping (NAM) population etc. are the several types of mapping populations being used for QTL mapping (Singh and Singh 2015). For biotic stress resistance BILs, RILs and populations derived from multi-parental lines such as MAGIC and NAMs are more specifically used (Arrones et al. 2020). Identification and mapping of important QTLs for pest and disease resistance in sorghum has enhanced with the use of genomic tools and mapping populations.

5.5.2 QTLs Mapped Using Different Mapping Populations

5.5.2.1 QTLs Associated with Diseases

The SNP markers linked to rust resistance have been identified and studied in detail (Upadhyaya et al. 2013b). The GWAS approach elucidated over 64 significant QTLs for rust including the earlier reported ones (Tao et al. 1998; Mohan et al. 2010; Upadhyaya et al. 2013b). Besides, a major QTL of the genome SC414-12E on chromosome 5 explained 20–39% of PVE in four environments (Kimball et al.

2019). Anthracnose resistance gene was identified by a closely linked RAPD marker *OPJ* 01_{1437} through bulk segregant analysis of derived RILs. QTLs for anthracnose on chromosome 9 found to be consistent across all the environments tested. The genomic regions reported earlier by Tao et al. (1998) and Klein et al. (2001) for rust and grain mold resistance, were found relevant to ergot disease resistance. Further, the presence of additive and non-additive gene actions for charcoal rot resistance has been noticed (Rao et al. 1993). Three traits, number of internodes crossed by the rot, crop lodging and length of infection conferred genetic basis to charcoal rot (Reddy et al. 2008). Haussmann et al. (2004) revealed five QTLs related to striga resistance in two RIL and were common across two mapping populations.

5.5.2.2 QTLs Associated with Insect Pests

Four major QTLs on chromosome 9 from PI 607900 resistant to greenbug biotype I were identified. Two major QTLs—*sbi09ii* and *sbi09iii* described up to 39.8 and 34.7 per cent variability for greenbug infestation (Punnuri et al. 2013). Three QTLs located on LG-A, LG-G and LG-J, respectively, explained 8.8%, 15% and 33.9%, phenotypic variation for gall midge resistance (Tao et al. 2003). Some shoot fly resistance (SFR) sources identified after evaluating the marker traits in sorghum germplasm have been exploited in breeding programs (Chamarthi et al. 2011; Kumar et al. 2014). Using crosses 296B (susceptible) × IS18551 (resistant) (Satish et al. 2012b) and cross 27B (susceptible) × IS2122 (resistant), SFR QTLs were mapped (Aruna et al. 2011). Four SFR QTLs were introgressed and the progenies harboring different combinations of major QTLs showed resistance which was evidenced by the fewer number of shoot flies (Abinaya et al. 2019). A set of 19 putative QTLs associated with resistance to shoot-fly including *qDH9.1* (dead heart) and *qEC9.1* (oviposition) explaining 15.03 and 18.89% phenotypic variance have been reported (Vikal et al. 2020). The genes producing allelochemicals, receptor kinases, and ubiquitin-proteasome degradation in the pathways as well as the candidate genes, like *cysteine protease* and cytochrome P450 were identified within the predicted QTL regions (Vikal et al. 2020).

5.6 Marker-Assisted Breeding for Biotic Stress Management in Sorghum

With the availability of large-scale sorghum genomic resources and use of DNA markers, breeding for desired agronomic traits and biotic stress resistance is becoming increasingly relevant. Affordable high-throughput genotyping coupled with throughput genome sequencing is rendering the use of molecular markers in germplasm diversity assessment, QTL mapping facilitating MAS. Resistance to

major pests and diseases is governed by multiple genes, which are seldom amenable to achieve an appreciable increase in resistance due to their strong influence by the environment (Tao et al. 2003; Mohammed et al. 2016). The molecular breeding approaches have been deployed in many crop species including sorghum to achieve delivery of results quickly with much greater precision (Kiranmayee et al. 2015).

5.6.1 Germplasm Characterization

Genetic resources as classified based on morphological characteristics, divided *Sorghum bicolour* into five major races: *bicolor*, *guinea*, *caudatum*, *kafir*, and *durra* and over ten possible hybrid groups (Harlan and de Wet 1972; Harlan and Stemler 1976; De Wet 1978). There are several 'wild' species and sub-species within *S. bicolor* and races within each subspecies (Snowden 1955). Sorghum has over 3475 accessions with over 242 mini core collection that include all five races and representation of geographic regions (Prasada Rao and Ramanatha Rao 1995; Upadhyaya et al. 2009; Dahlberg et al. 2012). Association mapping in mini-core collection for grain mold resistance using 14,739 SNP markers led to the identification of two linked marker to rust resistance (Upadhyaya et al. 2013b). Over 3367 accessions involving cultivated and wild relatives were genotyped using 41 SSR markers in which 78.3% of the SSR alleles were detected with a mean of 14.9 alleles per marker, comparable to the original allelic richness (Billot et al. 2013). Further, in an another attempt, a genome-wide association analysis using 268,289 SNPs, two loci linked to low seed deterioration and seedling emergence rate was identified (Cuevas et al. 2019).

5.6.2 Marker-Assisted Gene Introgression

Both the efficiency and precision of crop breeding can be achieved with the use of DNA markers. Molecular mapping of major QTLs for disease and pest resistance has facilitated the transfer of QTLs to the agronomically superior varieties in the shortest possible time using MAS strategies (Dormatey et al. 2020). Marker-assisted gene pyramiding (MAGP) can pyramid disease/pest resistance genes into single cultivar (Sanchez et al. 2000). Marker-assisted recurrent selection (MARS) is a strategy to accumulate favorable alleles i.e., multiple QTLs controlling resistance through genotypic selection and inter-crossing in repeated cycles of selection resulting in enhanced efficiency of recurrent selection and accelerated breeding (Ribaut et al. 2010; Dormatey et al. 2020). The process of stacking of genes/QTLs into a single elite cultivar background can now be efficiently performed using backcrossing or pedigree approaches with molecular markers thus eliminating the elaborate and costly process other ways (Kole 2006). Pyramiding of multiple genes/QTLs can lead to improved resistance (Werner et al. 2005).

Molecular breeding tools enable tracking the introgression of several *R*-genes from various sources into a single cultivar (Witcombe and Hash 2000). Three breeding strategies viz., stepwise transfer, simultaneous/synchronized, and convergent backcrossing are being employed for marker-assisted gene pyramiding (MAGP). MAS is needed to select pyramided resistance genes in the segregating progeny generation (Werner et al. 2005).

As many as five putative SFR QTLs for the component traits from IS18551 were introgressed through marker assisted back-cross breeding (MABCB) (Mehtre 2006; Jyothi et al. 2010). SFR QTLs were introgressed into 296B backgrounds and introgression lines (ILs) from 296B × IS18551 and BTx623 × IS18551 (Deshpande et al. 2010; Jyothi et al. 2010; Satish et al. 2012a) were field evaluated for the traits (Reddy et al. 2012). A total 136 BC_3 and 30 BC_4 plant progenies from crosses BC_2 X AKSV 13 R and BC3 X AKSV 13 R, respectively, were screened for the recovery of donor alleles in the elite background (Wagh et al. 2016). In addition, three QTLs associated with shoot-fly resistance were also introgressed into an elite cultivar ICSB 29004 and Parbhani Moti, all the derived introgression lines had higher shoot-fly resistance levels (Gorthy et al. 2017).

A gene associated with leaf blight resistance from G-118 was introgressed into the susceptible cultivar HC-136, using linked DNA marker (Mittal and Boora 2005). RILs with both resistant and susceptible reaction were screened individually with marker *Xtxp 309,* which produced amplification in 23 of the 26 resistant RILs, but no amplification in 25 susceptible RILs. This indicated the potential application of this marker in MAS for gene introgression (Mittal and Boora 2005). Further, eight putative QTLs were detected for resistance to sorghum downy mildew in a set of 50 inbred lines derived from the cross CML153 (susceptible) X CML226 (resistant) using 128 SSRs and 191 SNPs, introgression effort developed 33 resistant lines (Nagabhushan 2014). In a separate effort of using DNA markers for striga resistance, markers spanning through the QTLs conferring resistance to striga parasite were identified and the same markers were used in introgression to make headway towards developing resistant lines (Haussmann et al. 2004; Satish et al. 2012a; Mohamed et al. 2014; Yohannes et al. 2015). The QTLs of striga resistance in N13 were transferred to a farmer-preferred sorghum variety through MABCB using flanking SSR markers (Yohannes et al. 2016; Afolayan et al. 2019).

5.6.3 Limitations and Prospects of MAS and MABCB

MAS and MABCB approaches, even though adopted to breed resistance against biotic stresses, the complex quantitative traits have recorded marginal success as the QTLs for such traits partially explain the phenotype. The impact and application of MAS in plant breeding are still below the hypothetical possibilities. This could be attributed majorly due to the difficulty in identifying major QTLs with an adequate stable effect across environments and genetic backgrounds. The limited number of polymorphic markers in the breeding material and diverse mapping populations is

difficult to compare, assessment of QTL x environment interaction effect pose a complicate interpretation (Collard and Mackill 2008; Ribaut et al. 2010; Delannay et al. 2012). Further, genomic selection is a hope to solve this problem, where unmapped QTLs of small individual effects selected together by the plant breeders (Tuberosa 2012; Sakiyama et al. 2014). High throughput genotyping, phenotyping and more automatic ways would enhance the use of MAS in plant breeding (Gorthy et al. 2017).

5.7 Brief on Genetic Engineering for Resistance Traits

Conventional plant breeding methods used to develop cultivars resistant to multiple pests and diseases in sorghum are inadequate when the desirable genes are limited in the gene pool of cross-compatible species or when such genes restricted linkage-drag (Crews and Cattani 2018). Genetic transformation and genome editing enable incorporation of beneficial genes across genera into sorghum with limited genetic diversity in the desired traits (Liu et al. 2014). Insect pests with wide host range, evolving races of pathogens and low level of resistance in the cultivated sorghum germplasm have made molecular plant breeding approaches as highly desirable (Madhusudhana 2015). Insecticidal crystal proteins (CRY) from *Bacillus thuringiensis* (*Bt*) are very effective against the lepidopterans and dipterans. *Bt* and other genes including protease inhibitors, enzymes, secondary plant metabolites and plant lectins are being evaluated to reduce losses due to insect pests (Sharma et al. 2004; Visarada and Kishore 2007). Progress in sorghum transformation has been hindered by the challenges associated with recalcitrance to genetic transformation (Jeoung et al. 2002; Girijashankar et al. 2007). Different gene transfer methods are being used in sorghum so far, which include, Agrobacterium-mediated indirect gene transfer; electroporation and particle bombardment (Ahmed et al. 2018). *Agrobacterium*-mediated transformation is simple and precise in the integration of the transgene. However, monocotyledons such as sorghum are less responsive to agrobacterium infection. *PR* genes for *fusarium stalk rot* disease resistance were introduced into sorghum genotypes through *Agrobacterium*-mediated gene transfer. Despite the basic research, sorghum is still one of the most recalcitrant crops to transformation and regeneration (Raghuwanshi and Birch 2010).

5.7.1 Transgenic Resistance to Fungal Diseases

Sorghum is highly vulnerable to multiple fungal diseases causing decreased grain quality and yield loss. Genes encoding fungal cell wall hydrolyzing enzymes such as glucanases, chitinases and chitosanases are potential transgene candidates for developing fungal disease resistance in sorghum (Muthukrishnan et al. 2001). Chitinases and chitosanases degrade the components of fungal cell walls i.e., chitin

and chitosan and lyse the fungi. The first fungal resistance gene -*rice chitinase* (*G11*) was introduced into the sorghum inbred 'Tx430' along with *bar* gene and a plasmid DNA into the calli of immature zygotic embryos (Zhu et al. 1998). Thaumatin-like proteins (TLPs) are one more class of pathogenesis-related (PR) proteins that have shown antifungal activity and have been used as transgenes for enhancing fungal resistance (Mahdavi et al. 2012). Two *PR* genes viz., *rice chitinase* (*G11*) and *tlp* (Thaumatin-like protein) were introduced into three different sorghum inbred lines (Jeoung et al. 2002). Chitinase gene, *OschiII* fused with CaMV 35S promoter prospected for stalk rot resistance (Muthukrishnan et al. 2001). Transformation of sorghum with *tlp* gene along with green fluorescent protein (*gfp*) under the maize *ubi1* promoter exhibited enhanced resistance to fungal diseases. Expression of *gfp* was highly correlated with the expression of *tlp*, which was further confirmed by western blot analysis (Gao et al. 2005a). *In planta* and *ex planta* anthracnose infection assays revealed transgenic line KOSA-1 to be more resistant to anthracnose in comparison to its non-transgenic wild type AT412 (Ayoo 2008; Anami et al. 2016).

5.7.2 Transgenic Resistance to Insect Pests

Insecticidal crystal proteins are potential candidates for insect resistance in many crop plants (Roh et al. 2007; Jain et al. 2016). Many *Bt* toxin genes have been transferred into sorghum to attain resistance against insect pests. Stem borer is an important pest in sorghum. Sorghum genotype BT × 623 was transformed with the *cry1Ac* gene under the control of a wound-inducible promoter from the maize protease inhibitor gene (*mpiC1*) via particle bombardment of shoot apices. Transgenic lines showed up to 60% reduction in leaf damage, 40% larval mortality and 36% weight loss in the survived larvae of stem borer. However, *Bt* protein accumulation under the inducible promoter was very low at 1–8 ng/g of fresh tissue, which led to partial resistance (Girijashankar et al. 2005). Sorghum varieties 115, ICS21B and 5–27 were transformed with the *cry1Ab* gene and the transgenic lines showed high resistance levels to pink rice borer (Liu et al. 2015). Sweet sorghum varieties 'BABUSH' and 'MN-3025' transformed with *cry1Ah* using *Agrobacterium*-mediated transformation have shown high insect-resistance to Asian corn borer (*Ostrinia furnacalis*) (Zhao et al. 2011). Enhanced accumulation of the *Bt* protein in leaves by 30 to 50-fold (35–500 ng/g fresh leaf) by expression of *cry1Aa* and *cry1B* genes under the influence of maize *ubiquitin-1* promoter was reported during the susceptible plant growth period. Leaf consumption by the stem borer in the transgenic sorghum leaves was significantly lower (20–30%) compared to their feeding on non-transgenic lines (77–80%). Transgenic lines also showed a significant reduction in the leaf damage (55–78%) over their non-transgenic controls. Where, the larval mortality was appreciably high (60–90%) in transgenic lines as compared to (14–24%) non-transgenic control (Visarada et al. 2014). Higher expression of *Bt* protein is crucial for achieving superior insect control, which may

be achieved by placing the *Bt* genes under suitable promoters such as maize ubiquitin.

Transgenic glyphosate-resistant crops overexpressing 5-enolpyruvylshikimate-3-phosphate synthase (*cp4 epsps*) gene accelerated widespread use of glyphosate (Duke and Powles 2008) in controlling recalcitrant weeds such as Johnsongrass. RNAi is one of the most successful strategy in target trait improvement apart from its role in identifying gene function by silencing different pathogens/pests as well as plant genes (Stach and Good 2011; Banerjee et al. 2017; Majumdar et al. 2017; Zhang et al. 2017a). Virus-induced gene silencing (VIGS) efficiency in sorghum was significantly enhanced with an antisense strand of a gene in *Brome mosaic virus* (BMV) (Singh et al. 2018) (Table 5.1).

5.8 Brief Account on Bioinformatics as a Tool for Biotic Stress Resistance Breeding

Advances in disciplines that are contributing to the generation of genomic resources and data analytics have made a significant impact for structural and functional genomics of sorghum in the past decade. The next-generation sequencing platforms have greatly facilitated advanced assessment of sorghum genome, variety of transcriptome profiling attempts with deep insights into the structural organization of the genome; gene prediction; gene annotation and response of genes in variable biotic and abiotic conditions. The developed bioinformatics tools assist in filtering of data sets of various types, the correct interpretation of specific outcomes of *in silico* analytics of the data and its targeted views to elucidate the candidate gene sets that have potential applications in the breeding of sorghum for various biotic stress resistances (López de Maturana et al. 2019). The use of publicly available genomic data sets has helped the researchers to annotate key genes for their target traits in sorghum. Since the genome of sorghum is sequenced and high throughput datasets are publicly available, the bioinformatics pipelines can effectively identify putative candidate genes for various biotic stress responses. These potential candidate genes would be useful to develop the markers for the genotyping of breeding populations for the identification of a superior lines (de Oliveira et al. 2018). Databases in sorghum include; **SorGSD:** Web-portal with a comprehensive database of genomic variation across all types of cultivated and wild sorghums (Luo et al. 2016) and **SorghumFDB** covering transcription factors, regulators, protein kinases, ubiquitin, monolignol biosynthesis-related enzymes, carbohydrate-active enzymes, cytochrome P450, organelle-genes and R-genes. It acts as a genome browser for comprehensive coverage of gene annotations, miRNA information, gene loci conversions, orthologues in model plants like arabidopsis, maize and rice (Tian et al. 2016).

Through genomics, identified genomic regions could be incorporated to impart resistance to sorghum midge (Yazawa et al. 2013). Transcriptomic analysis of Cv.

Table 5.1 Transgenes conferring insect and disease resistance in sorghum

Transgene	Source	Target organism	Transformation method	Reference
Insect resistance				
CryIAc	*Bacillus thuringiensis*	Stem borer	Biolistic	Girijashankar et al. (2005)
cry1Ab	*Bacillus thuringiensis*	Pink rice borer	Agrobacterium	Liu et al. (2015)
cry1Ah	*Bacillus thuringiensis*	Asian corn borer	Agrobacterium	Zhao et al. (2011)
cry1Aa and *cry1B*	*Bacillus thuringiensis*	Stem borer	Biolistic and Agrobacterium	Visarada et al. (2014)
Disease resistance				
chitinase (*G11*)	*Oryza sativa*	Fungi	Biolistic	Zhu et al. (1998)
chitinase (*chiII*)	*Oryza sativa*	*Fusarium thapsinum*	Biolistic	Muthukrishnan et al. (2001)
chitinase	*Oryza sativa*	Fungi	Agrobacterium	Arulselvi et al. (2010)
chitinase (*HarChit*)	*Trichoderma harzianum*	*Colletotrichum sublineolum*	Biolistic	Ayoo (2008)
chitosanase (*HarCho*)	*Trichoderma harzianum*	*Colletotrichum sublineolum*	Biolistic	Ayoo (2008)
Thaumatin-like protein	–	Fungi	Agrobacterium	Gao et al. (2005b)

SIL-05 and *Bipolaris sorghicola* led to the identification of genes in host-pathogen interaction (Mizuno et al. 2012). The genes encoding hyphae related proteins and enzymes involved in plant cell wall degradation elucidated from pathogen transcriptome data sets besides genes encoding WRKY, receptors of LLR domain and class III peroxidase are relevant for functional genomics analysis in sorghum (Yazawa et al. 2013). Molecular interpretation of charcoal rot defense mechanism was unraveled by expression profiling of genes in resistant and susceptible cultivars (Sharma et al. 2014b). A major QTL on linkage group 5 in the cross of BTx623/SC748-5 for anthracnose resistance analyzed by sequencing genomic DNA of SC748-5 and compared to BTx623 genome sequence (Burrell et al. 2015; Poloni and Schirawski 2016). Transcriptional changes and network analysis were decoded in a resistant and a susceptible genotype of sorghum to sugarcane aphids. A suite of abundantly expressed genes were recovered across genotypes and nucleotide-binding-site -leucine-rich repeat (NBS-LRR) and disease resistance genes were recognized (Kiani and Szczepaniec 2018; Tetreault et al. 2019). Correlation-based network analyses vis-a-vis metabolic pathway analysis revealed that multi-component defense response characterized by a functional defense-related molecular cues are involved in pathogen invasion (Tugizimana et al. 2019). Metabolomics of white sorghum-isolated *Burkholderia andropogonis* interaction revealed the alterations in the levels of phytohormones that marked the onset of defense in sorghum (Mareya et al. 2019, 2020).

5.9 Recent Concepts and Strategies Developed

5.9.1 Genome Editing

A multitude of pathogens and insect pests comprising viruses, bacteria, fungi, insects and even parasitic plants affect sorghum globally with significant yield losses which in turn influence the food supply (Mushtaq et al. 2019; Yin and Qiu 2019). The strategy to control various diseases and pests involve widespread use of hazardous pesticides, which can be directly or indirectly deleterious to nature (Tyagi et al. 2020). Developing disease and insect pest resistant crops through various breeding approaches are sustainable and ecofriendly. In addition to the conventional transgenic approach, recent genome editing for biotic stress has greater potential in breeding programs. The biotic stress resistance being complex in nature is governed by several genes each with small effect. Some of these key genes could be potentially edited to create new alleles that can produce a larger desirable effect, thus re-orienting the process of breeding. More recently, genome editing technologies have emerged and evolved to enable rapid and precise manipulation of specific DNA sequences for developing biotic stress-resistant germplasm (Shi et al. 2017; Gao 2018; Yin et al. 2018). Genome editing involves engineered nucleases containing a non-specific nuclease domain fused with a

sequence-specific DNA binding domain, which can cleave the targeted gene precisely that can be repaired through specific genetics approaches. Zinc finger nucleases (ZFN), the first-generation editing technology are the chimeric proteins that consist of Fok1 cleavage domain and non-specific DNA cleavage domain (Fiaz et al. 2019; Ansari et al. 2020). Transcription activator-like effectors nucleases (TALENs) discovered in *Xanthomonas* consists of the amino acid repeats in the central DNA binding domain that recognizes one nucleotide in the target sequence. The repeat variable di-residue (RVD) which is located at 12 and 13 positions determines the specificity of TALEN. Once $TALEN_S$ are translocated to the nucleus, they bind to the target DNA strand in an opposite orientation. The FokI gets dimerized and cleaves at the spacer region resulting in double-strand breaks (DSB) in the target region (Jaganathan et al. 2018; Li et al. 2018). CRISPR/Cas System: clustered regularly interspaced short palindromic repeats (CRISPR), is a prokaryotic system observed for the first time in *Escherichia coli* that contains short repeated sequences separated by spacers with unique sequences (Ishino et al. 1987; Rath et al. 2015). A large recognition (REC) lobe determines the Cas9-specific function, whereas the small nuclease (NUC) incorporates two nuclease domains, RuvC and HNH, and a protospacer adjacent motif (PAM)-interacting domain (PI). The Cas9/single guide RNA (Cas9-sgRNA) complex probes a DNA sequence for rigorous protospacer adjacent motif (PAMs) using the Watson–Crick pairing principle (Song et al. 2016).

5.9.1.1 Genome Editing in Sorghum

The type II CRISPR/Cas, Cas9-sgRNA system was employed in sorghum as well as in arabidopsis and tobacco. *Agrobacterium tumefaciens* mediated method for green fluorescent protein-coding gene transfer was used and mutagenic effects of the Cas9/sgRNA system in immature sorghum embryos were observed (Jiang et al. 2013). CRISPR/Cas9 system has been investigated by targeted editing of cinnamyl alcohol dehydrogenase (CAD) and phytoene desaturase. Genotype TX430 was edited successfully with effective biolistic bombardment (Li et al. 2018). CRISPR/Cas9 approach was applied to edit the *chlorophyll*-a *oxidase* (CAO) gene in sorghum protoplasts (Meng et al. 2020). Fourteen protoplasts showed precise editing in target gene region which could be a possible model for precise editing study in sorghum for improvement concerning agronomically important traits. Although, till date, there is no study reported concerning the use of genome editing for biotic stress resistance in sorghum, the use of the conventional transgenic approach for improving resistance is reported by a number of studies. Transformation of sorghum with *rice chitinase* for resistance against stalk rot, expression of the *cry1Ac* gene against sorghum spotted stem borer, *chitinase & chitosanase* genes against anthracnose, expression of Bt *cry1Ah* gene (Zhu et al. 1998; Muthukrishnan et al. 2001; Girijashankar et al. 2005; Akosambo-Ayoo et al. 2011; Liu and Godwin 2012) envisages that the model transgenic studies in sorghum will pave the path for precise breeding and may facilitate the development of product germplasm governing biotic resistance through the editing of same genes.

5.9.2 *Nanotechnology*

Nanotechnology is currently being explored for agricultural applications, including, finding solutions for yield loss due to insect pests and diseases (Balaure et al. 2017; Sinha et al. 2017). Current pest management relies on the use of chemicals with all their side effects and environmental concern (Ghormade et al. 2011; Worrall et al. 2018). The nanoparticles, besides other ways, aid enhanced solubility of pesticides, increased shelf life and these protect plants from target pest (Hayles et al. 2017). Nanoparticles of Ag, Cu and Zn could be utilized as a potential method for suppressing diseases in crop plants (Elmer and White 2018; Malandrakis et al. 2019; Vanti et al. 2019). The application of nanotechnology with the use of emerged nanomaterials may heighten the sustainable productivity through effective insect pest and disease management (Giannousi et al. 2013; Imada et al. 2016).

5.10 Conclusion and Future Perspectives

Sorghum being an important cereal crop for low endowed and climatically challenging situations of the world, to achieve the sustainability for food and fodder in such regions, the development of biotic stress-resistant cultivars coupled with drought stress tolerance is crucial. As such, yield stability and grain quality are severely affected by various biotic stresses including insect pests, diseases and parasitic weeds, which hamper this crop at all stages including storage. Biotic stresses pose daunting challenges to the realization of its yield potential, and development of resistant cultivars through host plant resistance is most opted, as a great deal of germplasm diversity exists and serves as a source of resistant genes. However, on practical scale, attempts to increase the production of sorghum with the introduction of new high yielding varieties and hybrids have been largely unsuccessful because of their susceptibility to various biotic stresses (Kishore 2001; Kiranmayee et al. 2015). The limited number of resistant accessions and their overall phenotype may constrain the development of new varieties. The wide host range for many of the insect pests and low level of resistance in the cultivated germplasm necessities the use of wild relatives and new parental lines having the potential genes for various biotic stress resistance to mitigate the negative effect. Advent of molecular tools has great scope in accelerating the process of breeding, and in turn resulting the enhanced resistance in the form of horizontal as well as vertical resistance. Besides, the conventional process of breeding is highly labour-intensive and time-consuming (Sharma et al. 2005) and the resistance being highly complex, it is essential to deploy molecular markers linked to QTLs or any gene and these QTLs/genes are to be introgressed to increase the efficiency of conventional breeding (Kumar et al. 2014; Kiranmayee et al. 2015).

Fine mapping of the mapped QTL regions and significant maker trait associations through GWAS is needed. Further validation of QTLs provides great promise

for employing MAS in sorghum improvement. Genes responsible for resistance such as leaf blade glossiness and trichome density and other associated genomic regions need to be cloned and their introgression and expression level studies should be made to enhance the resistance related genetic architecture. Combinatorial approaches with conventional plant resistance along with novel genes such as *Bt* gene for increased resistance is highly desirable. An integrated synergistic system involving plant breeding and genomics research using advanced molecular tools such as high-throughput sequencing and large-scale genotyping technologies followed with MAS is a way forward to improve sorghum biotic stress resistance. Advances in new genomic tools such as genome sequencing, DNA microarrays, RNA-sequencing, real-time PCR, protein expression profiling, metabolomics strategies and bioinformatics allow more in-depth knowledge about the genetics of host defense and host-plant resistance mechanisms to biotic stresses (Kumar et al. 2014). In addition, sequencing of sorghum whole genome and its availability on publically available data sets of genomic resources of various types is expected to accelerate for rapid trait discovery and introgression (McCormick et al. 2018).

Transcription factors are candidates of choice to alter the agronomically relevant traits and to boost the resistance to biotic stresses and several transcription factors families, such as WRKY, NAC, MYB, DREB, and bZIP, in response to biotic stresses have been identified and characterized in sorghum. As such transcription factor responses to biotic stresses are highly complex with larger effects and complex cross-talk between different signal transduction pathways (Baillo et al. 2019). The findings from previous reports indicate the potential application of TF genes to enhance stress resistance in important crops, however, extensive studies for understanding the mechanisms of these TFs are required. Studies involving combinatorial approaches of TFs and small RNAs are expected to unravel the pathways and key genes for biotic stress resistance, such genes will be of key in utilizing the upcoming opportunities such as genome editing and genomics assisted breeding. The availability of complete genome sequences in sorghum and breakthroughs in sequencing technology have facilitated the identification and characterization of TFs (McCormick et al. 2018).

In future, it is crucial to pyramid multiple genes to achieve multiple resistant varieties through MABCB. So far, no QTL has been found to regulate multiple pest/disease resistance in sorghum (Romana et al. 2018). Hence, future research efforts should focus on identifying genetic loci responsible for multiple disease resistance, new sources of resistance, characterization of resistance genes, and dissecting the network of resistance gene regulation (Dormatey et al. 2020). Genomic selection has great promise in exploiting unmapped QTLs of small individual effects at the whole plant level which could be deployed in plant breeding endeavors, this approach expected to be relevant in sorghum as it has great genetic diversity (Yano and Tuberosa 2009). The newly developed genomic approaches would rapidly accelerate applications to many different research areas ranging from marker discovery; genetic diversity; and linkage/association mapping

to the genomic selection, physical mapping, gene discovery and genomic-assisted breeding to improve biotic stress resistance in sorghum.

References

Abera M, Alemayehu G (2012) Evaluation of improved and local/landrace/sorghum varieties for covered kernel smut. Arch Phytopathol Plant Protect 45:717–723

Abinaya M, Kumaravadivel N, Varanavasiappan S, Kavithamani D (2019) Screening the genotypes of sorghum [*Sorghum bicolor* (L.) Moench] BC_1F_3 generation of the cross CO (S) 28 × IS18551 for shoot-fly [*Atherigona soccata* (Rond.)] resistance. Elect J Plant Breed 10:1133–1139

Afolayan G, Aladele S, Deshpande S, Oduoye O, Nwosu D, Michael C, Blay E, Danquah E (2019) Marker-assisted foreground selection for identification of striga resistant backcross lines in *Sorghum bicolor*. Covenant J Physic Life Sci 7:29–36

Afolayan G, Aladele S, Deshpande S, Kolawole A, Nwosu D, Michael C, Blay E, Danquah E (2020) Genetic variation for *Striga hermonthica* resistance and yield among sorghum accessions in Nigeria. J Agric Sci 12:192–202

Ahmed RI, Ding A, Xie M, Kong Y (2018) Progress in optimization of Agrobacterium-mediated transformation in sorghum (*Sorghum bicolor*). Intl J Mol Sci 19:2983

Akosambo-Ayoo L, Bader M, Loerz H, Becker D (2011) Transgenic sorghum (*Sorghum bicolor* L. Moench) developed by transformation with chitinase and chitosanase genes from Trichoderma harzianum expresses tolerance to anthracnose. Afr J Biotechnol 10:3659–3670

Anami SE, Zhang Y-M, Zhang L-X, Zhu L, Jing H-C (2016) Sorghum genetic transformation: current status and future target traits. Biotechnol Major Cereals, pp 48

Ananda GK, Myrans H, Norton SL, Gleadow R, Furtado A, Henry RJ (2020) Wild sorghum as a promising resource for crop improvement. Front Plant Sci 11:1108

Anandan A, Huliraj H, Veerabadhiran P (2009) Analysis of resistance mechanism to *Atherigona soccata* in crosses of sorghum. Plant Breed 128:443–450

Andersen EJ, Ali S, Byamukama E, Yen Y, Nepal MP (2018) Disease resistance mechanisms in plants. Genes 9:339

Ansari WA, Chandanshive SU, Bhatt V, Nadaf AB, Vats S, Katara JL, Sonah H, Deshmukh R (2020) Genome editing in cereals: approaches, applications and challenges. Intl J Mol Sci 21:4040

Arrones A, Vilanova S, Plazas M, Mangino G, Pascual L, Díez MJ, Prohens J, Gramazio P (2020) The dawn of the age of multi-parent MAGIC populations in plant breeding: novel powerful next-generation resources for genetic analysis and selection of recombinant elite material. Biology 9:229

Arulselvi I, Michael P, Umamaheswari S, Krishanaveni S (2010) Agrobacterium mediated transformation of *Sorghum bicolor* for disease resistance. Intl J Pharma Bio Sci 1:272–281

Aruna C, Cheruku D (2019) Genetic improvement of grain sorghum. In: Aruna C, Visarada KBRS, Bhat BV, Tonapi VA (eds) Breeding sorghum for diverse end uses, pp 157–173. Woodhead Publishing, Cambridge, United Kingdom

Aruna C, Bhagwat V, Madhusudhana R, Sharma V, Hussain T, Ghorade R, Khandalkar H, Audilakshmi S, Seetharama N (2011) Identification and validation of genomic regions that affect shoot-fly resistance in sorghum [*Sorghum bicolor* (L.) Moench]. Theor Appl Genet 122:1617–1630

Ashok Kumar A, Reddy BV, Ramaiah B, Sharma R (2011a) Heterosis in white-grained grain mold resistant sorghum hybrids. J SAT Agric Res 9:6

Ashok Kumar A, Reddy BVS, Sharma HC, Hash CT, Srinivasa Rao P, Ramaiah B, Reddy PS (2011b) Recent advances in sorghum genetic enhancement research at ICRISAT. Amer J Plant Sci 2:589–600

Audilakshmi S, Das I, Ghorade R, Mane P, Kamatar M, Narayana Y, Seetharama N (2011) Genetic improvement of sorghum for grain mould resistance: I. Performance of sorghum recombinant inbred lines for grain mould reactions across environments. Crop Protect 30:753–758

Ayoo LMK (2008) Genetic transformation of Kenyan sorghum (*Sorghum bicolor* (L.) Moench) with anti-fungal genes and response to *Colletotrichum sublineolum* infection. Staats-und Universitätsbibliothek Hamburg Carl von Ossietzky

Baerson SR, Dayan FE, Rimando AM, Nanayakkara ND, Liu C-J, Schröder J, Fishbein M, Pan Z, Kagan IA, Pratt LH (2008) A functional genomics investigation of allelochemical biosynthesis in *Sorghum bicolor* root hairs. J Biol Chem 283:3231–3247

Baillo EH, Kimotho RN, Zhang Z, Xu P (2019) Transcription factors associated with abiotic and biotic stress tolerance and their potential for crops improvement. Genes 10:771

Balaure PC, Gudovan D, Gudovan I (2017) Nanopesticides: a new paradigm in crop protection. In: New pesticides and soil sensors, Academic Press. Elsevier, pp 129–192

Bandara AY, Weerasooriya DK, Tesso TT, Little CR (2019) Stalk rot resistant sorghum genotypes are resilient to pathogen-mediated photosystem II quantum yield retardation. Crop Protect 124: p104852

Bandyopadhyay R, Butler DR, Chandrashekar A, Reddy RK, Navi SS (2000) Biology, epidemiology, and management of sorghum grain mold. Technical and institutional options for sorghum grain mold management: proceedings of an international consultation. ICRISAT, Pattancheru, Andhra Pradesh, India, pp 18–19

Banerjee S, Banerjee A, Gill SS, Gupta OP, Dahuja A, Jain PK, Sirohi A (2017) RNA interference: a novel source of resistance to combat plant parasitic nematodes. Front Plant Sci 8:834

Bhattramakki D, Dong J, Chhabra AK, Hart GE (2000) An integrated SSR and RFLP linkage map of *Sorghum bicolor* (L.) Moench. Genome 43:988–1002

Billot C, Ramu P, Bouchet S, Chantereau J, Deu M, Gardes L, Noyer J-L, Rami J-F, Rivallan R, Li Y (2013) Massive sorghum collection genotyped with SSR markers to enhance use of global genetic resources. PLoS ONE 8:59714

Boozaya-Angoon D, Starks K, Weibel D, Teetes G (1984) Inheritance of resistance in sorghum, *Sorghum bicolor*, to the sorghum midge, *Contarinia sorghicola* (Diptera: Cecidomyiidae). Environ Entomol 13:1531–1534

Bora D, Saharia D, Hussain S (1994) Biology of yellow stem borer, *Scirpophagain certulas* (Wlk.). Crop Res Hissar 8:366–370

Bowden J, Neve R (1953) Sorghum midge and resistant varieties in the Gold Coast. Nature 172:551

Bowers JE, Abbey C, Anderson S, Chang C, Draye X, Hoppe AH, Jessup R, Lemke C, Lennington J, Li Z (2003) A high-density genetic recombination map of sequence-tagged sites for sorghum, as a framework for comparative structural and evolutionary genomics of tropical grains and grasses. Genetics 165:367–386

Bowling RD, Brewer MJ, Kerns DL, Gordy J, Seiter N, Elliott NE, Buntin GD, Way M, Royer T, Biles S (2016) Sugarcane aphid (Hemiptera: Aphididae): a new pest on sorghum in North America. J Integr Pest Manag 7(1):1–13

Bramel-Cox PJ, Cox TS (1988) Use of wild sorghums in sorghum improvement. In: Wilkinson D (ed) Proc 43rd Annu Corn & Sorghum Industry Res Conf Amer Seed Trade Assoc, Washington D.C, pp 13–26

Bueso FJ, Waniska RD, Rooney WL, Bejosano FP (2000) Activity of antifungal proteins against mold in sorghum caryopses in the field. J Agric Food Chem 48:810–816

Burrell AM, Sharma A, Patil NY, Collins SD, Anderson WF, Rooney WL, Klein PE (2015) Sequencing of an anthracnose-resistant sorghum genotype and mapping of a major QTL reveal strong candidate genes for anthracnose resistance. Crop Sci 55:790–799

Calvino M, Messing J (2012) Sweet sorghum as a model system for bioenergy crops. Curr Opin Biotechnol 23:323–329

Chamarthi S, Sharma H, Sahrawat K, Narasu L, Dhillon M (2011) Physico-chemical mechanisms of resistance to shoot-fly, *Atherigona soccata* in sorghum, *Sorghum bicolor*. J Appl Entomol 135:446–455

Chamarthi SK, Vijay PM, Sharma HC, Narasu LM (2012) Constitutive and inducible resistance to *Atherigona soccata* (Diptera: Muscidae) in *Sorghum bicolor*. J Econ Entomol 105:1069–1076

Collard BC, Mackill DJ (2008) Marker-assisted selection: An approach for precision plant breeding in the twenty-first century. Phil Trans Roy Soc B: Biol Sci 363:557–572

Cota LV, Souza AGC, Costa RV, Silva DD, Lanza FE, Aguiar FM, Figueiredo JEF (2017) Quantification of yield losses caused by leaf anthracnose on sorghum in Brazil. J Phytopathol 165:479–485

Cox T, House L, Frey KJ (1984) Potential of wild germplasm for increasing yield of grain sorghum. Euphytica 33:673–684

Crews TE, Cattani DJ (2018) Strategies, advances, and challenges in breeding perennial grain crops. Sustainability 10:1–7

Cuevas HE, Prom LK, Cruet-Burgos CM (2019) Genome-wide association mapping of anthracnose (*Colletotrichum sublineolum*) resistance in NPGS Ethiopian sorghum germplasm. G3: Genes Genomes Genet 9:2879–2885

Cui Y, Magill J, Frederiksen R, Magill C (1996) Chalcone synthase and phenylalanine ammonia-lyase mRNA levels following exposure of sorghum seedlings to three fungal pathogens. Physiol Mol Plant Pathol 49:187–199

Dahlberg J, Berenji J, Sikora V, Latković D (2012) Assessing sorghum [*Sorghum bicolor* (L) Moench] germplasm for new traits: food, fuels and unique uses. Maydica 56:85–92

Das IK (2019) Advances in sorghum disease resistance. Breeding sorghum for diverse end uses. Woodhead Publishing, Elsevier, pp 313–324

Das IK, Aruna C, Tonapi V (2020) Sorghum grain mold. ICAR-Indian Institute of Millets Research, Hyderabad, India

De Oliveira AA, Pastina MM, da Costa Parrella RA, Noda RW, Simeone MLF, Schaffert RE, de Magalhães JV, Damasceno CMB, Margarido GRA (2018) Genomic prediction applied to high-biomass sorghum for bioenergy production. Mol Breed 38:49

De Wet J (1978) Special paper: systematics and evolution of sorghum sect. Sorghum (Gramineae). Amer J Bot 65:477–484

Delannay X, McLaren G, Ribaut J-M (2012) Fostering molecular breeding in developing countries. Mol Breed 29:857–873

Deshpande S, Jyothi T, Folkertsma R, Sharma H, Bhasker Raj A, Yousuf A, Hash C (2010) Marker-assisted backcrossing of shoot-fly resistance in sorghum [*Sorghum bicolor* (L.) Moench]. In: Abstracts, national symposium on genomics and crop improvement: relevance and reservations, pp 25–27

Dhillon M, Sharma H, Reddy B, Singh R, Naresh J (2006) Inheritance of resistance to sorghum shoot-fly, *Atherigona soccata*. Crop Sci 46:1377–1383

Diarisso NY, Diourté M, Pendleton B (2005) Use of local plants to control sorghum insect pests in the field. Intl Sorghum Millets News 146:60–62

Dicko MH, Gruppen H, Barro C, Traoré AS, van Berkel WJ, Voragen AG (2005) Impact of phenolic compounds and related enzymes in sorghum varieties for resistance and susceptibility to biotic and abiotic stresses. J Chem Ecol 31:2671–2688

Dormatey R, Sun C, Ali K, Coulter JA, Bi Z, Bai J (2020) Gene pyramiding for sustainable crop improvement against biotic and abiotic stresses. Agronomy 10:1255

Duke SO, Powles SB (2008) Glyphosate: a once-in-a-century herbicide. Pest Manag Sci (Formerly Pesticide Science) 64:319–325

Dweikat I (2005) A diploid, interspecific, fertile hybrid from cultivated sorghum, *Sorghum bicolor*, and the common Johnson grass weed *Sorghum halepense*. Mol Breed 16:93–101

Ejeta G, Gressel J (2007) The Striga scourge in Africa: a growing pandemic. Integrating new technologies for Striga control—towards ending the Witch-Hunt'. World Scientific, Singapore, pp 3–16

Elmer W, White JC (2018) The future of nanotechnology in plant pathology. Annu Rev Phytopathol 56:111–133

Esele J (1995) Foliar and head diseases of sorghum. Afr Crop Sci J 3:185–189

Fiaz S, Ahmad S, Noor MA, Wang X, Younas A, Riaz A, Riaz A, Ali F (2019) Applications of the CRISPR/Cas9 system for rice grain quality improvement: perspectives and opportunities. Intl J Mol Sci 20:888

Franzmann B (1988) Components of resistance to sorghum midge in grain sorghum. In: McWhirter KS, Downes RW, Read BJ (eds) Proceedings of 9th Australian plant breeding conference, agriculture research institute. Private Mail Bag, Wagga-Wagga, New South Wales, Australia, pp 277–278

Franzmann B, Vaschina B (1989) Sorghum midge oviposition in preflowering and flowering panicles. Agric Sci 119–129

Freeman BC, Beattie GA (2008) An overview of plant defenses against pathogens and herbivores. Plant Health Instructor. https://doi.org/10.1094/phi-i-2008-0226-01

Gao C (2018) The future of CRISPR technologies in agriculture. Nat Rev Mol Cell Biol 19:275–276

Gao Z, Jayaraj J, Muthukrishnan S, Claflin L, Liang G (2005a) Efficient genetic transformation of sorghum using a visual screening marker. Genome 48:321–333

Gao Z, Xie X, Ling Y, Muthukrishnan S, Liang GH (2005b) Agrobacterium tumefaciens-mediated sorghum transformation using a mannose selection system. Plant Biotechnol J 3:591–599

Ghormade V, Deshpande MV, Paknikar KM (2011) Perspectives for nano-biotechnology enabled protection and nutrition of plants. Biotechnol Adv 29:792–803

Ghosh T, Biswas M, Guin C, Roy P (2018) A review on characterization, therapeutic approaches and pathogenesis of *Macrophomina phaseolina*. Plant Cell Biotechnol Mol Biol 19:72–84

Giannousi K, Avramidis I, Dendrinou-Samara C (2013) Synthesis, characterization and evaluation of copper-based nanoparticles as agrochemicals against *Phytophthora infestans*. RSC Adv 3:21743–21752

Girijashankar V, Sharma HC, Sharma KK, Swathisree V, Prasad LS, Bhat B, Royer M, San Secundo B, Narasu ML, Altosaar I (2005) Development of transgenic sorghum for insect resistance against the spotted stem borer (*Chilo partellus*). Plant Cell Rep 24:513–522

Girijashankar V, Sharma K, Balakrishna P, Seetharama N (2007) Direct somatic embryogenesis and organogenesis pathway of plant regeneration can seldom occur simultaneously within the same explant of sorghum. J SAT Agric Res 3:1–3

Gorthy S, Narasu L, Gaddameedi A, Sharma HC, Kotla A, Deshpande SP, Are AK (2017) Introgression of shoot-fly (*Atherigona soccata* L. Moench) resistance QTLs into elite post-rainy season sorghum varieties using marker-assisted backcrossing (MABC). Front Plant Sci 8:1494

Gressel J (2010) Needs for and environmental risks from transgenic crops in the developing world. New Biotechnol 27:522–527

Hariprasanna K, Rakshit S (2016) Economic importance of sorghum. In: Rakshit S, Wang Y-H (eds) The sorghum genome. Springer, Cham, Switzerland, pp 1–25

Harlan JR, de Wet JM (1972) A simplified classification of cultivated sorghum 1. Crop Sci 12:172–176

Harlan JR, Stemler A (1976) The races of sorghum in Africa. Origins African Plant Domestication 465:478

Harris HB, Johnson BJ, Dobson JW, Luttrell ES (1964) Evaluation of anthracnose on grain sorghum 1. Crop Sci 4:460–462

Haussmann B, Hess D, Omanya G, Folkertsma R, Reddy B, Kayentao M, Welz H, Geiger H (2004) Genomic regions influencing resistance to the parasitic weed *Striga hermonthica* in two recombinant inbred populations of sorghum. Theor Appl Genet 109:1005–1016

Hayles J, Johnson L, Worthley C, Losic D (2017) Nanopesticides: a review of current research and perspectives. New pesticides and soil sensors. Elsevier, pp 193–225

Henzell RG, Franzmann BA, Brengman RL (1994) Sorghum midge resistance research in Australia. Intl Sorghum Millets Newsl 35:41–47

Hodges R, Hall A, Jayaraj K, Jaiswal P, Potdar N, Yogand B (2000) Quality changes in farm-stored sorghum grain grown in the wet or dry season in southern India-a technical and social study. ACIAR proceedings, pp 333–344

Hooker AL (1985) Corn and sorghum rusts. In: Roelfs AP, Bushnell WR (eds) The Cereal Rusts. Vol. II. Diseases, Distribution, Epidemiology, and Control. Academic Press, Orlando, FL, pp 207–236

Hulvova H, Galuszka P, Frébortová J, Frébort I (2013) Parasitic fungus *Claviceps* as a source for biotechnological production of ergot alkaloids. Biotechnol Adv 31:79–89

Hussain B, War AR, Sharma HC (2014) Jasmonic and salicylic acid-induced resistance in sorghum against the stem borer *Chilo partellus*. Phytoparasitica 42:99–108

Imada K, Sakai S, Kajihara H, Tanaka S, Ito S (2016) Magnesium oxide nanoparticles induce systemic resistance in tomato against bacterial wilt disease. Plant Pathol 65:551–560

Ishino Y, Shinagawa H, Makino K, Amemura M, Nakata A (1987) Nucleotide sequence of the *iap* gene, responsible for alkaline phosphatase isozyme conversion in *Escherichia coli*, and identification of the gene product. J Bacteriol 169:5429–5433

Jadhav R, Jadhav L (1978) Studies on preliminary screening of some sorghum hybrid and varieties against earhead midge (*Contarinia sorghicola* Coq.). J Maharashtra Agric Univ 3:187–188

Jaganathan D, Ramasamy K, Sellamuthu G, Jayabalan S, Venkataraman G (2018) CRISPR for crop improvement: an update review. Front Plant Sci 9:985

Jain D, Saharan V, Pareek S (2016) Current status of *Bacillus thuringiensis*: insecticidal crystal proteins and transgenic crops. In: Al-Khayri JM, Jain M, Johnson DV (eds) Advances in plant breeding strategies: agronomic, abiotic and biotic stress traits. Springer International Publishing, New York, pp 657–698

Jeoung J, Krishnaveni S, Muthukrishnan S, Trick H, Liang G (2002) Optimization of sorghum transformation parameters using genes for green fluorescent protein and β-glucuronidase as visual markers. Hereditas 137:20–28

Jiang W, Zhou H, Bi H, Fromm M, Yang B, Weeks DP (2013) Demonstration of CRISPR/Cas9/sgRNA-mediated targeted gene modification in Arabidopsis, tobacco, sorghum and rice. Nucleic Acids Res 41:e188–e188

Jotwani M, Marwaha K, Srivastava K, Young W (1970) Seasonal incidence of shoot-fly *(Atherigona varia soccata* Rond) in jowar hybrids at Delhi. Indian J Entomol 32:7–15

Jotwani MG, Knndu GG, Kishore P, Srivastava KP, Sukhani TR, Singh SP (1979) Evaluation of some high yielding sorghum derivatives for resistance to stem borer, *Chilo partellus* (Swinhoe). Indian J Entomol 41:1–4

Jyothi T, Fölkertsma R, Sharma H, Bhasker Raj A, Anwar Y, Hash C (2010) P-128: marker-assisted transfer of shoot-fly resistance in *Sorghum bicolor*. In: National symposium on genomics and crop improvement: relevance and reservations institute of biotechnology. Acharya NG Ranga Agricultural University, Rajendranagar, Hyderabad, India, pp 25–27

Kamala V, Singh S, Bramel P, Rao DM (2002) Sources of resistance to downy mildew in wild and weedy sorghums. Crop Sci 42:1357–1360

Kamala V, Sharma H, Manohar Rao D, Varaprasad K, Bramel P (2009) Wild relatives of sorghum as sources of resistance to sorghum shoot-fly, *Atherigona soccata*. Plant Breed 128:137–142

Kamala V, Sivaraj N, Pandravada S, Rameash K, Sharma H, Sarath Babu B (2016) Potential of wild relatives in sorghum improvement through molecular approaches. In: Conference on national priorities in plant health management February 4–5, 2016, Tirupati, Andhra Pradesh, India, pp 124–125

Khan ZR, Midega CA, Hassanali A, Pickett JA, Wadhams LJ, Wanjoya A (2006) Management of witchweed, *Striga hermonthica*, and stem borers in sorghum, *Sorghum bicolor*, through intercropping with green leaf desmodium, *Desmodium intortum*. Intl J of Pest Manag 52:297–302

Kiani M, Szczepaniec A (2018) Effects of sugarcane aphid herbivory on transcriptional responses of resistant and susceptible sorghum. BMC Genom 19:1–18

Kimball J, Cui Y, Chen D, Brown P, Rooney WL, Stacey G, Balint-Kurti PJ (2019) Identification of QTL for target leaf spot resistance in *Sorghum bicolor* and investigation of relationships between disease resistance and variation in the MAMP response. Sci Rep 9:1–9

Kiranmayee K, Hash CT, Deshpande SP, Varaprasad K, Kishor P (2015) Biotechnological approaches to evolve sorghum (*Sorghum bicolor* (L.) Moench) for drought stress tolerance and shoot-fly resistance. Curr Trends Biotechnol Pharm 9:281–292

Kishore P (2001) Resistance to shoot-fly, *Atherigona soccata* Rondani and stem borer, *Chilo partellus* (Swinhoe) in new germplasm of sorghum. J Entomol Res 25:273–282

Klein R, Rodriguez-Herrera R, Schlueter J, Klein P, Yu Z, Rooney W (2001) Identification of genomic regions that affect grain-mould incidence and other traits of agronomic importance in sorghum. Theor Appl Genet 102:307–319

Klittich CJ, Leslie JF, Nelson PE, Marasas WF (1997) *Fusarium thapsinum* (*Gibberella thapsina*): a new species in section Liseola from sorghum. Mycologia 89:643–652

Kole C (2006) Genome mapping and molecular breeding in plants. Vol on Cereals and Millets. Springer, Berlin, New York

Komolong B, Chakraborty S, Ryley M, Yates D (2003) Ovary colonization by Claviceps africana is related to ergot resistance in male-sterile sorghum lines. Plant Pathol 52:620–627

Kumar VK, Sharma H, Reddy KD (2006) Antibiosis mechanism of resistance to spotted stem borer, *Chilo partellus* in sorghum, *Sorghum bicolor*. Crop Protec 25:66–72

Kumar AA, Gorthy S, Sharma HC, Huang Y, Sharma R, Reddy BV (2014) Understanding genetic control of biotic stress resistance in sorghum for applied breeding. In: Wang Y-H, Upadhyay HD, Kole C (eds) Genetics, genomics and breeding of sorghum. CRC Press, USA, pp 198–225

Kumari A, Goyal M, Kumar R, Sohu R (2020) Morpho-physiological and biochemical attributes influence intra-genotypic preference of shoot-fly [*Atherigona soccata* (Rondani)] among sorghum genotypes. Protoplasma 1–16

Li J, Shi Y, Veeranampalayam-Sivakumar A-N, Schachtman DP (2018) Elucidating sorghum biomass, nitrogen and chlorophyll contents with spectral and morphological traits derived from unmanned aircraft system. Front Plant Sci 9:1406

Liu G, Godwin ID (2012) Highly efficient sorghum transformation. Plant Cell Rep 31:999–1007

Liu G, Campbell BC, Godwin ID (2014) Sorghum genetic transformation by particle bombardment. Methods Mol Biol 1099:219–234

Liu G, Gilding EK, Godwin ID (2015) A robust tissue culture system for sorghum [*Sorghum bicolor* (L.) Moench]. S Afr J Bot 98:157–160

López de Maturana E, Alonso L, Alarcón P, Martín-Antoniano IA, Pineda S, Piorno L, Calle ML, Malats N (2019) Challenges in the integration of omics and non-omics data. Genes 10:238

Lu J, Ehsani R, Shi Y, de Castro AI, Wang S (2018) Detection of multi-tomato leaf diseases (late blight, target and bacterial spots) in different stages by using a spectral-based sensor. Sci Rep 8:1–11

Luo H, Zhao W, Wang Y, Xia Y, Wu X, Zhang L, Tang B, Zhu J, Fang L, Du Z (2016) SorGSD: a sorghum genome SNP database. Biotechnol Biofuels 9:6

Luthra Y, Gandhi S, Joshi U, Arora S (1988) Total phenols and their oxidative enzymes in sorghum leaves resistant and susceptible to *Ramulisporasorghicola* Harris. Acta Phytopathol Entomol Hung 23:393–399

M Perez-de-Castro A, Vilanova S, Cañizares J, Pascual L, M Blanca J, J Diez M, Prohens J, Picó B (2012) Application of genomic tools in plant breeding. Curr Genom 13:179–195

Mace ES, Rami J-F, Bouchet S, Klein PE, Klein RR, Kilian A, Wenzl P, Xia L, Halloran K, Jordan DR (2009) A consensus genetic map of sorghum that integrates multiple component maps and high-throughput Diversity Array Technology (DArT) markers. BMC Plant Biol 9:13

Madhusudhana R (2015) Linkage mapping. In: Madhusudhana R, Rajendrakumar P, Patil JV (eds) Sorghum molecular breeding, pp 47–70. Springer, New Delhi

Mahdavi F, Sariah M, Maziah M (2012) Expression of rice thaumatin-like protein gene in transgenic banana plants enhances resistance to Fusarium wilt. Appl Biochem Biotechnol 166:1008–1019

Majumdar R, Rajasekaran K, Cary JW (2017) RNA interference (RNAi) as a potential tool for control of mycotoxin contamination in crop plants: concepts and considerations. Front Plant Sci 8:200

Malandrakis AA, Kavroulakis N, Chrysikopoulos CV (2019) Use of copper, silver and zinc nanoparticles against foliar and soil-borne plant pathogens. Sci Total Environ 670:292–299

Mareya CR, Tugizimana F, Piater LA, Madala NE, Steenkamp PA, Dubery IA (2019) Untargeted metabolomics reveal defensome-related metabolic reprogramming in *Sorghum bicolor* against infection by *Burkholderiaandropogonis*. Metab 9:8

Mareya CR, Tugizimana F, Di Lorenzo F, Silipo A, Piater LA, Molinaro A, Dubery IA (2020) Adaptive defence-related changes in the metabolome of *Sorghum bicolor* cells in response to lipopolysaccharides of the pathogen *Burkholderiaandropogonis*. Sci Rep 10:1–17

Mbuvi DA, Masiga CW, Kuria EK, Masanga J, Wamalwa M, Mohamed A, Odeny D, Hamza N, Timko MP, Runo SM (2017) Novel sources of witchweed (striga) resistance from wild sorghum accessions. Front Plant Sci 8:116

McCormick RF, Truong SK, Sreedasyam A, Jenkins J, Shu S, Sims D, Kennedy M, Amirebrahimi M, Weers BD, McKinley B (2018) The *Sorghum bicolor* reference genome: improved assembly, gene annotations, a transcriptome atlas, and signatures of genome organization. Plant J 93:338–354

Mehtre SP (2006) Genetic diversity analysis, QTL mapping and marker-assisted selection for shoot fly resistance in sorghum [*Sorghum bicolor* (L,) Moench]. Ph.D dissertation, Marathwada Agricultural University, Parbhani, Maharashtra, India

Meng R, Wang C, Wang L, Liu Y, Zhan Q, Zheng J, Li J (2020) An efficient sorghum protoplast assay for transient gene expression and gene editing by CRISPR/Cas9. Peer J 8:

Mengistu G, Shimelis H, Laing M, Lule D (2019) Assessment of sorghum genetic resources of Ethiopia for anthracnose (*Colletotrichum sublineolum* Henn.) resistance and agronomic traits. J Phytopathol 167:667–678

Menkir A, Ejeta G, Butler L, Melakeberhan A (1996) Physical and chemical kernel properties associated with resistance to grain mold in sorghum. Cereal Chem 73:613–617

Menz M, Klein R, Mullet J, Obert J, Unruh N, Klein P (2002) A high-density genetic map of *Sorghum bicolor* (L.) Moench based on 2926 AFLP, RFLP and SSR markers. Plant Mol Biol 48:483–499

Miller magazine (2020) World milling and pulses technologies refereed journal, 132. https://www.millermagazine.com/english/archive

Mittal M, Boora KS (2005) Molecular tagging of gene conferring leaf blight resistance using microsatellites in sorghum [*Sorghum bicolo*r (L.) Moench]. Indian J Exp Biol 43(5):462–466

Mizuno H, Kawahigashi H, Kawahara Y, Kanamori H, Ogata J, Minami H, Itoh T, Matsumoto T (2012) Global transcriptome analysis reveals distinct expression among duplicated genes during sorghum-*Bipolarissorghicola* interaction. BMC Plant Biol 12:121

Mohamed A, Ali R, Elhassan O, Suliman E, Mugoya C, Masiga CW, Elhusien A, Hash CT (2014) First products of DNA marker-assisted selection in sorghum released for cultivation by farmers in sub-saharan Africa. J Plant Sci Mol Breed 3:1–10

Mohammed R, Are AK, Munghate RS, Bhavanasi R, Polavarapu KKB, Sharma HC (2016) Inheritance of resistance to sorghum shoot-fly, *Atherigona soccata*in sorghum, *Sorghum bicolor* (L.) Moench. Front Plant Sci 7:543

Mohan SM, Madhusudhana R, Mathur K, Chakravarthi D, Rathore S, Reddy RN, Satish K, Srinivas G, Mani NS, Seetharama N (2010) Identification of quantitative trait loci associated with resistance to foliar diseases in sorghum [*Sorghum bicolor* (L.) Moench]. Euphytica 176:199–211

Mughogho L, Pande S (1983) Charcoal rot of sorghum. In: Mughogho LK (ed) Sorghum root and stalk rots—a critical review: proceedings of the consultative group discussion on research

needs and strategies for control of sorghum root and stalk rot diseases, 27 Nov–2 Dec 1983, Bellagio, Italy. ICRISAT Patancheru, A.P. 502324, India, pp 11–24

Mundia CW, Secchi S, Akamani K, Wang G (2019) A regional comparison of factors affecting global sorghum production: the case of North America, Asia and Africa's Sahel. Sustainability 11:2135

Mushtaq M, Sakina A, Wani SH, Shikari AB, Tripathi P, Zaid A, Galla A, Abdelrahman M, Sharma M, Singh AK (2019) Harnessing genome editing techniques to engineer disease resistance in plants. Front Plant Sci 10:550

Muthukrishnan S, Jeoung J, Liang G, Krishnaveni S (2001) Transgenic sorghum plants constitutively expressing a rice chitinase gene show improved resistance to stalk rot [*Sorghum bicolor* (L.) Moench]. J Genet Breed 55:151–158

Nagabhushan (2014) QTL Identification and Marker assisted selection for sorghum downy mildew resistance in maize (*Zea mays* L.). Doctoral dissertation, University of Agricultural Sciences GKVK, Bangalore, India

Nagarajan K, Perumal K, Shanmugan N (1957) The red hairy caterpillar and its field scale control. Madras Agric J 4:150–153

Navi SS, Bandyopadhyay R, Reddy R, Thakur R, Yang X-B (2005) Effects of wetness duration and grain development stages on sorghum grain mold infection. Plant Dis 89:872–878

Ngugi H, King S, Holt J, Julian A (2001) Simultaneous temporal progress of sorghum anthracnose and leaf blight in crop mixtures with disparate patterns. Phytopathol 91:720–729

Padmaja P, Shwetha B, Swetha G, Patil J (2014) Oxidative enzyme changes in sorghum infested by shoot-fly. J Insect Sci 14(1):2–6

Parh D, Jordan D, Aitken E, Mace E, Jun-Ai P, McIntyre C, Godwin I (2008) QTL analysis of ergot resistance in sorghum. Theor Appl Genet 117:369–382

Park S-J, Huang Y, Ayoubi P (2006) Identification of expression profiles of sorghum genes in response to greenbug phloem-feeding using cDNA subtraction and microarray analysis. Planta 223:932–947

Parker C (2009) Observations on the current status of orobanche and striga problems worldwide. Pest Manag Sci 65:453–459

Passlow T (1965) Bionomics of sorghum midge [*Contarinia sorghicola* (Coq.)] in Queensland, with particular reference to diapause. Queensland J Agric Anim Sci 22:149–167

Paterson AH, Bowers JE, Bruggmann R, Dubchak I, Grimwood J, Gundlach H, Haberer G, Hellsten U, Mitros T, Poliakov A (2009) The *Sorghum bicolor* genome and the diversification of grasses. Nature 457:551–556

Patil S (2011) Genome-wide QTL mapping for post-flowering drought tolerance and validation of charcoal rot resistance QTLs NILs of sorghum. PhD Thesis. Univ Agric Sci, Dharwad, Karnataka, India

Paudyal S, Armstrong JS, Giles KL, Payton ME, Opit GP, Limaje A (2019) Categories of resistance to sugarcane aphid (Hemiptera: Aphididae) among sorghum genotypes. J Econ Entomol 112:1932–1940

Pazoutova S, Frederickson D (2005) Genetic diversity of *Claviceps africana* on sorghum and Hyparrhenia. Plant Pathol 54:749–763

Perumal R, Tomar SS, Bandara A, Maduraimuthu D, Tesso TT, Prasad PV, Upadhyaya HD, Little CR (2020) Variation in stalk rot resistance and physiological traits of sorghum genotypes in the field under high temperature. J Gen Plant Pathol 86:350–359

Poloni A, Schirawski J (2016) Host specificity in *Sporisorium reilianum* is determined by distinct mechanisms in maize and sorghum. Mol Plant Pathol 17:741–754

Prasada Rao K, Ramanatha Rao V (1995) The use of characterization data in developing a core collection of sorghum. Core Collections of Plant Genetic Resources IPGRI. John Wiley and Sons, New York, pp 109–115

Prom L, Perumal R, Erattaimuthu S, Little C, No E, Erpelding J, Rooney W, Odvody G, Magill C (2012) Genetic diversity and pathotype determination of *Colletotrichum sublineolum* isolates causing anthracnose in sorghum. Eur J Plant Pathol 133:671–685

Punnuri S, Huang Y, Steets J, Wu Y (2013) Developing new markers and QTL mapping for greenbug resistance in sorghum [*Sorghum bicolor* (L.) Moench]. Euphytica 191:191–203

Raghuwanshi A, Birch RG (2010) Genetic transformation of sweet sorghum. Plant Cell Rep 29:997–1005

Ramu P, Kassahun B, Senthilvel S, Kumar CA, Jayashree B, Folkertsma R, Reddy LA, Kuruvinashetti M, Haussmann B, Hash CT (2009) Exploiting rice–sorghum synteny for targeted development of EST-SSRs to enrich the sorghum genetic linkage map. Theor Appl Genet 119:1193–1204

Rao G, Patil S, Anahosur K (1993) Genetics of charcoal rot resistance in Rabi sorghum. Karnataka J Agric Sci 6:113–116

Rashid Z, Singh PK, Vemuri H, Zaidi PH, Prasanna BM, Nair SK (2018) Genome-wide association study in Asia-adapted tropical maize reveals novel and explored genomic regions for sorghum downy mildew resistance. Sci Rep 8:1–12

Rath D, Amlinger L, Rath A, Lundgren M (2015) The CRISPR-Cas immune system: biology, mechanisms and applications. Biochimie 117:119–128

Reddy KS (1988) Assessment of on-farm yield losses in sorghum due to insect pests. Int J Trop Insect Sci 9:679–685

Reddy BV, Bandyopadhyay R, Ramaiah B, Ortiz R (2000) Breeding grain mold resistant sorghum cultivars. Technical and institutional options for sorghum grain mold management. In: Proceedings of an international consultation. ICRISAT, Patancheru, India, pp 195–224

Reddy B, Ramesh S, Reddy P (2004) Sorghum breeding research at ICRISAT-goals, strategies, methods and accomplishments. Intl Sorghum Millets Newsl 45:5–12

Reddy PS, Rao V, Reddy BV, Ramesh S, Thakur R (2005) Grain mold resistance in advanced sorghum B-lines. Intl Sorghum Millets Newsl 46:29–32

Reddy PS, Fakrudin B, Punnuri S, Arun S, Kuruvinashetti M, Das I, Seetharama N (2008) Molecular mapping of genomic regions harboring QTLs for stalk rot resistance in sorghum. Euphytica 159:191–198

Reddy RN, Madhusudhana R, Mohan SM, Chakravarthi D, Seetharama N (2012) Characterization, development and mapping of Unigene-derived microsatellite markers in sorghum [*Sorghum bicolor* (L.) Moench]. Mol Breed 29:543–564

Reed J, Ramundo B, Claflin L, Tuinstra M (2002) Analysis of resistance to ergot in sorghum and potential alternate hosts. Crop Sci 42:1135–1138

Reynolds MP, Quilligan E, Aggarwal PK, Bansal KC, Cavalieri AJ, Chapman SC, Chapotin SM, Datta SK, Duveiller E, Gill KS (2016) An integrated approach to maintaining cereal productivity under climate change. Glob Food Secur 8:9–18

Ribaut J, De Vicente M, Delannay X (2010) Molecular breeding in developing countries: challenges and perspectives. Curr Opin Plant Biol 13:213–218

Riyazaddin M, Kavi Kishor PB, Ashok Kumar A, Reddy BV, Munghate RS, Sharma HC (2015) Mechanisms and diversity of resistance to sorghum shoot-fly, *Atherigona soccata*. Plant Breed 134:423–436

Rodriguez-Herrera R, Rooney W, Rosenow D, Frederiksen R (2000) Inheritance of grain mold resistance in grain sorghum without a pigmented testa. Crop Sci 40:1573–1578

Rodríguez-Herrera R, Waniska RD, Rooney WL (1999) Antifungal proteins and grain mold resistance in sorghum with non-pigmented testa. J Agric Food Chem 47:4802–4806

Roh JY, Choi JY, Li MS, Jin BR, Je YH (2007) *Bacillus thuringiensis* as a specific, safe, and effective tool for insect pest control. J Microbiol Biotechnol 17:547

Romana KK, Chander G, Deshpande S, Gupta R (2018) Genomic-assisted enhancement in stress tolerance for productivity improvement in sorghum. In: Biotechnologies of Crop Improvement, vol 3, pp 265–288. Springer, Cham, Switzerland

Sakiyama NS, Ramos HCC, Caixeta ET, Pereira MG (2014) Plant breeding with marker-assisted selection in Brazil. Crop Breed Appl Biotechnol 14:54–60

Salama EA, Kumaravadivel N, Mohankumar S, Muthukrishnan N (2020) Correlation study of traits associated with shoot-fly resistance in recombinant inbred lines (RILs) population of sorghum [*Sorghum bicolor* (L.) Moench]. Electron J Plant Breed 11:110–115

Sanchez A, Brar D, Huang N, Li Z, Khush G (2000) Sequence tagged site marker-assisted selection for three bacterial blight resistance genes in rice. Crop Sci 40:792–797

Santos Jd, Carmo Cd (1974) Evaluation of resistance to *Contarinia sorghicola* by sorghum lines from the Cameroon, Africa collection. Ceara, Brazil. Sorghum Newsl 17:10–11

Satish K, Srinivas G, Madhusudhana R, Padmaja P, Reddy RN, Mohan SM, Seetharama N (2009) Identification of quantitative trait loci for resistance to shoot-fly in sorghum [*Sorghum bicolor* (L.) Moench]. Theor Appl Genet 119:1425–1439

Satish K, Gutema Z, Grenier C, Rich PJ, Ejeta G (2012a) Molecular tagging and validation of microsatellite markers linked to the low germination stimulant gene (lgs) for Striga resistance in sorghum [*Sorghum bicolor* (L.) Moench]. Theor Appl Genet 124:989–1003

Satish K, Madhusudhana R, Padmaja P, Seetharama N, Patil J (2012b) Development, genetic mapping of candidate gene-based markers and their significant association with the shoot-fly resistance quantitative trait loci in sorghum [*Sorghum bicolor* (L.) Moench]. Mol Breed 30:1573–1591

Savary S, Ficke A, Aubertot J-N, Hollier C (2012) Crop losses due to diseases and their implications for global food production losses and food security. Food Secur 4:519–537

Seifers DL, Perumal R, Little CR (2012) New sources of resistance in sorghum (*Sorghum bicolor*) germplasm are effective against a diverse array of *Potyvirus* spp. Plant Dis 96:1775–1779

Sharma H (1985) Strategies for pest control in sorghum in India. Intl J Pest Manag 31:167–185

Sharma H (1993) Host-plant resistance to insects in sorghum and its role in integrated pest management. Crop Protec 12:11–34

Sharma HC, Teetes GL (1995) Yield loss assessment and economic injury levels for panicle-feeding insects of sorghum. In: Nwanze KF, Youm O (eds) Panicle insect pests of sorghum and pearl millet: proceedings of an international consultative workshop, 4–7 Oct 1993, ICRISAT Sahelian Center, Niamey, Niger: (In En. Summaries in En, Fr, Es.), ICRISAT, Patancheru, Andhra Pradesh, India, pp 320

Sharma H, Vidyasagar P (1994) Antixenosis component of resistance to sorghum midge, *Contarinia sorghicola* Coq. in *Sorghum bicolor* (L.) Moench. Ann Appl Biol 124:495–507

Sharma HC, Taneja SL, Rao NK, Rao KP (2003) Evaluation of sorghum germplasm for resistance to insect pests. Information Bulletin No. 63. International Crops Research Institute for the Semi-Arid Tropics, Patancheru, Andhra Pradesh, India, pp 177

Sharma AD, Thakur M, Rana M, Singh K (2004) Effect of plant growth hormones and abiotic stresses on germination, growth and phosphatase activities in *Sorghum bicolor* (L.) Moench seeds. Afr J Biotechnol 3:308–312

Sharma H, Reddy BV, Dhillon M, Venkateswaran K, Singh B, Pampapathy G, Folkertsma R, Hash C, Sharma K (2005) Host-plant resistance to insects in sorghum: present status and need for future research. Intl Sorghum Millets Newsl 46:36–43

Sharma H, Dhillon M, Pampapathy G (2006) Multiple-resistance to sorghum shoot-fly, spotted stemborer and sugarcane aphid in sorghum. Intl J Trop Insect Sci 26:239–245

Sharma H, Dhillon M, Pampapathy G, Reddy B (2007) Inheritance of resistance to spotted stem borer, *Chilo partellus*, in sorghum, *Sorghum bicolor*. Euphytica 156:117–128

Sharma R, Rao V, Upadhyaya H, Reddy VG, Thakur R (2010) Resistance to grain mold and downy mildew in a mini-core collection of sorghum germplasm. Plant Dis 94:439–444

Sharma R, Upadhyaya H, Manjunatha S, Rao V, Thakur R (2012) Resistance to foliar diseases in a mini-core collection of sorghum germplasm. Plant Dis 96:1629–1633

Sharma HC, Bhagwat VR, Daware DG, Pawar DB, Munghate RS, Sharma SP, Kumar AA, Reddy BV, Prabhakar KB, Ambekar SS (2014a) Identification of sorghum genotypes with resistance to the sugarcane aphid (*Melanaphis sacchari)* under natural and artificial infestation. Plant Breed 133:36–44

Sharma I, Kumari N, Sharma V (2014b) Defense gene expression in *Sorghum bicolor* against *Macrophomina phaseolina* in leaves and roots of susceptible and resistant cultivars. J Plant Interact 9:315–323

Sharma HC, Bhagwat VR, Munghate RS, Sharma SP, Daware DG, Pawar DB, Kumar AA, Reddy BV, Prabhakar KB, Mehtre SP (2015) Stability of resistance to sorghum shoot-fly, *Atherigona soccata*. Field Crops Res 178:34–41

Shayanowako AT, Laing M, Shimelis H, Mwadzingeni L (2018) Resistance breeding and biocontrol of *Striga asiatica* (L.) Kuntze in maize: a review. Acta Agric Scand B 68:110–120

Shi TQ, Liu GN, Ji RY, Shi K, Song P, Ren LJ, Huang H, Ji XJ (2017) CRISPR/Cas9-based genome editing of the filamentous fungi: the state of the art. Appl Microbiol Biotechnol 101:7435–7443

Singh S, Bandyopadhyay R (2000) Grain mold. Compendium of sorghum diseases, pp 38–40

Singh BD, Singh AK (2015) Marker-assisted plant breeding: principles and practices. Springer, New Delhi, India

Singh B, Padmaja P, Seetharama N (2004a) Biology and management of the sugarcane aphid, *Melanaphis sacchari* (Zehntner) (Homoptera: Aphididae) in sorghum: a review. Crop Protec 23:739–755

Singh B, Padmaja P, Seetharama N (2004b) Stability of biochemical constituents and their relationships with resistance to shoot-fly, *Atherigona soccata* (Rondani) in seedling sorghum. Euphytica 136:279–289

Singh DK, Lee HK, Dweikat I, Mysore KS (2018) An efficient and improved method for virus-induced gene silencing in sorghum. BMC Plant Biol 18:123

Sinha K, Ghosh J, Sil PC (2017) New pesticides: a cutting-edge view of contributions from nanotechnology for the development of sustainable agricultural pest control. In: New pesticides and soil sensors, Elsevier, pp 47–79

Snowden J (1955) The wild fodder sorghums of the section Eu-sorghum. Biol J Linn Soc Lond 55:191–260

Song G, Jia M, Chen K, Kong X, Khattak B, Xie C, Li A, Mao L (2016) CRISPR/Cas9: a powerful tool for crop genome editing. Crop J 4:75–82

Stach JE, Good L (2011) Synthetic RNA silencing in bacteria–antimicrobial discovery and resistance breaking. Front Microbiol 2:185

Stenhouse JW, Bandyopadhyay R, Singh SD, Subramanian V (1997) Breeding for grain-mould resistance in sorghum. In: Proc Int Conf Genetic Improvement of Sorghum and Pearl Millet, 22–27 Sept 1996, Lubbock, Texas, pp 326–336

Subbarayudu B (2002) Shoot bug incidence on sorghum in South India. Intl Sorghum Millets Newsl 43:56–57

Subudhi PK, Nguyen HT (2000) Linkage group alignment of sorghum RFLP maps using a RIL mapping population. Genome 43:240–249

Tao Y, Jordan D, Henzell R, McIntyre C (1998) Identification of genomic regions for rust resistance in sorghum. Euphytica 103:287–292

Tao Y, Hardy A, Drenth J, Henzell R, Franzmann B, Jordan D, Butler D, McIntyre C (2003) Identifications of two different mechanisms for sorghum midge resistance through QTL mapping. Theor Appl Genet 107:116–122

Te-Beest D, Kirkpatrick T, Cartwright R (2004) Common and important diseases of grain sorghum. In: Espinoza L, Kelley J (eds) Grain sorghum production handbook. Univ Ark Coop Ext, USA MP297

Teetes GL, Becerra M, Peterson GC (1986) Sorghum midge (Diptera: Cecidomyiidae) management with resistant sorghum and insecticide. J Econ Entomol 79:1091–1095

Tenkouano A, Miller F, Frederiksen R, Rosenow D (1993) Genetics of non-senescence and charcoal rot resistance in sorghum. Theor Appl Genet 85:644–648

Tesso TT, Perumal R, Little CR, Adeyanju A, Radwan GL, Prom LK, Magill CW (2012) Sorghum pathology and biotechnology-a fungal disease perspective: Part II. Anthracnose, stalk rot, and downy mildew. Eur J Plant Sci Biotechnol 6:31–44

Tetreault HM, Grover S, Scully ED, Gries T, Palmer NA, Sarath G, Louis J, Sattler SE (2019) Global responses of resistant and susceptible sorghum (*Sorghum bicolor*) to sugarcane aphid (*Melanaphis sacchari*). Front Plant Sci 10:145

Tian T, You Q, Zhang L, Yi X, Yan H, Xu W, Su Z (2016) SorghumFDB: sorghum functional genomics database with multidimensional network analysis. Database 2016: baw099

Tsedaley B, Adugna G, Lemessa F (2016) Distribution and importance of sorghum anthracnose (*Colletotrichum sublineolum*) in southwestern and western Ethiopia. Plant Pathol J 15:75–85

Tuberosa R (2012) Phenotyping for drought tolerance of crops in the genomics era. Front Physiol 3:347

Tugizimana F, Djami-Tchatchou AT, Fahrmann JF, Steenkamp PA, Piater LA, Dubery IA (2019) Time-resolved decoding of metabolic signatures of in-vitro growth of the hemibiotrophic pathogen *Colletotrichum sublineolum*. Sci Rep 9:1–12

Tuinstra MR, Soumana S, Al-Khatib K, Kapran I, Toure A, van Ast A, Bastiaans L, Ochanda NW, Salami I, Kayentao M (2009) Efficacy of herbicide seed treatments for controlling striga infestation of sorghum. Crop Sci 49:923–929

Tyagi D, Wang H, Huang W, Hu L, Tang Y, Guo Z, Ouyang Z, Zhang H (2020) Recent advances in two-dimensional-material-based sensing technology toward health and environmental monitoring applications. Nanoscale 12:3535–3559

Upadhyaya H, Ortiz R (2001) A mini core subset for capturing diversity and promoting utilization of chickpea genetic resources in crop improvement. Theor Appl Genet 102:1292–1298

Upadhyaya H, Pundir R, Dwivedi S, Gowda C, Reddy VG, Singh S (2009) Developing a mini core collection of sorghum for diversified utilization of germplasm. Crop Sci 49:1769–1780

Upadhyaya HD, Wang Y-H, Sharma R, Sharma S (2013a) Identification of genetic markers linked to anthracnose resistance in sorghum using association analysis. Theor Appl Genet 126:1649–1657

Upadhyaya HD, Wang Y-H, Sharma R, Sharma S (2013b) SNP markers linked to leaf rust and grain mold resistance in sorghum. Mol Breed 32:451–462

Van Rensburg N, Hamburg HV (1975) Grain sorghum pests: an integrated control approach. Entomological society of Southern Africa: proceedings of the first congress of the entomological society of Southern Africa, 1974, Stellenbosch. Entomol Soc South Afr, pp 151–162

Vanti GL, Nargund VB, Vanarchi R, Kurjogi M, Mulla SI, Tubaki S, Patil RR (2019) Synthesis of *Gossypium hirsutum*-derived silver nanoparticles and their antibacterial efficacy against plant pathogens. Appl Organomet Chem 33:e4630

Venkateswaran K (2003) Diversity analysis and identification of sources of resistance to downy mildew, shoot fly and stem borer in wild sorghums. PhD thesis. Department of Genetics, Osmania University, Hyderabad, Andhra Pradesh, India

Venkateswaran K, Elangovan M, Sivaraj N (2019) Chapter 2: origin, domestication and diffusion of *Sorghum bicolor*. In: Aruna C, Visarada KBRS, Bhat BV, Tonapi VA (eds) Breeding Sorghum for diverse end uses. Woodhead Publishing Series in Food Science, Technology and Nutrition, Elsevier, pp 15–31

Vikal Y, Kaur A, Jindal J, Kaur K, Pathak D, Garg T, Singh A, Singh P, Yadav I (2020) Identification of genomic regions associated with shoot-fly resistance in maize and their syntenic relationships in the sorghum genome. PLoSOne 15:e0234335

Visarada K, Kishore NS (2007) Improvement of Sorghum through transgenic technology. Information system for biotechnology news report (Virginia tech, US), Rajendranagar, India, pp 1–3

Visarada K, Padmaja P, Saikishore N, Pashupatinath E, Royer M, Seetharama N, Patil J (2014) Production and evaluation of transgenic sorghum for resistance to stem borer. Vitro Cell Dev Biol Plant 50:176–189

Wagh AD, Gahukar SJ, Gangurde SS (2016) Marker assisted selection for shoot-fly tolerance in sorghum, *Sorghum bicolor*. Biosci Biotechnol Res Commun 9:179–188

Wang ML, Zhu C, Barkley NA, Chen Z, Erpelding JE, Murray SC, Tuinstra MR, Tesso T, Pederson GA, Yu J (2009) Genetic diversity and population structure analysis of accessions in the US historic sweet sorghum collection. Theor Appl Genet 120:13–23

Wang F, Zhao S, Han Y, Shao Y, Dong Z, Gao Y, Zhang K, Liu X, Li D, Chang J (2013) Efficient and fine mapping of RMES1 conferring resistance to sorghum aphid *Melanaphis sacchari*. Mol Breed 31:777–784

Waniska R, Venkatesha R, Chandrashekar A, Krishnaveni S, Bejosano F, Jeoung J, Jayaraj J, Muthukrishnan S, Liang G (2001) Antifungal proteins and other mechanisms in the control of sorghum stalk rot and grain mold. J Agric Food Chem 49:4732–4742

Wegulo S, Carlson M (2011) Ergot of small grain cereals and grasses and its health effects on humans and livestock. University of Nebraska, Extension, EC1880

Weir TL, Park S-W, Vivanco JM (2004) Biochemical and physiological mechanisms mediated by allelochemicals. Curr Opin Plant Biol 7:472–479

Werner K, Friedt W, Ordon F (2005) Strategies for pyramiding resistance genes against the barley yellow mosaic virus complex (BaMMV, BaYMV, BaYMV-2). Mol Breed 16:45–55

Williams R, Rao K (1981) A review of sorghum grain moulds. Intl J Pest Manag 27:200–211

Witcombe J, Hash C (2000) Resistance gene deployment strategies in cereal hybrids using marker-assisted selection: gene pyramiding, three-way hybrids, and synthetic parent populations. Euphytica 112:175–186

Worrall EA, Hamid A, Mody KT, Mitter N, Pappu HR (2018) Nanotechnology for plant disease management. Agronomy 8:285

Xu GW, Magill C, Schertz K, Hart G (1994) A RFLP linkage map of *Sorghum bicolor* (L.) Moench. Theor Appl Genet 89:139–145

Yano M, Tuberosa R (2009) Genome studies and molecular genetics from sequence to crops: genomics comes of age. Curr Opin Plant Biol 12:103–106

Yazawa T, Kawahigashi H, Matsumoto T, Mizuno H (2013) Simultaneous transcriptome analysis of Sorghum and *Bipolaris sorghicola* by using RNA-seq in combination with de-novo transcriptome assembly. PLoS ONE 8:e62460

Yin K, Qiu J-L (2019) Genome editing for plant disease resistance: applications and perspectives. Philos Trans Roy Soc Lond B Biol Sci 374:1–8

Yin H, Song CQ, Suresh S, Kwan SY, Wu Q, Walsh S, Ding J, Bogorad RL, Zhu LJ, Wolfe SA (2018) Partial DNA-guided *Cas9* enables genome editing with reduced off-target activity. Nat Chem Biol 14:311

Yohannes T, Abraha T, Kiambi D, Folkertsma R, Hash CT, Ngugi K, Mutitu E, Abraha N, Weldetsion M, Mugoya C (2015) Marker-assisted introgression improves striga resistance in an Eritrean farmer-preferred sorghum variety. Field Crops Res 173:22–29

Yohannes T, Ngugi K, Emanuel A, Abraha T, Yao N, Asami P, Ahonsi M (2016) Genotypic variation for low striga germination stimulation in *Sorghum* (L.) moench landraces from eritrea. Amer J Plant Sci 7:2470–2482

Young W, Teetes G (1977) Sorghum entomology. Annu Rev Entomol 22:193–218

Zhang J, Khan SA, Heckel DG, Bock R (2017a) Next-generation insect-resistant plants: RNAi-mediated crop protection. Trends Biotechnol 35:871–882

Zhang Y, Ngu DW, Carvalho D, Liang Z, Qiu Y, Roston RL, Schnable JC (2017b) Differentially regulated orthologs in sorghum and the subgenomes of maize. Plant Cell 29:1938–1951

Zhao Y, Li X, Chen W, Peng X, Cheng X, Zhu S, Cheng B (2011) Whole-genome survey and characterization of MADS-box gene family in maize and sorghum. Plant Cell Tiss Org 105:159–173

Zhu H, Muthukrishnan S, Krishnaveni S, Wilde G, Jeoung JM, Liang GH (1998) Biolistic transformation of sorghum using a rice chitinase gene [*Sorghum bicolor* (L.) Moench-*Oryza sativa* L.]. J Genet Breed 52:243–252

Zou G, Zhai G, Feng Q, Yan S, Wang A, Zhao Q, Shao J, Zhang Z, Zou J, Han B (2012) Identification of QTLs for eight agronomically important traits using an ultra-high-density map based on SNPs generated from high-throughput sequencing in sorghum under contrasting photoperiods. J Exp Bot 63:5451–5462