AGRONOMY SCIENCE AND BIOTECHNOLOGY

REVIEW ARTICLE

The effects of a few important gene families on sorghum agronomic traits

Mesfin Hailemariam[1,*]

[1]Addid Ababa University, Ethiopian Institutes of Agricultural Research, Departmente of Microbial, Cellular and Molecular Biology, Addis Ababa, Shewa, Ethiopia. *Corresponding author, E-mail: mesfin.hailemariam@aau.edu.et

ABSTRACT

Sorghum (*Sorghum bicolor* [L.] Moench), a main food for more than 500 million impoverished and food insecure people in arid and semi-arid regions of Sub-Saharan Africa (SSA) and South Asia, is an important crop for food and nutritional security (SA). Sorghum has the most acceptance in these drought-prone areas due to its good tolerance to harsh settings, high yield, and use as a good source of forages. In this review, the objective of this study is to document the production and use Sorghum in improvement programmed through a literature review, we used publications from journals to explore gene families, how they evolved, gene family theories, how gene families influenced agronomic features in sorghum, and in-depth studies of the key ten gene families in sorghum. The future prospects on sorghum enhancement include genomic selections and gene families, as well as comparative genomic selections. Furthermore, understanding the mechanism of these gene families is important for addressing problems that plague sorghum production, including as infections, drought, and heat stress. We can accurately improve traits using modern techniques such as marker-assisted selection, Genomic selections (GS), Marker-assisted backcrossing (MABC), Marker-assisted recurrent selection (MARS), Marker-assisted selections (MAS), and Genome-wide selections (GWAS) if we have the above gene families of interest (GWAS). Sorghum as a desirable breed: future paths and prospects.

Keywords: Molecular breeding, biotic and Abiotic stress, Genomic selections (GS), Genome-wide selections (GWAS), group of genes, multigene families, homologous genes.

Citation: Hailemariam, M. (2023). The effects of a few important gene families on sorghum agronomic traits. *Agronomy Science and Biotechnology*, 9, 1-11 https://doi.org/10.33158/ASB.r163.v9.2023

Received: February 15, 2022.
Accepted: June 30, 2022.
Published: January 10, 2023.

English by: Mesfin Hailemariam.

INTRODUCTION

Sorghum (*Sorghum bicolor* [L] Moench 2n=2x=20), the fifth most significant cereal crop in terms of production and cultivation area, has got a huge amount of interest in recent years as a possible "star" crop for addressing global food security concerns (Hao et al., 2021). It is also a versatile food crop that may be used for food, fodder, feed, and fuel, and it has a lot of promise for phytoremediation of contaminated soil (Liu, Fernie, & Yan, 2020). Sorghum is a historically important staple food source and is now developing as a crop with varied end-uses as food, feed, fuel, and forage, as well as a model for functional genetics and genomics of tropical grasses (Ananda et al., 2020). It is a short-day C4 grass that is used as a model crop for other C4 grasses because of its compact genome (Patil et al., 2015), with ten chromosomes (Kim et al., 2005). The crop can withstand a variety of biotic and abiotic challenges and it is commonly cultivated in less productive areas. Plants in the environment face a variety of abiotic and biotic challenges that threaten their life and productivity; yet, plants have evolved complex molecular machinery to detect and avoid these pressures (Singh et al., 2016).

A gene family is a collection of homologous genes found in a single organism, or a group of genes generated by duplication of a single original gene with comparable biochemical activity. For each gene family, the rate of homogeneity through uneven crossing-over, gene conversion, and so on has been evolutionarily adjusted. When organisms require additional activities, gene families may evolve into superfamilies, in which no further concerted evolution occurs and each family member acquires an essential function (Pandey, Singh, Achary, & Reddy, 2015).

Sorghum gene families were similar in quantity and size to Arabidopsis, rice, and poplar. Gene families are playing an increasingly important role in plant breeding and genetics research for sorghum yield improvement. These studies mostly focused on disease resistance/tolerance, drought, salinity, and heat stress genes identification and characterization using various mechanisms and methods, with the goal of improving polygenic trait yielding. Sorghum cystatins gene family, nucleotide-binding site plus leucine-rich repeat gene family, Auxin related gene families, Sorghum SWEET gene family, polyphenol oxidase genes, intermediate domain family, Ascorbate-Glutathione. Pathway, Carotenoid dioxyglutathione. With a yield gap compared to more intensively grown cereals, it is required to successfully combine innovative breeding procedures to generate new cultivars with improved goal features in sorghum breeding strategies. We are also concerned about the biotic and abiotic challenges that distinct gene families govern. So, the objective of this study is to document the production and use Sorghum in improvement program.

DEFINITION, EVOLUTION AND THEORIES GENE FAMILIES

A gene family is a group of genes that have similar biochemical functions and are created by duplication of a single original gene. It is more difficult to address a plant's reaction to challenges that are dictated by multiple genes than it is to address single-gene features. When the genes in a gene family encode proteins, the word protein family is sometimes used interchangeably with the phrase gene family.

Although it is well known that concerted evolution is prevalent among gene families that have existed for a long time, there are many distinct forms of multigene families, ranging from uniform to diversified (Ohta, 1990). QTLs governed the majority of sorghum domestication and improvement features, with just minimal genetic influences. Ohta (1990) explained that while concerted evolution is prevalent in gene families that have existed for a long time, there are many distinct forms of multigene families, ranging from uniform to varied. For each gene family, the rate of homogeneity through uneven crossing-over, gene conversion, and so on has been evolutionarily adjusted. When organisms require additional activities, gene families may evolve into superfamilies, in which no further concerted evolution occurs and each family member acquires an essential function. A particularly fascinating example of such a superfamily is the homeobox-containing gene family.

Agronomic features are influenced by gene families

Agronomically relevant traits, in general, are complex features controlled by poly- and/or oligogenic loci. For continual crop yield enhancement, genetic dissection of critical agronomic traits is required. For continual crop production enhancement to satisfy the demands of the world's rising population, genetic dissection of major agronomic features is required (Sattler et al., 2009). Varshney et al. (2017) discovered that pearl millet shares 14,398 genes with sorghum and foxtail millet, 13,027 genes with maize and rice, and 11,369 genes with barley and wheat in their study. Knowing and comprehending on Table 1.

Gene families are groups of genes that have similar biochemical functions and are created by duplication of a single initial gene. Within a single organism, a gene family is a group of homologous genes. The situation known as "redundancy" occurs when a gene is present in two or more copies per genome. Members of a gene family can be found in clusters, spread over several chromosomes, or a combination of both. The concepts of the various sorghum gene families are briefly discussed here. However, comprehensive and up-to-date reviews can be found in various journals and papers.

Sorghum *cystatins* (*SbCys*) gene family-The cystatin family in Sorghum is poorly understood. However, a recent work by Li, Liu, Wang, Sun and He (2021) discovered that sorghum has 18 cystatin families, which are more or less similar to soybean (20 genes), which is a higher number than rice (11 genes) and Arabidopsis (7 genes) (Wang et al., 2010) According to the findings, the change in cystatin number could reflect plant adaptation to the environment, according to Li et al. (2021). *2.1.3. WRKY* genes family - Baillo et al. (2020) reported 94 WRKY genes in sorghum after undertaking characterization and categorization, gene structure analysis, chromosome mapping, and conserved motif analysis. qRT-PCR was also used to look at numerous sbWRKY genes that were induced by drought stress. The vast WRKY family of transcription factors are also known to alter a wide range of phenotypes, some of which are linked to abiotic stress responses in acidic soil Barros et al., 2020. Ascorbate-Glutathione Pathway (AsA-GSH) -The APX, MDHAR, DHAR, and GR enzymes, as well as two anti-oxidants, AsA and GSH, make up the AsA-GSH pathway (Pandey et al., 2015).

The gene family for carotenoid dioxygenase-In sorghum (*Sorghum bicolor* L.), carotenoid candidate genes have been found, and linkage disequilibrium (LD) mapping has been successfully used to investigate the connection of these genes with carotenoid content in grain endos perm for human consumption. If specific genes are responsible for variable photosy nthetic capacity in diverse germplasm and superior alleles can be identified, they co uld be exploited in breeding programs to improve photosynthesis and crop producti vity.

The effect of carotenoid candidate genes on the photosynthetic capacity of sorghum as assessed by Linkage Disequilibrium mapping. Genes encoding enzymes involved in the production of carotenoids have been discovered. Despite the fact that most carotenoid biosynthetic genes have been cloned and identified, significant aspects of carotenoid synthesis and manipulation, particularly in higher plants, remain unknown (Singh et al., 2016).

Table 1. Major QTL/genes for important agronomical and adaptive traits in sorghum.

Genes Family Type	Functions	References
PHY gene family	Flowering time and shade-avoidance behavior.	White *et al*., (2004)
Sorghum *cystatins* (*SbCys*) gene fami	18 *SbCys* genes were identified in Sorghum Genes participated in the regulation of seed formation an or two abiotic stresses (dehydration, salt, and ABA stresses)	Li et al., *(*2021)
WRKY genes family	Identified a total of 94 *SbWRKY* genes Regulates diverse biological processes in plants includi toxicity, low-P availability and drought stress Response for critical stresses like drought	Baillo et al., (2020); Barros et al., (2020)
SbGA20*ox*l and SbGAl*ox*1	They were highlighted as a key regulatory gene in stem bio	Wang et al (2010)
IDD gene family (The INTERMEDIATE family)	They are involved in seed maturation and germination, G naling, root development, sugar metabolism, leaf polarity ch metabolism, cold-stress signaling, auxin biosynthesis a ansport, flowering, plant architecture, shoot gravitropism monium uptake, and endosperm development	
Hsp gene family	The first detailed molecular characterization of the heat s protein 70 (Hsp70) gene from *Sorghum bicolor*, MN1618 designated as SbHsp70-1	Han et al., (2015)
SWEET gene family *SbSWEET8-1* for efflux of sucrose fro leaf; *SbSWEET4-3* for unloading sucrose the phloem in the stem; *SbSWEET2-1* and *SbSWEET7-1* for development; *SbSWEET9-3* for pollen nutrition	Plays a key role in the efflux of photosynthesized sucrose the leaf Sugar transporter that unloads sucrose from the phloem stem Play a key role in seed development Pollen nutrition	Mizuno et al. (2016)
Sucrose transporters *(SUT)* genes	SUTs transport sucrose across membranes, and have proposed to function in sucrose partitioning differ between sweet and grain sorghums	
Aux/IAA, ARF, GH3 and LBD genes) SbIAA1, SbGH3-13, and SbLBD32	They may a role in a cross talk between the auxin, BR abiotic stress signaling pathways	Wang et al., (2010)
NBS-LRR family	Enriched in the regions of the genome containing fungal gen disease resistance QTL and Diversity of the NBS-enc genes influenced by the type of co-locating biotic stress resis QTL	Mace et al., (2014)
Aquaporins (AQPs) *PIP2-6*, *PIP2-7*, *TIP2-2*, *TIP4-4*, and *TI*	Five expression was differentially regulated in to compared to sensitive genotypes	Li et al., *(*2021)

Sorghum *cystatins* (*SbCys*) gene family

The cystatin family in Sorghum is poorly understood. However, a recent work by Li *et al*., 2021, discovered that sorghum has 18 cystatin families, which are more or less similar to soybean (20 genes), which is a higher number than rice (11 genes) and Arabidopsis (7 genes) (Wang et al., 2010). According to the findings, the change in cystatin number could reflect plant adaptation to the environment, according to Li *et al*., 2021. *2.1.3. WRKY* genes family - Baillo et al. (2020) reported 94 WRKY genes in sorghum after undertaking characterization and categorization, gene structure analysis, chromosome mapping, and conserved motif analysis. qRT-PCR was also used to look at numerous sbWRKY genes that were induced by drought stress. The vast WRKY family of transcription factors are also known to alter a wide range of phenotypes, some of which are linked to abiotic stress responses in acidic soil (Barros et al., 2020).

Ascorbate-Glutathione Pathway (AsA-GSH)

The APX, MDHAR, DHAR, and GR enzymes, as well as two anti-oxidants, AsA and GSH, make up the AsA-GSH pathway (Pandey et al., 2015).

The gene family for carotenoid dioxygenase

In sorghum (*Sorghum bicolor* L.), carotenoid candidate genes have been found, and linkage disequilibrium (LD) mapping has been successfully used to investigate the connection of these genes with carotenoid content in grain endosperm for human consumption. If specific genes are responsible for variable photosynthetic capacity in diverse germplasm and superior alleles can be identified, they could be exploited in breeding programs to improve photosynthesis and crop productivity. The effect of carotenoid candidate genes on the photosynthetic capacity of sorghum as assessed by Linkage Disequilibrium mapping. Genes encoding enzymes involved in the production of carotenoids have been discovered. Despite the fact that most carotenoid biosynthetic genes have been cloned and identified, significant aspects of carotenoid synthesis and manipulation, particularly in higher plants, remain unknown.

Family of Intermediate Domain (IDD gene family)

Plant-specific transcription factors that have primary activities in inflorescence, leaf architecture, root architecture, seed development, and sugar homeostasis make up the IDD protein family (Kumar et al., 2019).

Polyphenol oxidase genes

Plant polyphenol oxidases (PPOs) are enzymes that oxidize ortho-diphenols to ortho-quinones using molecular oxygen (Tran, Taylor, & Constabel, 2012). Polyphenol oxidase (PPO) is a multifunctional enzyme that helps plants grow and respond to environmental stimuli. However, there is still a scarcity of molecular data on sorghum PPO genes. However, there are several exceptions. In two grain sorghum genotypes, BTx623, eight different PPO gene members, denoted as SbPPO1–SbPPO8, were found (HN16). Sorghum chromosomes 3 (SbPPO1 and SbPPO2), 6 (SbPPO3 and SbPPO4), 7 (SbPPO5–SbPPO7), or 10 (SbPPO8) had zero (SbPPO6–SbPPO8), one (SbPPO1, SbPPO2, and SbPPO5), or two (SbPPO1, SbPPO2, and SbPPO5), or these are known to elicit browning reactions after tissue damage and may play a role in plant defense. Although some PPOs serve as hydroxylases or in cross-linking processes, their physiological activities in most plants remain unknown. PPO gene families were investigated in 25 sequenced genomes from chlorophytes, bryophytes, lycophytes, and flowering plants to better understand their role in the plant kingdom. After that, the PPO genes were evaluated for gene structure, phylogenetic connections, and targeting signals in silico.

SWEET gene family of sorghum

According to Mizuno, Kasuga and Kawahigashi, (2016), a genome-wide analysis in sorghum (*Sorghum bicolor*) identified variable 23 of SWEET genes, and they concluded that the key SWEET genes for technological improvement of sorghum in the production of biofuels are: SbSWEET8-1 for sucrose efflux from the leaf; SbSWEET4-3 for sucrose unloading from the phloem in the stem; SbSWEET2-1. Sorghum accumulates sucrose in the stem, which is a unique trait among plants, making it a valuable bioethanol source Calvino and Messing, 2012.

Auxin-associated gene families

Are a group of genes that are connected to auxin. Different authors have reported on the effects of auxin-related gene families on biotic and abiotic agronomic parameters in sorghum. Auxin-responsive genes, such as the Auxin/Indole-3-Acetic Acid (Aux/IAA) family, the auxin response factor (ARF) family, short auxin upregulated RNA (SAUR), and the auxin-responsive Gretchen Hagen and Guilfoyle, (2002). (GH3) family, can sense and respond to changes in auxin levels swiftly Luo, Zhou and Zhang et al., 2018.

The expression profile of those gene families was also studied in sorghum following IAA, BR, salt, and drought treatments, according to Wang et al. 2010. Furthermore, Furthermore, the number of members in each gene family in sorghum is similar to that in Arabidopsis and rice. Furthermore, real-time PCR research revealed that these genes are expressed differently in the leaf/root of sorghum and revealed the expression profile of these gene families under the effects of IAA, brassinosteroid (BR), salt, and drought Wang et al., 2010.

The nucleotide-binding site plus leucine-rich repeat (NBS-LRR) family

The nucleotide-binding site plus leucine-rich repeat (NBS-LRR) family is the most widespread and ancient of the disease resistance gene families, according to Mace et al., 2014. It is also one of the largest gene families known in plants. Furthermore, the nucleotide binding site-leucine-rich repeat (NBS-LRR) class of resistance genes is the most prevalent (Marone, Russo, Laidò, Leonardis, & Mastrangelo, 2013).

Gene family of aquaporins (AQP)

The aquaporin (AQP) gene family, according to Reddy, Rao, Sharma and Vadez (2015), is the most conserved class of gene families and plays a critical role in water transport and conservation in plants. According to the same authors' work on the

AQP gene families, there are a total of 41 AQP genes in Sorghum that are divided into four groups. Furthermore, the gene expression analysis in Sorghum implies functional divergence. The phylogeny, gene organization, and chromosome placements were all studied. In silico study was used to analyze SbAQP promoter sequences. This is the first of a genome-wide investigation of AQP genes in Sorghum that has been published.

Crops for food, fodder, and biofuel sorghum gene families

Despite the importance of the sorghum crop in the biofuel and fodder industries, there is a lack of comprehensive information on cell wall related genes and gene families. It is also critical to identify cell wall related genes in order to better understand the cell wall biosynthetic process and to facilitate biomass manipulation (Rai et al., 2016). So, based on these findings, a genome-wide analysis using a gene family-specific Hidden Markov Model of conserved domains identified 520 genes spread across 20 gene families that are involved in the biosynthesis/modification of various cell wall polymers like cellulose, hemicellulose, pectin, and lignin.

Genomic selection (GS) and gene families

In recent years, rapid advancements in high-throughput experimental and data processing technologies have dramatically accelerated sorghum genome research (Hao et al., 2021; Crossa et al., 2017), and genomic selection (GS) promotes the quick selection of superior genotypes and speeds up the breeding cycle. The importance and potential of the multi-purpose crop sorghum in global food security has yet to be fully realized, and it will require the integration of cutting-edge genomics and high-throughput, technologies into breeding practice, as well as rapid advancements in high-throughput experimental and data processing technologies.

Sorghum comparative genomics

Scientists are rapidly progressing toward a comprehensive framework for comparative genomics of the grass family, which will allow comparative studies to reach unprecedented levels of complexity Andrew *et al*. (2009) Hao *et al*. (2021) used comparative genomics analysis to investigate the genetic diversity between sweet and grain sorghums. Previously, two sweet and one-grain sorghum genomes were re-sequenced, and a substantial number of SNPs, InDels, PAVs, and CNVs were discovered. Furthermore, nearly 1500 genes were discovered that differentiate sweet and grain-type sorghums, some of which are involved in starch and sucrose metabolism, lignin, and coumarin synthesis.

Several QTL traits were studied by different authors on the different traits this is included the traits like grain yield, grain quality, flowering, height, tillering and stress tolerance. For the shattering the protein encoding was reported Lin *et al*. (2012). Grain weight the expression protein was reported by Han et al. (2015), grain size similar to putative fibre protein Fb34 and similar to H0801D08.10 protein was reported Zhang et al. (2015), seed number encoding protein of Ent-kaurene synthase reported by Zheng et al. (2011), for the tillering the encoding protein transcription factor was reported by Mizuno, Kasuga and Kawahigashi. (2016). for the stress tolerance that includes the Aluminium tolerance encoding protein Multidrug and toxic compound extrusion transporter was reported by P deficiency and Waxy bloom encoding protein Long chain acyl coA oxidase was reported by Burow, Franks, Acosta-Martinez and Xin (2009).

Perspectives on sorghum future successes

The multi-purpose crop sorghum's importance and promise in global food security have yet to be completely realized, necessitating the incorporation of cutting-edge genomics and high-throughput technology into breeding practice. Genomic selections (GS) are a type of marker-assisted selection in which genetic markers covering the entire genome are employed to ensure that all quantitative trait loci (QTL) are in linkage disequilibrium with at least one marker-assisted backcrossing is a technique for incorporating a significant gene from a source that is agronomically inferior into an elite cultivar or breeding line.

FINAL COMMENTS

We revealed abiotic-stress responsive genes that could assist in enhancing sorghum plant flowering time and shade avoidance behaviour, identifying a critical regulatory gene in stem biomass, and water transport and conservation in plants, as well as abiotic and biotic stresses.

With a greater understanding of the gene families that affect our features of interest, future sorghum varieties and hybrids will be more resilient to climate change.

The findings will serve as a baseline for future research using various current techniques for cloning and functional validation of gene families in sorghum crop improvement initiatives, as well as for genetic engineering approval.

REFERENCES

Ananda, G. K. S., Myrans, H., Norton, S. L., Gleadow, R., Furtado, A., & Henry, R. J. (2020). Wild Sorghum as a Promising Resource for Crop Improvement. *Frontiers in Plant Science*, *11*, 1–14. https://doi.org/10.3389/fpls.2020.01108

Baillo, E. H., Hanif, M. S., Guo, Y., Zhang, Z., Xu, P., & Algam, S. A. (2020). Genome-wide identification of WRKY transcription factor family members in sorghum (*Sorghum bicolor* (L.) moench). *PLoS ONE*, *15*(8), 1–24. https://doi.org/10.1371/journal.pone.0236651

Barros, V. A., Chandnani, R., Sousa, S. M., Maciel, L. S., Tokizawa, M., Guimaraes, C. T., … Kochian, L. V. (2020). Root Adaptation via Common Genetic Factors Conditioning Tolerance to Multiple Stresses for Crops Cultivated on Acidic Tropical Soils. *Frontiers in Plant Science*, *11*, 1–25. https://doi.org/10.3389/fpls.2020.565339

Burow, G. B., Franks, C. D., Acosta-Martinez, V., & Xin, Z. (2009). Molecular mapping and characterization of BLMC, a locus for profuse wax (bloom) and enhanced cuticular features of Sorghum (Sorghum bicolor (L.) Moench.). *Theoretical and Applied Genetics*, *118*(3), 423–431. https://doi.org/10.1007/s00122-008-0908-y

Calvino, M., & Messing, J. (2012). Sweet sorghum as a model system for bioenergy crops. *Current Opinion in Biotechnology*, *23*(3), 323–329. https://doi.org/10.1016/j.copbio.2011.12.002

Crossa, J., Pérez-Rodríguez, P., Cuevas, J., Montesinos-López, O., Jarquín, D., Campos, G., … Varshney, R. K. (2017). Genomic Selection in Plant Breeding: Methods, Models, and Perspectives. *Trends in Plant Science*, *22*(11), 961–975. https://doi.org/10.1016/j.tplants.2017.08.011

Hagen, G., & Guilfoyle, T. (2002). Auxin-responsive gene expression: Genes, promoters and regulatory factors. *Plant Molecular Biology*, *49*(3–4), 373–385. https://doi.org/10.1023/A:1015207114117

Han, L., Chen, J., Mace, E. S., Liu, Y., Zhu, M., Yuyama, N., … Cai, H. (2015). Fine mapping of qGW1, a major QTL for grain weight in sorghum. *Theoretical and Applied Genetics*, *128*(9), 1813–1825. https://doi.org/10.1007/s00122-015-2549-2

Hao, H., Li, Z., Leng, C., Lu, C., Luo, H., Liu, Y., … Jing, H. C. (2021). Sorghum breeding in the genomic era: opportunities and challenges. *Theoretical and Applied Genetics*, *134*(7), 1899–1924. https://doi.org/10.1007/s00122-021-03789-z

Kim, J. S., Klein, P. E., Klein, R. R., Price, H. J., Mullet, J. E., & Stelly, D. M. (2005). Chromosome identification and nomenclature of Sorghum bicolor. *Genetics*, *169*(2), 1169–1173. https://doi.org/10.1534/genetics.104.035980

Kumar, M., Le, D. T., Hwang, S., Seo, P. J., & Kim, H. U. (2019). Role of the INDETERMINATE DOMAIN genes in plants. *International Journal of Molecular Sciences*, *20*(9), 1–16. https://doi.org/10.3390/ijms20092286

Li, J., Liu, X., Wang, Q., Sun, J., & He, D. (2021). Genome-wide identification and analysis of cystatin family genes in Sorghum (*Sorghum bicolor* (L.) Moench). *PeerJ*, *9*(Group I), 1–24. https://doi.org/10.7717/peerj.10617

Li, J., Li, S., Han, B., Yu, M., Li, G., & Jiang, Y. (2013). A novel cost-effective technology to convert sucrose and homocelluloses in sweet sorghum stalks into ethanol. *Biotechnology for Biofuels and Bioproducts*, *6*(1), 1–12. https://doi.org/10.1186/1754-6834-6-174

Liu, F. H., & Yang, F. (2020). Male sterility induction and evolution of cytoplasmic male sterility related atp9 gene from Boehmeria nivea (L.) Gaudich. *Industrial Crops and Products*, *156*(August), 112861. https://doi.org/10.1016/j.indcrop.2020.112861

Liu, J., Fernie, A. R., & Yan, J. (2020). The Past, Present, and Future of Maize Improvement: Domestication, Genomics, and Functional Genomic Routes toward Crop Enhancement. *Plant Communications*, *1*(1), 1–19. https://doi.org/10.1016/j.xplc.2019.100010

Luo, J., Zhou, J. J., & Zhang, J. Z. (2018). Aux/IAA gene family in plants: Molecular structure, regulation, and function. *International Journal of Molecular Sciences*, *19*(1), 1–17. https://doi.org/10.3390/ijms19010259

Mace, E., Tai, S., Innes, D., Godwin, I., Hu, W., Campbell, B., … Jordan, D. (2014). The plasticity of NBS resistance genes in sorghum is driven by multiple evolutionary processes. *BMC Plant Biology*, *14*(1), 1–14. https://doi.org/10.1186/s12870-014-0253-z

Mace, G. M., Reyers, B., Alkemade, R., Biggs, R., Chapin, F. S., Cornell, S. E., … Woodward, G. (2014). Approaches to defining a planetary boundary for biodiversity. *Global Environmental Change*, *28*(1), 289–297. https://doi.org/10.1016/j.gloenvcha.2014.07.009

Marone, D., Russo, M. A., Laidò, G., Leonardis, A. M., & Mastrangelo, A. M. (2013). Plant nucleotide binding site-leucine-rich repeat (NBS-LRR) genes: Active guardians in host defense responses. *International Journal of Molecular Sciences*, *14*(4), 7302–7326. https://doi.org/10.3390/ijms14047302

Mizuno, H., Kasuga, S., & Kawahigashi, H. (2016). The sorghum SWEET gene family: Stem sucrose accumulation as revealed through transcriptome profiling. *Biotechnology for Biofuels and Bioproducts*, *9*(1), 1–12. https://doi.org/10.1186/s13068-016-0546-6

Ohta, T. (1990). How gene families evolve. *Theoretical Population Biology*, *37*(1), 213–219. https://doi.org/10.1016/0040-5809(90)90036-U

Pandey, P., Singh, J., Achary, V. M. M., & Reddy, M. K. (2015). Redox homeostasis via gene families of ascorbate-glutathione pathway. *Frontiers in Environmental Science*, *3*, 1–14. https://doi.org/10.3389/fenvs.2015.00025

Patil, G., Valliyodan, B., Deshmukh, R., Prince, S., Nicander, B., Zhao, M., … Nguyen, H. T. (2015). Soybean (Glycine max) SWEET gene family: Insights through comparative genomics, transcriptome profiling and whole genome re-sequence analysis. *BMC Genomics*, *16*(1), 1–16. https://doi.org/10.1186/s12864-015-1730-y

Rai, K. M., Thu, S. W., Balasubramanian, V. K., Cobos, C. J., Disasa, T., & Mendu, V. (2016). Identification, characterization, and expression analysis of cell wall related genes in Sorghum bicolor (L.) moench, a food, fodder, and biofuel crop. *Frontiers in Plant Science*, *7*(AUG2016), 1–19. https://doi.org/10.3389/fpls.2016.01287

Reddy, P. S., Rao, T. S. R. B., Sharma, K. K., & Vadez, V. (2015). Genome-wide identification and characterization of the aquaporin gene family in *Sorghum bicolor* (L.). *Plant Gene*, *1*, 18–28. https://doi.org/10.1016/j.plgene.2014.12.002

Sattler, S. E., Singh, J., Haas, E. J., Guo, L., Sarath, G., & Pedersen, J. F. (2017). Two distinct waxy alleles impact the granule-bound starch synthase in sorghum. *Molecular Breeding*, *24*(4), 349–359. https://doi.org/10.1007/s11032-009-9296-5

Singh, R. K., Jaishankar, J., Muthamilarasan, M., Shweta, S., Dangi, A., & Prasad, M. (2016). Genome-wide analysis of heat shock proteins in C 4 model, foxtail millet identifies potential candidates for crop improvement under abiotic stress. *Scientific Reports*, *6*(6), 1–14. https://doi.org/10.1038/srep32641

Tran, L. T., Taylor, J. S., & Constabel, C. P. (2012). The polyphenol oxidase gene family in land plants: Lineage-specific duplication and expansion. *BMC Genomics*, *13*(1), 1–12. https://doi.org/10.1186/1471-2164-13-395

Varshney, R. K., Shi, C., Thudi, M., Mariac, C., Wallace, J., Qi, P., … Xu, X. (2017). Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. *Nature Biotechnology*, *35*(10), 969–976. https://doi.org/10.1038/nbt.3943

Wang, S., Bai, Y., Shen, C., Wu, Y., Zhang, S., Jiang, D., … Qi, Y. (2010). Auxin-related gene families in abiotic stress response in Sorghum bicolor. *Functional and Integrative Genomics*, *10*(4), 533–546. https://doi.org/10.1007/s10142-010-0174-3

White, G. M., Hamblin, M. T., & Kresovich, S. (2004). Molecular Evolution of the Phytochrome Gene Family in Sorghum: Changing Rates of Synonymous and Replacement Evolution. *Molecular Biology and Evolution*, *21*(4), 716–723. https://doi.org/10.1093/molbev/msh067

Zhang, D., Li, J., Compton, R. O., Robertson, J., Goff, V. H., Epps, E., … Paterson, A. H. (2015). Comparative Genetics of seed size traits in divergent cereal lineages represented by sorghum (Panicoidae) and Rice (Oryzoidae). *G3: Genes, Genomes, Genetics*, *5*(6), 1117–1128. https://doi.org/10.1534/g3.115.017590

Zheng, L. Y., Guo, X. Sen, He, B., Sun, L. J., Peng, Y., Dong, S. S., … Jing, H. C. (2011). Genome-wide patterns of genetic variation in sweet and grain sorghum (Sorghum bicolor). *Genome Biology*, *12*(11), 1–15. https://doi.org/10.1186/gb-2011-12-11-r114