

Chapter 6

Genomic Designing for Sesame Resistance to Abiotic Stresses



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Abstract Abiotic stress conditions result from climate change and the water-supply shortage affect plant growth and cause extensive losses to agricultural production worldwide. Sesame, one of the oldest and important oil-yielding crops, is highly valued for its high quality oil rich in antioxidants with health benefits. We describe here the abiotic stresses that significantly curtail the productivity of sesame and the progresses in the genetics and breeding research for abiotic stress tolerance improvement in sesame. The potential of genomics-assisted breeding for improvement in abiotic stress tolerance in sesame is also discussed.

Keywords Sesame · *Sesamum indicum* · Abiotic stresses · Waterlogging · Drought · Breeding · QTLs · Genomics-assisted selection

6.1 Introduction

Sesame (*Sesamum indicum* L.), belonging to the genus *Sesamum*, is one of the world's most ancient oilseed crops with evidence that it has been cultivated in Asia for more than 5000 years (Bedigian 2004). Sesame is an annual self-pollinating oilseed crop and widely grown in tropical and subtropical areas mainly for its seed. Sesame seeds have higher oil content than other oilseed crops, contain approximately 55% oil and 25% protein (Wang et al. 2014). Besides high oil content, sesame is known for its nutritional and medicinal properties. The seed contains all essential amino acids and is a good source of unsaturated fatty acids and minerals such as calcium. It is worth noting that sesame seeds are also rich in antioxidants and bioactive compounds (such

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as sesamum, sesamol, tocopherol and phytosterols) that are beneficial to human health (Pathak et al. 2014). Seed of sesame is widely used for edible products like edible oil, paste, cakes, flour, and confectioneries due to its high nutrients, unique taste and flavor (Hama 2016). Sesame oil also can be used for pharmaceutical or industrial uses such as raw material of cosmetics, soap, and lubricants (Myint et al. 2020).

Global sesame production was about 6.55 million tons in 2019, of which about 61% was produced in Africa and 34% in Asia (FAO 2019). Sudan is the world's largest producer of sesame, followed by Myanmar, India, Tanzania, Nigeria, China, Burkina Faso, Ethiopia, South Sudan, and Chad. With the improvement of consumers' health awareness and the deepening understanding of the benefits of sesame, the global demand for sesame is growing steadily (Dossa et al. 2017a; Myint et al. 2020). However, the abiotic stresses such as waterlogging and drought caused by climate anomalies seriously affect the yield and quality of sesame around the world.

6.2 Reduction in Yield and Quality Due to Abiotic Stresses in Sesame

6.2.1 Types and Distribution of Abiotic Stresses in Sesame

Sesame can grow in harsh environments and do not need much fertilizer or water. However, yield varies greatly with growing environment and cultivation practices. Waterlogging and drought are the main abiotic stresses in sesame. In China, the production of sesame often suffers from abiotic stresses during the growing season from June to August. About 20–35% and 10–30% of the planting areas suffer from waterlogging and drought, respectively. Waterlogging stress mainly occurred in Henan, Hubei, and Anhui provinces, occasionally a seasonal drought, while Liaoning, Hebei, Shanxi and Jiangxi were dominated by drought. Both waterlogging and drought stress occurred in the whole growth stage of sesame, and the frequency of waterlogging and drought stress occurred in different growth stage was 46% in seedling stage, 44% in early flowering stage, 52% in full flowering stage, 45% in final flowering stage, 41% in filling stage and 29% in maturity stage. In Myanmar, 18% of dryland sesame growers reported that excessive rainfall was the main cause of reduced dryland sesame production (Myint et al. 2020). Likewise, a short monsoon season resulting in drought stress also reduces the sesame yield in Myanmar (Myint and Kyaw 2019). In Ethiopia, sesame production is carried out under rain-fed conditions. Reduced rainfall and prolonged drought caused by climate change are the major challenges for sesame production in Ethiopia (Girmay 2018).

6.2.2 Waterlogging and Evaluation of Tolerance in Sesame

Sesame usually grows in rainfed regions. Waterlogging stress is the most common disaster for sesame (Fig. 6.1). Waterlogging stress leads to damage due to lack of oxygen in plant tissues. For sesame, waterlogging inhibits the respiration of root, reduces the photosynthesis rate, inhibits the growth and development of plants, and finally cause serious yield losses (Wang et al. 2000; Sun et al. 2008, 2010b; Wei et al. 2013). Continuous waterlogging would reduce the yield and seed quality (Wang et al. 1999; Sun et al. 2010b; Sarkar et al. 2016; Yuan et al. 2018). Exposed with waterlogging, the yield of sesame could decrease by 44.8%–100% (Ding et al. 2012). Yuan et al. (2018) found that the plant height of six genotypes was reduced by 19.50%–46.76%, and the zone length of capsule was decreased by 24.02%–67.03% under 24–60 h waterlogging exposure. After waterlogging stress for 60 h, the plant yield of some varieties was reduced by 88.2%. On the other hand, the content of oil, protein, and polysaccharide in the six varieties varied from 51.99%–58.61%, 19.08%–22.05%, to 9.12%–13.68%, respectively. The content of fiber, polysaccharide, and ash also changed significantly in most varieties. For most test varieties treated under the 36 h waterlogging stress, the acid value and peroxide value of sesame oil varied significantly.

Morphological observations showed that the waterlogging tolerance was significantly correlated with root vigor, pubescence intensity on stem, and seed coat color (Liu et al. 1993; Wang et al. 2000). In order to evaluate waterlogging tolerance in



Fig. 6.1 Waterlogging stress in sesame field caused by excessive rainfall

sesame, Sun et al. (2010b) determined the capsule number per plant and seed weight per plant as the top two indicators for waterlogging tolerance assay from the 13 morphological and agronomic traits. Zhang et al. (2014) applied normal plant rate and plant survival rate to evaluate the waterlogging tolerance of sesame at flowering stage.

6.2.3 Drought and Evaluation for Tolerance in Sesame

Sesame originated from the tropical regions and has a certain drought tolerance. However, drought or water deficit also inhibits the growth and development of sesame plants (Fig. 6.2). Drought in the seedling stage leads to restrained growth and development of root and leaves, reduced plant height and biomass (Sun et al. 2010a; Harfi et al. 2016). Drought stress at flowering stage had significant effects on plant height, capsule size, seed per capsule and seed per plant, which resulted in decreased yield of sesame (Sun et al. 2010a; Golestani and Pakniyat 2015). Drought generally results in a reduction of 150–375 kg/ha, with an average reduction rate of about 23%. Serious drought can result in a 50–80% reduction of production. Eskandari et al. (2009) found that severe water stress reduced the yield of oil and protein by 38.18 and 10.77%, respectively, which affected the quality of sesame.



Fig. 6.2 Insufficient rainfall and lack of irrigation induced drought stress in sesame

Morphological comparison using scanning microscope reflected the specific surface structure of leaf hairs and the variation among the various sesame varieties (Su et al. 2016). The variation of the structure and secretory components of sesame glandular hairs can be used to evaluate the drought resistance of sesame. Meanwhile, the amount of wax on leaves also indicates the tolerance level to drought stress and the seed yield (coefficient $r = 0.466^*$) (Kim et al. 2007). In order to determine the ideal indicators for drought resistance in sesame, the effects of drought on growth and yield, biochemical and physio-morphological indices were evaluated (Sun et al. 2010a; Dossa et al. 2017c; Gholinezhad and Darvishzadeh 2018; Li et al. 2018a).

6.2.4 Strategies to Tackle Abiotic Stresses in Sesame

The counter measures to mitigate abiotic stresses include: (1) Planting varieties with strong stress resistance, which can increase the yield by 10–15% under stress condition; (2) use cultivation measures to deal with abiotic stress. To prevent and control waterlogging, the fields are usually made into “deep furrows and narrow block” or ridging, and clear the furrows in time for drainage after the rain. Measures such as mulching, drip irrigation and timely irrigation are often adopted to prevent and control drought. The application of these cultivation measures can increase production by 10–35%; and (3) spraying waterlogging-resistant inducers or drought-resistant agents on sesame leaves during the growth period, increasing production by 6–8%.

6.3 Traditional Breeding and Sesame Varieties with High Tolerance to Abiotic Stresses

6.3.1 Use of Morphological Markers

Identification of waterlogging tolerance of sesame was mainly carried out during germination and flowering stage. The evaluation index of waterlogging tolerance in germination period was relatively normal at seedling rate. The varieties with relatively normal seedling rate $\geq 80.00\%$ was considered as high tolerance, 60.00–79.99% was tolerance, 40.00–59.99% was moderate tolerance, 20.00–39.99% was intolerance, and $< 20.00\%$ was extremely intolerance. The evaluation index of waterlogging tolerance at the full flowering stage was relatively waterlogging-tolerance index, which was calculated by the number of withering plants, the withering grades and the number of surviving plants. The varieties with relative waterlogging-tolerance index ≥ 0.8 was considered as high tolerance, 0.6–0.79 was tolerance, 0.4–0.59 was moderate tolerance, 0.2–0.39 was intolerance, and < 0.2 was extremely intolerance.

Drought tolerance of sesame was evaluated in germination stage and adult period. The evaluation index of drought tolerance at germination stage was relatively drought

tolerance index, which was calculated by different drought tolerance grades and seedling numbers. The varieties with relatively drought tolerance index $\geq 90.00\%$ was considered as high tolerance, 80.00–89.99% was tolerance, 70.00–79.99% was medium tolerance, 50.00–69.99% was intolerance, and $< 50.00\%$ was extreme intolerance. The evaluation index of drought resistance at adult period was drought tolerance index, which was calculated by the number of withering plants, the withering grades and the number of surviving plants. The varieties with drought tolerance index $\geq 90.00\%$ was considered as high tolerance, 70.00–89.99%, was tolerance, 50.00–69.99% was medium tolerance, 20.00–49.99% was intolerance, and $< 20.00\%$ was extreme intolerance.

6.3.2 Breeding Objectives: Positive and Negative Selection

The positive selection targets in stress tolerance breeding include the survival rate and yield-related traits of plants under abiotic stress, which directly or indirectly reflects the resistance of plants to abiotic stress. The negative selection targets are traits related to quality and disease resistance, as well as yield under normal conditions. In other words, the improvement of stress tolerance should not bring negative effects on yield potential, quality and disease resistance.

6.3.3 Classical Breeding Achievements in Yield, Quality, and Stress Tolerance

The genetic improvement of tolerance of sesame in China began in the 1960s. At first, it mainly used line breeding methods. In the past decades, since the 1970s, a variety of breeding methods including conventional hybridization, radiation mutagenesis, space mutagenesis, line selection, distant hybridization, and the utilization of two-line heterosis of nuclear male sterility have been applied for sesame breeding. Some excellent Chinese elite varieties and local varieties, such as Zhongzhi 13, Yuzhi 1, Yiyangbai and Henan 1, showed high weather resistance and met the production requirements (Liu et al. 1993; Ding et al. 2012). Under the artificial waterlogging conditions, more representative varieties with high waterlogging tolerance such as Zhongzhi 5, Zhongzhi 7, Zhongzhi 11, Zhongzhi 13, Zhongzhi 20, Henan 1, Yiyangbai, Yuzhi 4, Zhengzhi 98N09, Zhengzhi 97C01, Zhengzhi 13, Ezhi 1, Ezhi 6, Jizhi 1, Luozhi 12, Zhuzhi 14, Zhuzhi 18 have been bred or screened. The drought-resistant varieties are Jinhuangma, Jinzhi 2, and Liaozhi 1 (data not shown, Xiongrong Zhang). Some sesame cultivars with tolerant to drought stress have been released in different states of India, such as Usha (OMT-11-6-5), Gouri, Madhavi, Uma (OMT-11-6-3), and Prachi (ORM 17) (Tripathy et al. 2019). Gholamhoseini

(2020) identified Sudan 94 as a drought-tolerant genotype with the best yield stability based on its agronomic traits under water deficiency.

6.3.4 Limitations of Traditional Breeding and Rationale for Molecular Breeding

Traditional breeding is a method of breeding new varieties based on phenotypic selection, which generally refers to selection, mutation and hybridization methods of breeding. One of the limitations of conventional breeding is that it is not easy to obtain the desired material with excellent characters, and the other is that the breeding cycle is long. Molecular breeding is based on molecular selection technology for the selection of new varieties, generally refers to molecular marker-assisted breeding. By using the genotypes of molecular markers closely linked to the target genes (or traits), molecular marker-assisted breeding can obtain individuals with the target genes (or traits) in the conventional breeding program through molecular selection, thus improving the selection efficiency and accelerating the breeding process. Transgenic breeding uses DNA recombination technology and DNA transfer technology to introduce the target gene into the recipient organism and obtain transgenic individuals, so as to realize directional breeding.

6.4 Genetic Diversity Related to Abiotic Stress Tolerance in Sesame

6.4.1 Phenotype-Based Diversity Analysis

The *Sesamum* genus has 23 species (IPGRI and NBPGR 2004) and *S. indicum* is the well-known and widely cultivated species within this genus. Several wild relatives of sesame with the adaptive features including hairiness, linear leaves, fleshy roots, more stomata located on the paraxial plane of leaf, and increased seed setting rate in dry season, have been proved tolerant to some abiotic stresses (Nimmakayala et al. 2011). For example, *S. laciniatum*, *S. occidentale* and *S. radiatum* were tolerant to drought stress, and *S. malabaricum* was reported resistant to waterlogging stress (Nimmakayala et al. 2011). These wild relatives of sesame are precious resources for abiotic stress tolerance improvement in sesame.

Beside wild related sesame species, over 25,000 genetic materials of cultivated sesame are currently preserved in some genebanks worldwide, including Oil Crops Research Institute, Chinese Academy of Agricultural Sciences in China, National Agrobiodiversity Center, Rural Development Administration in South Korea, and NBPGR National Gene Bank in India (Dossa et al. 2017a). Based on germplasm resources, several studies were performed to analyze the diversity of abiotic stress

tolerance and screen for tolerance sources in sesame (Boureima et al. 2012, 2016; Zhang et al. 2014; Liu et al. 2017; Priyadharshini et al. 2018). Ding et al. (2012) evaluated the waterlogging tolerance of 43 main sesame cultivars from China at full flowering stage. They found most of the present sesame cultivars were sensitive to waterlogging stress, and two cultivars, Xiongzhi No. 1 and Zhongzhi No. 13, with higher percentage of normal plant and with higher harvest yield after waterlogging stress, respectively, showed relatively higher waterlogging tolerance among these cultivars. The results also indicated that waterlogging tolerance of the southern cultivars was higher than those from northern regions. Zhang et al. (2014) screened for tolerance sources of waterlogging stress in sesame core collections containing 186 landraces, and identified eight waterlogging tolerant germplasm. Liu et al. (2017) selected 12 sesame germplasms with high drought-tolerance from 100 sesame germplasm by a comprehensive evaluation method. Dossa et al. (2019a) analyzed the drought tolerance of 400 different sesame genotypes from 29 different countries around the world. Five traits associated with drought tolerance, including survival rate, stem length, capsule number, wilting level, and seed yield were investigated, and extensive variations of these traits were observed among the sesame genotypes under normal and drought stress condition. It was found that the drought resistance of the genotypes from tropical regions was significantly higher than that from northern regions. Li et al. (2018b) investigated the tolerance to drought and salinity of 490 sesame lines at germination stage. Most of the genotypes were moderately tolerant to drought and salt stresses, while the tolerant genotypes and sensitive ones were less represented for both stresses. In total, only 27 accessions were commonly tolerant to drought and salt stresses. Similarly, the correlation of traits between drought and salt was significantly weak, indicating the responses of different sesame genotypes to drought and excess salt stresses were quite distinct at germination stage.

6.4.2 Gene Pool of the Sesame Resources with High Toleranceto Abiotic Stresses

With continuous application of “omics” tools in sesame, more and more abiotic stress resistance-related gene resources have been discovered. Using whole-genome RNA-Seq analysis, Wang et al.(2012) identified 13,307 waterlogging-responsive genes in sesame. Later, a comparative time-course transcriptome analysis between waterlogging-sensitive and waterlogging-tolerant genotypes were performed to explore the molecular mechanisms of waterlogging stress response in sesame (Wang et al. 2016a). A total of 1379 genes, which were significantly differentially expressed at all time-point during waterlogging stress, were identified as the core genes responsible for the waterlogging response in sesame. Furthermore, 66 genes were identified as key components for improving waterlogging tolerance of sesame through a comparative analysis between two distinct genotypes. Recently, a high resolution

dynamic transcriptome data of two contrasting sesame genotypes during the waterlogging and recovery stages were released (Dossa et al. 2019c). Clustering analysis of 126 RNA-seq data revealed three stages of sesame seed response to waterlogging stress: early response stage (0–12 h), delayed response stage (12–36 h) and recovery stage (36–48 h) (Wang et al. 2021a). Further analysis showed that WRKY and ERF transcription factor family members played an important role in transcriptional regulation of waterlogging-responsive genes during stress. By constructing a time-series expression regulation network of transcription factors and their target genes, several key transcription factors, such as SiRAP2.2 and SiERF056, which simultaneously regulate the three waterlogging response periods, were discovered (Wang et al. 2021a). For drought stress, a RNA-seq analysis of sesame root identified 722 genes as core drought-responsive genes and 61 genes showed different expression profiles in two sesame cultivars during drought stress (Dossa et al. 2017b). In another study, transcriptional profiling in sesame leaves of two contrasting genotypes for drought stress tolerance was characterized, and 684 up-regulated genes as well as 1346 down-regulated genes in both genotypes were revealed (You et al. 2019). Zhang et al. (2019a) analyzed the transcriptomic changes in sesame seedlings under salt stress. A total of 1946 and 1275 genes were identified in all time-point of salt-sensitive and salt-tolerant genotype, respectively. Notably, 59 genes were specific and robustly upregulated in salt tolerance genotypes under salt treatment, and were identified as resources for enhancing salt tolerance. Transcription factors play an important role in plant adaptation to abiotic stress. A series of TFs, such as ERF, bZIP, WRKY, MYB, NAC and HD-Zip, have been genome-wide analyzed in sesame, and several stress-responsive TF members of these family have been identified (Dossa et al. 2016; Li et al. 2017; Mmadi et al. 2017; Wang et al. 2018; Zhang et al. 2018; Wei et al. 2019). By a meta-analysis of sesame transcriptome datasets under drought, salt, waterlogging, and osmotic stresses, Dossa et al. (2019b) identified 543 genes as core abiotic stress-responsive genes (CARG) that robustly differentially expressed in all stress conditions. Transcription factor members belong to ERF, bHLH, MYB, and WRKY families were overrepresented in CARGs, indicating that these TF families are the main regulatory factors in response to various abiotic stresses in sesame. Moreover, overexpression of two transcription factors (SiERF5 and SiNAC104) in *Arabidopsis thaliana* increased tolerance to waterlogging, drought, and osmotic stresses. In another study, a R2-R3 MYB transcription factor, *SiMYB75*, strongly induced by drought, ABA, salinity and osmotic stresses was identified in sesame. Overexpression of *SiMYB75* in *Arabidopsis* increased ABA content and ABA sensitivity, as well as improved tolerance to salinity and drought stresses, suggesting that *SiMYB75* modulates abiotic stresses through an ABA-dependent manner (Dossa et al. 2020). Chowdhury et al. (2017) overexpressed an osmotin-like gene from *Solanum nigrum* (SindOLP) in sesame. The transgenic sesame enhanced tolerance to salinity and drought stresses, as well as the charcoal rot pathogen through the integrated activation of multiple components of the defense signaling cascade.

6.5 Molecular Genetics and Breeding for Abiotic Stress Tolerance in Sesame

6.5.1 Mapping QTLs Related to Stress Tolerance in Sesame

Quantitative trait locus (QTL) mapping based on high-density linkage maps is an approach widely used for investigating genetic variants responsible for phenotypic variation of complex traits. Zhang et al. (2014) mapped quantitative trait loci (QTLs) linked to waterlogging tolerance in sesame using a population of recombinant inbred lines derived from a cross between Zhongzhi 13 and Yiyangbai. The length of constructed genetic map was 592.4 cM, and 70 marker loci were distributed into 15 linkage groups (LGs), with an average distance of 8.46 cM. A total of six QTLs (*qWH09CHL15*, *qEZ09ZCL13*, *qEZ10CHL07*, *qEZ10ZCL07*, *qWH10CHL09* and *qWH10ZCL09*) related to waterlogging tolerance at flowering stage were identified in sesame (Fig. 6.3), with individual QTLs explaining 5.67–17.19% of the phenotype variance. Furthermore, ZM428, a simple sequence repeat (SSR) marker tightly linked with *qWH10CHL09* (QTL explaining the most phenotype variance) was confirmed as an effective molecular marker for marker-assisted selection (MAS) to improve waterlogging tolerance of sesame.

6.5.2 Association of Molecular Markers and Target Genes Regulating Stress Tolerance in Sesame

Genome-wide association study (GWAS) has certain advantages over traditional linkage analysis and has been considered as a powerful tool for detecting the genetic architecture of complex traits in crops. Li et al. (2018b) performed GWAS in 490 diverse sesame accessions to analyze the genetic bases of drought (polyethylene glycol-induced) and salinity (NaCl-induced) tolerances at germination stage. There are 120 and 132 significant single nucleotide polymorphisms (SNPs) resolved to 15 and 9 QTLs identified for salinity and drought stresses, respectively. Only two QTLs were detected under both salinity and drought stress conditions, suggesting distinct genetic bases of salinity and drought tolerance in sesame. A total of 13 potential drought-tolerant genes and 27 potential salt-tolerant genes were identified in the QTL region, closely involving in signal transduction, hormone synthesis or ion sequestration. Dossa et al. (2019a) investigated the genetic basis of sesame drought tolerance at flowering stage by GWAS based on drought tolerance related traits (survival rate, stem length, capsule number, wilting level, and yield in control and stress conditions). Ten stable QTLs (constitutively detected in two years or different traits) located in four LGs explained more than 40% of phenotypic variation. Two pleiotropic QTLs harboring known and unreported genes related to drought resistance, including *SiSAM*, *SiABI4*, *SiGOLS1*, *SiTTM3*, and *SiNIMIN1* were reported.

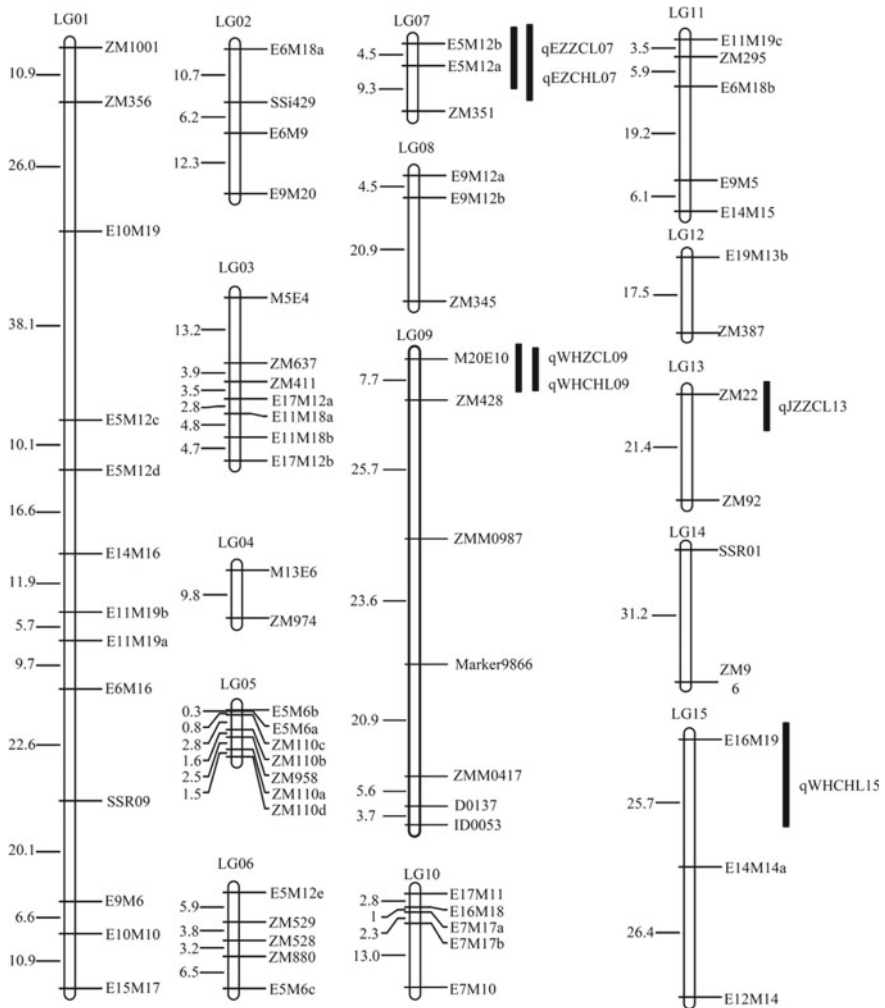


Fig. 6.3 Mapping of sesame waterlogging tolerance QTL (Zhang et al. 2014)

Moreover, the authors found that a missense mutation in the coding region of *SiSAM* may contribute to the natural variation of sesame drought tolerance.

6.6 Genomics-Aided Breeding for Stress Tolerance Traits

Research on genetics and molecular biology of sesame was almost blank before 2010. However, the release of the draft sesame genome (Wang et al. 2014) and the application of various omics technologies (Wei et al. 2011, 2014b, 2015; Zhang et al.

2019b) have greatly promoted the research on genetics and functional genomics in sesame. With these invaluable efforts, a large number of genetic resources included informative molecular markers (Zhang et al. 2012; Wei et al. 2014a, b; Dossa 2016; Purru et al. 2018; Kizil et al. 2020), ultra-dense genetic maps (Wang et al. 2016b; Zhang et al. 2016; Mei et al. 2017), transcriptome assemblies (Wei et al. 2011; Wang et al. 2012; Dossa et al. 2017b, 2019c; You et al. 2019; Zhang et al. 2020), integrative online databases (Wang et al. 2015, 2021b; Dossa et al. 2017d; Wei et al. 2017) etc. were developed in sesame, which provide an important basis for the genetic improvement of important agronomic traits including abiotic stress resistance in sesame.

Marker-assisted selection (MAS) is an indirect selection process based on molecular markers associated with the traits of interest, which makes efficient selection in breeding programs. Although numerous QTLs for traits associated with abiotic stress tolerance were identified in various crops, few of them were successfully used in stress tolerance breeding mainly due to strong genotype-by-environment interaction (Mishra et al. 2013; Priyadarshan 2019). Some SSR or SNP markers associated with abiotic stress tolerance related traits were detected in sesame (Zhang et al. 2014; Li et al. 2018b; Dossa et al. 2019a), but their effectiveness in breeding for stress tolerance through MAS needs further evaluation. Besides MAS, transgenic technique is also an efficient way to enhance resistance to abiotic stresses in crop breeding. Although the protocol of genetic transformation through *Agrobacterium* in sesame need to be further optimized, some successful attempts have provided opportunities for improve abiotic stress tolerance of sesame by transgenic breeding (Yadav et al. 2010; Al-Shafeay et al. 2011; Chowdhury et al. 2014). In a recent study, an exogenous gene from *Solanum nigrum* was introduced into sesame that enhanced stress and disease resistance in transgenic plants (Chowdhury et al. 2017).

Global planting area and production of sesame have remarkably increased in recent years, but the productivity of sesame is still very low mainly due to its poor yield stability in various adverse conditions. Over the last two decades, substantial progress has been made in revealing the genetic basis of traits related to abiotic stress tolerance and molecular mechanisms of tolerance to abiotic stress in sesame. More importantly, several QTLs and functional genes related to abiotic stress tolerance were identified and could be used in breeding progress. More genetic sources of tolerance to abiotic stresses characterized in valuable germplasm resources, and more applications of molecular breeding technique, will help to accelerate the genetic improvement of abiotic stress tolerance in sesame.

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