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REVIEW

Research progress on plant tolerance to soil salinity and alkalinity in sorghum

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Abstract

Sorghum is an important source of food, feed and raw material for brewing, and is expected to be a promising bioenergy crop. Sorghum is well known for its strong resistance to abiotic stress and wide adaptability, and salt tolerance is one of its main characteristics. Increasing sorghum planting acreage on saline-alkalien land is one way to effectively use this kind of marginal soil. In this paper, domestic and overseas research on plant tolerance to soil salinity and alkalinity in sorghum, including salt-tolerant genetics and breeding, physiology, cultivation, and identification of tolerant germplasms, are reviewed. Suggestions for further studies on salinity and alkalinity tolerance in sorghum are given, and the prospects for sorghum production in saline-alkalien land are discussed.

Keywords: sorghum, saline-alkaline resistance, genetics and breeding, stress physiology, resistance evaluation

1. Introduction

Saline-alkaline soil accounts for a considerable share, nearly 1 billion hectares, of the world's total land resources according to the incomplete statistics of the United Nations Educational, Scientific and Cultural Organization (UNESCO) and the Food and Agriculture Organization (FAO). The total area of saline-alkaline soil in China is approximately 100 million hectares and represents an important land resource (Wang *et al*. 1993). Improvement and utilization of saline-alkaline land has been brought to the attention of the government, and remarkable achievements have been made, such as in the ecological environment governance of tens of millions of acres of saline-alkaline land in the Huang-Huai-Hai Plain. However, due to the complexity of the factors that affect saline-alkaline soil formation, coupled with the action of the secondary salinization, there is an increasing trend of regional salt accumulation, and across the country, especially in North China, the area of saline-alkaline soil is increasing. In addition, the widespread inappropriate use of fertilization and irrigation is also a cause of soil salinization (Zhao *et al*. 2007). Soil salinization is always a practical ecological problem of agricultural production in China and the world.

Sorghum is one of the world's five major cereal crops and is widely grown in arid, semiarid tropical, subtropical, and temperate regions. It is an important source of food, feed, and raw material for brewing and is expected to be a promising bioenergy crop. Sorghum was once one of the most important food crops in North China; however, in recent decades it has gradually changed from being mainly used for food consumption to being mainly used as raw material

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for brewing, and it is now mainly grown in Northeast and Southwest China. Sorghum is famous for its strong stress resistances and wide adaptability, and salt tolerance is one of its main characteristics (Igartua *et al*. 1994). Enhancing sorghum production on saline-alkaline land is one of the best choices for effective use of this marginal soil. Domestic and overseas studies on plant tolerance to soil salinity and alkalinity in sorghum have led to many achievements. These mainly include the improvements in genetics and breeding, physiology, production, and evaluation of saline-alkaline resistance.

2. Genetic research in sorghum saline-alkaline tolerance

Plants under salt stress show a series of physiological and ecological adaptabilities (Li *et al*. 2012). These adaptive responses are induced by environmental factors and hormones and are regulated by the relevant genes. The expression of many important plant functional genes is induced or suppressed by salt stress, and gene expression regulation has become a hot research topic in recent years. These studies have focused on the transcriptional regulation of genes encoding proteins that are involved in the synthesis of osmotic regulation substances, ion transport, cell detoxification, and antioxidant defense, and protecting cells against stress damage, salt-stress signal transduction, and expression regulation.

2.1. Genetics of sorghum saline-alkaline tolerance

Plant tolerance to soil salinity and alkalinity has been shown to be genetically determined in many plant species (Tal 1985). A strong genotype×salinity interaction was observed while evaluating salt tolerance of sorghum (Azhar and McNeilly 1987; Krishnamurthy *et al*. 2003). Salt tolerance in sorghum is inherited mainly along the male line and is controlled by several non-allelic genes that condition dominant or overdominant expression of resistance (Spivakov 1990). Similarly, Igartua *et al*. (1994) also reported that salt tolerance in sorghum is a very complex quantitative trait controlled by polygenes. They observed substantial genetic variation for salt tolerance during sorghum germination and emergence. In the tested hybrids, these differences in salt tolerance were due to special combining ability (SCA) and female general combining ability (GCA) for emergence, and female GCA for germination, although the male GCA was also significant for both characters. Line *per se* performance was significantly correlated with individual GCA estimates for emergence, but not for germination. Heterosis was also detected in some crosses for germination and final emergence. Wang H L *et al*. (2014) studied the quantitative trait loci (QTLs) for three traits (germination vigor, germination percentage, and relative salt-injury rate) at the germination stage and nine traits (salt injury index, root dry weight, total dry weight, shoot height, root length, shoot fresh weight, root fresh weight, total fresh weight, and shoot dry weight) at the seedling stage of sorghum and identified 12 and 29 QTLs at the germination and seedling stages, respectively. Six major QTLs and five chromosome regions were found to play a crucial role in salt tolerance of sorghum and could be applied in marker-assisted selection and in further investigations of salt tolerance.

2.2. Genes and proteins related to sorghum saline-alkaline tolertance

The osmolyte proline accumulates when plants are subjected to abiotic stress (Tripathi *et al*. 2007). Delta 1-pyrroline-5-carboxylate synthetase (P5CS) is a key regulatory enzyme that plays a crucial role in proline biosynthesis. Su *et al*. (2011) isolated two closely related *P5CS* genes from sweet sorghum, designated *SbP5CS1* (GenBank accession number: GQ377719) and *SbP5CS2* (GenBank accession number: GQ377720), which are located on chromosomes 3 and 9 and encode 729 and 716 amino acid polypeptides, respectively. Expression analysis revealed that *SbP5CS1* and *SbP5CS2* transcripts were up-regulated after drought and salt treatment of 10-day-old sweet sorghum seedlings. Under high salt treatment, *SbP5CS1* and *SbP5CS2* expression peaked in roots at 4 and 8 h, respectively, and the level of *SbP5CS1* up-regulation was higher than that of *SbP5CS2*. Proline concentration increased after stress application and was correlated with the expression of both *SbP5CS* genes. These findings suggest that these two genes could potentially be used in improving stress tolerance of sweet sorghum.

Dalal *et al*. (2013) identified four genes encoding LEA3 proteins in the sorghum genome and further classified them into LEA3A and LEA3B subgroups based on the conservation of LEA3 specific motifs. The changes in the expression levels of the *SbLEA3* genes in response to abiotic stresses, such as soil moisture deficit and osmotic, salt and temperature stress suggest that the *LEA3* genes have non-redundant functions in stress tolerance in sorghum. Wang *et al*. (2013) characterized a member of the stress-associated protein (SAP) gene family from *Sorghum bicolor* (*SbSAP14*) with A20 and AN1 zinc-finger domains. Expression profiling revealed that *SbSAP14* is specifically induced in response to dehydration, salt, and oxidative stress as well as abscisic acid treatment. They proposed that *SbSAP14* may play a key role in antioxidant defense systems and possibly be involved in the induction