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Salt Tolerant Mechanism in Crops

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ABSTRACT

Salinity often construed as one of the serious constraint in crop production under ground level source of irrigation. Ambiance of salinity mechanism utters negative impact on crop production process, growth and development. Also, plant adapt on saline situation triggering salt tolerant genes to face the osmotic or oxidative reactions induced by soil salinity. Further, genetic improvement of pulses under increased salinity is quite complex and less proven progress. Gene alteration for saline resistant considered as a quite complex phenomenon besides the advances in resign the crop phenotype for this trait over years construed very dawdling in nature. Cited data on crop genetics and genomics failed to project innovative ideas on the synthesis of saline tolerant genotypes. Though substantial advancement have been made in studying the crop mechanism on abiotic stresses, still obstacles remain trendy elaborating the translation and molecular behavior of individual crop.

INTRODUCTION

Salinity stress always remains as dignified among the abiotic stresses imparting significant reduction in yield reduction in Mung bean production. The salt properties in soil construed to cause decline in seed viability, poor vigour besides reduced root and shoot growth. Also, the crop exhibit clear cut indications of chlorosis, necrosis and reduced quantum of chlorophyll factors including carotenoids. Experimental results projected the impact of salt stress in abridged growth of root and shoots, greater reduction in root hairs besides stout, brittle and brown roots leading lowly nutrient scavenging activity. Salt stress further increased the deposition of superoxide dismutase and catechol peroxidase in both roots and leaves besides steady fall in chlorophyll, carotenoid pigment contents and their fluorescence intensities. Balasubramaniam *et al.,* (2023) had shown that salt stress can be combined with any other stress components that result in organ specific changes in mung bean plants. Studies had also shown the greater linkage of plant metabolism with the morphological, physiological and biochemical pathway on soil salinity.

FINE MAPPING OF TOLERANCE GENE IN CROPS

Conventional breeding in crops had triggered a significant progress in evolution of salt tolerant genotypes. Only few remarkable achievements have been made till date due to poor studies in its genetic, physiological and biochemical mechanisms of salt tolerance. Concrete efforts are to be taken for screening greater numbers of germplasm to identify novel genes for the trait besides developing suitable DNA markers thereby locating suitable genes constituting significant levels of tolerance to soil salinity. Also, constant efforts are being enforced to recognise the molecular, physiological and biochemical attributes of abiotic stress tolerance most particularly drought and salt stress factors. However, researches should get diversified to intensify the learning of ion exclusion principles operating under saline stress situations facilitating ideal evolution of salt tolerant genotypes in crops. Projection of QTLs to salt stress seems very remote when very many QTLs have been reported for different traits in different crops. Continuous efforts need to get drenched to expose and determine novel genes attributing tolerance to salinity stress situations. Wild relatives and traditional genotypes concerned to crops have to be explored at a greater height to aid manipulations at genetic levels triggering stable tolerance to the stress factors as envisaged by Luo *et al*. (2005). Efforts on diversifying the key points attached to development of new QTL besides fortitude of gene action on salt stress will bring improvement in tolerance to drought and salinity inter-mediating the crop growth.

PYRAMIDING GENES BY MARKER ASSISTED SELECTION IN CROP BREEDING

Pyramiding of genes at more than two loci could be accomplished by marker assisted selection (MAS) to address salt stress tolerance in crops. The limitations or constraints in DNA marker technology have been overcome by the identification and utilization of gene specific SNP markers. Further, SNP related markers have assisted in development of high density genetic map for major crops thereby helped to document and characterize the QTLs pertaining to traits positively associated with salinity tolerance in crops. During 2008, United States Department of Energy and Joint Genome Institute had come out with the whole genome shotgun which served as platform to integrate genetic and physical map besides traits specific SNP markers to target the abiotic stress associated traits. Construction of genetic and physical map along with genome sequencing had proved to be effective approach to reach out genes concerned to major abiotic stresses most particularly drought and salt stress resistance in crops. In rice and canola crops, genes associated to stress tolerance traits identified and genetically engineered to evolve crop genotypes. In this regard, highly elevated technologies like QTL mapping, gene cloning, gene transformation and DNA microarray and gene expression analysis related to specific QTL regions could play a vital role in the development of stress tolerant varieties. Genetic resources concerned with tolerance mechanism have been also lined up to construct genomic map of a crop illuminating towards well designed crop breeding strategies to achieve greater yield under salt stress situations. As such genetic markers closely associated with salt-tolerant/susceptible alleles exploited to select saline tolerant and better yielding genotypes (Lee *et al*., 2004). Zhang *et al*., (2005) evaluated Chinese soybean genotypes by SSR marker linked to salt tolerant QTL wherein the 212bp at SSR locus Satt339 accounted for 74 per cent which had shown the potential usefulness of this marker for salt tolerance in crops. Reports also detailed the conversion of the RAPD marker into SCAR marker and reported the similarity of 85.10 per cent in genotype and phenotype of fifty five salinity tolerant and 90 salt susceptible genotypes which proved the efficiency of marker assisted breeding for stress tolerant genes in crops.

CHALLENGES AND FUTURE PROSPECTS

Everyone would not deny the cereal based diet system for human. More importantly, age old practices are all concerned with cereal domestication which had ultimately conquered the major food resource for the global people. As such, soil salinity is playing an adverse issue imparting major yield barrier accounting war foot technologies to evolve salt loving genotypes in cereal crops.

Concerning over few decades, crop breeding strategies are primarily planned to target better economic yield under salt stress situations and we have also marched successful in evolving many salinity resistance crop genotypes. However, it is always warranted to diversify our molecular technologies in production of salt resistant genotypes in cereals, particularly in rice, wheat and maize. Genetic manipulations with identified gene sequence reported to be advantageous for rice and as such many genes have been successfully transferred to rice genome. Successful reports of genetic engineering in evolving salt tolerant maize have been reported by Afzal *et al.* (2023). As such achievements for salt tolerance in oat, barley, sorghum, and pearl millet are very limited. Detailed protocols and technologies have been constantly evolved for chief cereal crops but practical applications of the findings are very meagre. Factors such as environmental variation, soil texture and structure, rainfall pattern and extent of salinity chiefly determine the limitations in varietal evolution. It was established fact that most of the crops have specific adaptations for its life cycle tethering its performance under different agro-ecological regions. The complexity of genes controlling the salt tolerance under different crop growth phases always trigger significant deviations in exhibition of salt tolerance. Similarly, the salinity stress susceptibility of crops seems to be not uniform over its period of growth as such action of many genes triggered at appropriate time. Few studies pronounced that mere manipulation of single gene in a crop can provoke multiple reactions upon salt tolerance mechanism. Main stream reports suggested the influence of NaCl for induction of salt stress besides influence of several other salts like sulphate ions might also been involved.

Sulfate induced salt stress may not favour the genetically engineered plants been greater positive response to prolonged salt stress to perform explicit superior. As such the transgenic plants were successfully exploited in model plants revolving around Arabdiopsis and Tobacco. However, it is pertinent important to target the salt tolerance in cereals through introgressing alien gene from other crops.

CONCLUSION

Salt tolerance in crops has been reported to be in control of multiple genes and complex biochemical pathways leading complexity in study of genetics of salt tolerance. Updation and genetic engineering of crop genomics through novel tools and methods constituted a clear visionary on the salinity tolerance mechanism. Moreover gene discovery or sequence manipulations triggered clarity in study of molecular mechanism that controls the crop phenotype concerned to salinity tolerance.

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